metabolomics

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36055054	Integrated transcriptional and metabolomics signature pattern of pigmented wheat to insight the seed pigmentation and other associated features	Saloni Sharma Ashish Kumar Dalwinder Singh Anita Kumari Payal Kapoor Satveer Kaur Bhawna Shreon Monika Garg	Anthocyanin biosynthesis in plants is complex, especially in a polyploid monocot wheat plant. Using whole-genome sequencing, transcriptomics, and LC-MS/MS, we investigated anthocyanin pigmentation patterns in (black, blue, and purple) colored wheat seeds. According to differential gene expression profiling, 2AS-MYC, 7DL-MYB, and WD40 regulatory genes control purple pericarp coloration, 4DL-MYC, 2AS-MYC, 7DL-MYB, WD40 control blue aleurone coloration, and 4DL-MYC, 7DL-MYB, WD40 controls black...	pmid:36055054 doi:10.1016/j.plaphy.2022.08.008	Fri, 02 Sep 2022 06:00:00 -0400
2	pubmed:36055202	Gut bacterial nutrient preferences quantified in vivo	Xianfeng Zeng Xi Xing Meera Gupta Felix C Keber Jaime G Lopez Ying-Chiang J Lee Asael Roichman Lin Wang Michael D Neinast Mohamed S Donia Martin Wühr Cholsoon Jang Joshua D Rabinowitz	Great progress has been made in understanding gut microbiomes' products and their effects on health and disease. Less attention, however, has been given to the inputs that gut bacteria consume. Here, we quantitatively examine inputs and outputs of the mouse gut microbiome, using isotope tracing. The main input to microbial carbohydrate fermentation is dietary fiber and to branched-chain fatty acids and aromatic metabolites is dietary protein. In addition, circulating host lactate,...	pmid:36055202 doi:10.1016/j.cell.2022.07.020	Fri, 02 Sep 2022 06:00:00 -0400
3	pubmed:36055244	Integrating transcriptomics, metabolomics, and GWAS helps reveal molecular mechanisms for metabolite levels and disease risk	Xianyong Yin Debraj Bose Annie Kwon Sarah C Hanks Anne U Jackson Heather M Stringham Ryan Welch Anniina Oravilahti Lilian Fernandes Silva FinnGen Adam E Locke Christian Fuchsberger Susan K Service Michael R Erdos Lori L Bonnycastle Johanna Kuusisto Nathan O Stitziel Ira M Hall Jean Morrison Samuli Ripatti Aarno Palotie Nelson B Freimer Francis S Collins Karen L Mohlke Laura J Scott Eric B Fauman Charles Burant Michael Boehnke Markku Laakso Xiaoquan Wen	Transcriptomics data have been integrated with genome-wide association studies (GWASs) to help understand disease/trait molecular mechanisms. The utility of metabolomics, integrated with transcriptomics and disease GWASs, to understand molecular mechanisms for metabolite levels or diseases has not been thoroughly evaluated. We performed probabilistic transcriptome-wide association and locus-level colocalization analyses to integrate transcriptomics results for 49 tissues in 706 individuals from...	pmid:36055244 doi:10.1016/j.ajhg.2022.08.007	Fri, 02 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
4	pubmed:36055403	GC×GC-TOFMS Metabolomics Analysis Identifies Elevated Levels of Plasma Sugars and Sugar Alcohols in Diabetic Mellitus Patients with Kidney Failure	Kassaporn Duangkumpha Narumol Jariyasopit Kwanjeera Wanichthanarak Esha Dhakal Pattipong Wisanpitayakorn Sansanee Thotsiri Yongyut Sirivatanauksorn Chagriya Kitiyakara Nuankanya Sathirapongsasuti Sakda Khoomrung	Two dimensional GC (GC×GC)-TOFMS has been used to improve accurate metabolite identification in the chemical industry, but this method has not been applied as readily in biomedical research. Here, we evaluated and validated the performance of high-resolution GC×GC-TOFMS against that of GC-TOFMS, for metabolomics analysis of two different plasma matrices, from healthy individuals (CON) and diabetes mellitus (DM) patients with kidney failure (DM with KF). We found GC×GC-TOFMS outperformed...	pmid:36055403 doi:10.1016/j.jbc.2022.102445	Fri, 02 Sep 2022 06:00:00 -0400
5	pubmed:36055428	Analysis of fruit ripening in Theobroma cacao pod husk based on untargeted metabolomics	Adriana M Gallego Romer A Zambrano Martha Zuluaga Anyela V Camargo Rodríguez Mariana S Candamil-Cortés Angela P Romero Vergel Jorge W Arboleda Valencia	The pod husk of Theobroma cacao (CPH) plays an important agronomical role, as its appearance is used as indicator of ripening, guiding the farmers in the harvest process. Cacao harvesting is not a standardized practice because farmers harvest between six up to eight months from flowering, guided by pod's color and shape. The mixture of cacao beans from different ripening stages (RS), negatively affecting the quality and price of grain. A way to help the farmers in the harvest standardization...	pmid:36055428 doi:10.1016/j.phytochem.2022.113412	Fri, 02 Sep 2022 06:00:00 -0400
6	pubmed:36055508	Multi-omics reveals response mechanism of liver metabolism of hybrid sturgeon under ship noise stress	Yong Zhang Chunhua Liu Jiehao Liu Ximei Liu Zhihan Tu Yueping Zheng Jianan Xu Houyong Fan Youji Wang Menghong Hu	Underwater noise from ship engines can affect the metabolism and immune system of various fish species. Meanwhile, changes in the metabolic pathways in liver are important for fish to adapt to adverse environments. We used a combined multi-omics analysis to investigate the response mechanism of hybrid sturgeon to continuously played ship noise. A control group and a noise group (simulated ship noise: 12 h) were set up, and liver tissues were extracted for high-throughput transcriptome and...	pmid:36055508 doi:10.1016/j.scitotenv.2022.158348	Fri, 02 Sep 2022 06:00:00 -0400
7	pubmed:36055557	Taurine promotes Oreochromis niloticus survival against Edwardsiella tarda infection	Liao-Tian Peng De-Li Li Dai-Xiao Yang Bo Peng	Edwardsiella tarda represents one of the most important pathogens that infects a variety of hosts including aquatic animals and humans. The outbreak of E. tarda infection is frequently reported in aquaculture that causes huge economic loss. Due to the widespread of antibiotic resistance, available antibiotics to treat bacterial infection are limited. Therefore, enhancing aquatic animals to survive upon E. tarda infection become an urgent issue. In this study, we profiled the metabolomic change...	pmid:36055557 doi:10.1016/j.fsi.2022.08.065	Fri, 02 Sep 2022 06:00:00 -0400
8	pubmed:36055574	Metabolomic and transcriptomic analysis of roots of tobacco varieties resistant and susceptible to bacterial wilt	Haoqi Shi Peiwen Xu Wen Yu Yazhi Cheng Anming Ding Weifeng Wang Shengxin Wu Yuhe Sun	Ralstonia solanacearum severely damages the growth of tobacco (Nicotiana tabacum L.) and causes great economic losses in tobacco production. To investigate the root metabolism and transcriptional characteristics of tobacco bacterial wilt susceptible variety Cuibi-1 (CB-1) and resistant new line KCB-1 (derived from an ethyl methanesulfonate (EMS) mutant of CB-1) after infestation with R. solanacearum, root metabolism and transcriptional characteristics were investigated using RNA-Seq and liquid...	pmid:36055574 doi:10.1016/j.ygeno.2022.110471	Fri, 02 Sep 2022 06:00:00 -0400

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9	pubmed:36055779	Prenatal Metabolomic Profiles Mediate the Effect of Maternal Obesity On Early Childhood Growth Trajectories and Obesity Risk: the CANDLE Study	Zunsong Hu Luhang Han Jiawang Liu Jay H Fowke Joan C Han David Kakhniashvili Kaja Z LeWinn Nicole R Bush W Alex Mason Qi Zhao	CONCLUSIONS: Our study provided further evidence that prenatal metabolomic profiles might mediate the effect of maternal OWO on early childhood growth trajectories and OWO risk in offspring. The metabolic pathways including identified metabolite mediators might provide novel intervention targets for preventing the intrauterine development of obesity in offspring of mothers with obesity.	pmid:36055779 doi:10.1093/ajcn/nqac244	Fri, 02 Sep 2022 06:00:00 -0400
10	pubmed:36056096	Metabolomic changes in crown of alfalfa (Medicago sativa L.) during de-acclimation	Zhensong Li Feng He Zongyong Tong Xianglin Li Qingchuan Yang David B Hannaway	Alfalfa is a high-quality forage legume species that is widely cultivated at high latitudes worldwide. However, a decrease in cold tolerance in early spring seriously affects regrowth and persistence of alfalfa. There has been limited research on the metabolomic changes that occur during de-acclimation. In this study, a liquid chromatography-mass spectrometry system was used to compare the metabolites in two alfalfa cultivars during a simulated overwintering treatment. In four pairwise...	pmid:36056096 doi:10.1038/s41598-022-19388-x	Fri, 02 Sep 2022 06:00:00 -0400
11	pubmed:36056162	Tissue-wide metabolomics reveals wide impact of gut microbiota on mice metabolite composition	Iman Zarei Ville M Koistinen Marietta Kokla Anton Klåvus Ambrin Farizah Babu Marko Lehtonen Seppo Auriola Kati Hanhineva	The essential role of gut microbiota in health and disease is well recognized, but the biochemical details that underlie the beneficial impact remain largely undefined. To maintain its stability, microbiota participates in an interactive host-microbiota metabolic signaling, impacting metabolic phenotypes of the host. Dysbiosis of microbiota results in alteration of certain microbial and host metabolites. Identifying these markers could enhance early detection of certain diseases. We report LC-MS...	pmid:36056162 doi:10.1038/s41598-022-19327-w	Fri, 02 Sep 2022 06:00:00 -0400
12	pubmed:36056205	Identifying a metabolomics profile associated with masked hypertension in two independent cohorts: Data from the African-PREDICT and SABPA studies	Michél Strauss-Kruger Ruan Kruger Esmé Jansen Van Vuren Adriaan Jacobs Roan Louw Carina Mels	Individuals with masked hypertension (MHT) have a greater risk of adverse cardiovascular outcomes than normotensive (NT) individuals. Exploring metabolomic differences between NT and MHT individuals may help provide a better understanding of the etiology of MHT. We analyzed data from 910 young participants (83% NT and 17% MHT) (mean age 24 ± 3 years) from the African-PREDICT and 210 older participants (63% NT and 37% MHT) from the SABPA (mean age 42 ± 9.6 years) studies. Clinic and ambulatory...	pmid:36056205 doi:10.1038/s41440-022-01010-2	Fri, 02 Sep 2022 06:00:00 -0400
13	pubmed:36056220	An approach to assess and adjust for the influence of multicollinear covariates on metabolomics association patterns-applied to a study of the associations between a comprehensive lipoprotein profile and the homeostatic model assessment of insulin resista	Olav M Kvalheim Tarja Rajalahti Eivind Aadland	CONCLUSION: The presented covariate projection approach to obtain net association patterns, made it possible to quantify and interpret the influence of adiposity and physical (in)activity on the association pattern of HOMA-IR to the lipoprotein features.	pmid:36056220 doi:10.1007/s11306-022-01931-6	Fri, 02 Sep 2022 06:00:00 -0400

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14	pubmed:36056292	Intestinal Microbiomics and Metabolomics Insights into the Hepatoprotective Effects of Lactobacillus paracasei CCFM1222 Against the Acute Liver Injury in Mice	Weiling Guo Shumao Cui Xin Tang Qiuxiang Zhang Jianxin Zhao Bingyong Mao Hao Zhang	In recent years, acute liver injury (ALI) has received wide-range attention in the world due to its relatively high morbidity and mortality. This study aimed to explore the hepatoprotective effect of Lactobacillus paracasei CCFM1222 against lipopolysaccharide (LPS)-induced ALI mice and further elaborate its mechanism of action from the perspective of intestinal microbiomics and metabolomics. The results displayed that L. paracasei CCFM1222 pretreatment significantly decreased the serum ALT, and...	pmid:36056292 doi:10.1007/s12602-022-09986-6	Fri, 02 Sep 2022 06:00:00 -0400
15	pubmed:36056402	Metabolomic changes in polyunsaturated fatty acids and eicosanoids as diagnostic biomarkers in Mycobacterium avium ssp. paratuberculosis (MAP)-inoculated Holstein-Friesian heifers	Emma N Taylor Manfred Beckmann Glyn Hewinson David Rooke Luis A J Mur Ad P Koets	Mycobacterium avium subspecies paratuberculosis (MAP) is the causative organism of Johne's disease, a chronic granulomatous enteritis of ruminants. We have previously used naturally MAP-infected heifer calves to document metabolomic changes occurring in MAP infections. Herein, we used experimentally MAP-inoculated heifer calves to identify biomarkers for MAP infections. At 2-weeks of age, 20 Holstein-Friesian (HF) calves were experimentally inoculated with MAP. These calves, along with 20...	pmid:36056402 doi:10.1186/s13567-022-01087-0	Fri, 02 Sep 2022 06:00:00 -0400
16	pubmed:36056641	Glucose metabolism enhancement by 10-hydroxy-2-decenoic acid *via* the PI3K/AKT signaling pathway in high-fat-diet/streptozotocin induced type 2 diabetic mice	Xiyi Hu Zhenguo Liu Yuntao Lu Xuepeng Chi Kai Han Hongfang Wang Ying Wang Lanting Ma Baohua Xu	10-Hydroxy-2-decenoic acid (10-HDA) is a principal active ingredients of royal jelly. Several recent studies demonstrated that 10-HDA has potential anti-type 2 diabetes mellitus (T2DM) properties. To evaluate the anti-T2DM effect of 10-HDA and explore its underlying molecular mechanisms, we used high fat diet (HFD) combined with streptozotocin (STZ) injection to establish a diabetes model. Mice were randomly divided into four groups (8 mice per group): control group, 10-HDA group, T2DM group,...	pmid:36056641 doi:10.1039/d1fo03818d	Sat, 03 Sep 2022 06:00:00 -0400
17	pubmed:36056681	Transcriptomics and metabolomics reveal the role of CYP1A2 in psoralen/isopsoralen-induced metabolic activation and hepatotoxicity	Cai Zhang Song Fan Jin-Quan Zhao Yan Jiang Jia-Xing Sun Hui-Jun Li	Psoralen and isopsoralen are the pharmacologically important but hepatotoxic components in Psoraleae Fructus. The purpose of this study was to reveal the underlying mechanism of psoralen/isopsoralen-induced hepatotoxicity. Initially, we applied integrated analyses of transcriptomic and metabolomic profiles in mice treated with psoralen and isopsoralen, highlighting the xenobiotic metabolism by cytochromes P450 as a potential pathway. Then, with verifications of expression levels by qRT-PCR and...	pmid:36056681 doi:10.1002/ptr.7604	Sat, 03 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
18	pubmed:36056694	Exploring the mechanism of Shendi Bushen capsule in anti-renal fibrosis using metabolomics theory and network analysis	Tianwei Meng Hong Chang Hongyu Meng	Shendi Bushen capsule (SDBS) is a Chinese patent medicine used for the treatment of renal fibrosis (RF). However, its mechanism of action in the treatment of RF is still unclear, which seriously restricts its clinical application. This study integrated metabolomics and biological network analysis of SDBS against RF mechanism. Metabolomic analysis of rat urine samples identified biomarkers of differential progression of RF and key metabolites regulated by SDBS. The key metabolic pathways and the...	pmid:36056694 doi:10.1039/d2mo00141a	Sat, 03 Sep 2022 06:00:00 -0400