

metabolomics

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36063685	Progress and opportunities in microbial community metabolomics	Amrisha Bhosle Ya Wang Eric A Franzosa Curtis Huttenhower	The metabolome lies at the interface of host-microbiome crosstalk. Previous work has established links between chemically diverse microbial metabolites and a myriad of host physiological processes and diseases. Coupled with scalable and cost-effective technologies, metabolomics is thus gaining popularity as a tool for characterization of microbial communities, particularly when combined with metagenomics as a window into microbiome function. A systematic interrogation of microbial community...	pmid:36063685 doi:10.1016/j.mib.2022.102195	Mon, 05 Sep 2022 06:00:00 -0400
2	pubmed:36063700	Network pharmacology combined with metabolomics reveals the mechanism of Fuzi decoction against chronic heart failure in rats	Taixiang Gao Rui Wang Hongxiong Zhang Feng Zhao	Chronic heart failure (CHF) is the end stage of many severe heart diseases. Fuzi decoction (FZD) originates from Zhang Zhongjing's Treatise on Febrile Diseases and is widely used in the treatment of CHF in the clinic, but the potential mechanism of FZD in CHF is unclear. In this study, an integrated approach combining network pharmacology and metabolomics was adopted to explore the mechanism of FZD in CHF. Network pharmacological studies indicated that the most significant signaling pathway was...	pmid:36063700 doi:10.1016/j.jchromb.2022.123435	Mon, 05 Sep 2022 06:00:00 -0400
3	pubmed:36063854	Comparative plasma metabolomic analysis to identify biomarkers for lead-induced cognitive impairment	Yuqin Wang Yuan Nong Xing Zhang Tingyu Mai Jiansheng Cai Jiaqi Liu Keng Po Lai Zhiyong Zhang	CONCLUSIONS: The findings of this report provide novel insights into the use of plasma metabolites to assess metal-induced cognitive impairment.	pmid:36063854 doi:10.1016/j.cbi.2022.110143	Mon, 05 Sep 2022 06:00:00 -0400
4	pubmed:36063990	Metabolomics reveals inosine 5'-monophosphate is increased during mice adipocyte browning	Haruya Takahashi Motohiro Tokura Satoko Kawarasaki Hiroyuki Nagai Mari Iwase Kento Nishitani Haruka Okaze Shinsuke Mohri Tetsuro Ito Takeshi Ara Huei-Fen Jheng Wataru Nomura Teruo Kawada Kazuo Inoue Tsuyoshi Goto	Adipocyte browning is one of the potential strategies for the prevention of obesity-related metabolic syndromes, but it is a complex process. Although previous studies make it increasingly clear that several transcription factors and enzymes are essential to induce browning, it is unclear what dynamic and metabolic changes occur in induction of browning. Here, we analyzed the effect of a beta-adrenergic receptor agonist (CL316243, accelerator of browning) on metabolic change in mice adipose...	pmid:36063990 doi:10.1016/j.jbc.2022.102456	Mon, 05 Sep 2022 06:00:00 -0400
5	pubmed:36064220	Assessment of type I interferon responses as a feature of immunogenic cell death	Sabrina Forveille Allan Sauvat Shuai Zhang Liwei Zhao Guido Kroemer Oliver Kepp	The radiochemotherapy- or chemotherapy-induced stimulation of immunogenic cell death (ICD) affecting malignant cells ignites antitumor immune responses that are clinically relevant as they allow to achieve durable responses beyond treatment discontinuation. The mechanistic exploration of ICD and the discovery of agents and interventions that are endowed with the capacity to elicit ICD is of the utmost importance. Here, we describe an assay for the assessment of type I interferon (IFN)...	pmid:36064220 doi:10.1016/bs.mcb.2021.12.028	Mon, 05 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
6	pubmed:36064227	Assessment of transcription inhibition as a characteristic of immunogenic cell death	Giulia Cerrato Juliette Humeau Allan Sauvat Oliver Kepp Guido Kroemer	Anticancer drugs that suppress DNA-to-RNA transcription are particularly efficient in stimulating immunogenic cell death and hence eradicate malignant cells in a way that they will ignite an antitumor immune response. This is therapeutically relevant as it allows treatment response to last beyond drug discontinuation. For this reason, it is important to measure transcription inhibition in a precise fashion. Here, we detail two complementary assays for the assessment of transcription inhibition,...	pmid:36064227 doi:10.1016/bs.mcb.2021.12.026	Mon, 05 Sep 2022 06:00:00 -0400
7	pubmed:36064228	Assessment of eIF2 phosphorylation during immunogenic cell death	Lucillia Bezu Juliette Humeau Marion Leduc Hui Pan Guido Kroemer Oliver Kepp	Immunogenic cell death (ICD) is a modality of cellular demise that when it is induced by certain anticancer treatments can ignite an adaptive anticancer immune response. ICD is characterized by the emission of a specific set of danger-associated molecular patterns (DAMPs) including calreticulin exposure at the plasma membrane, ATP liberation, HMGB1 exodus and type-I IFN release. The apical signaling triggering the appearance of these hallmarks involves the phosphorylation on serine 51 of the...	pmid:36064228 doi:10.1016/bs.mcb.2022.01.003	Mon, 05 Sep 2022 06:00:00 -0400
8	pubmed:36064229	Interference of immunogenic chemotherapy by artificially controlled calreticulin secretion from tumor cells	Liwei Zhao Shuai Zhang Hui Chen Guido Kroemer Oliver Kepp Peng Liu	The exposure of calreticulin (CALR) on the cell surface of apoptotic cancer cells is an important "eat-me" signal that stimulates the engulfment by antigen presenting cells (APCs). When cells are exposed to immunogenic cell death (ICD) inducers, CALR translocates from the lumen of the endoplasmic reticulum (ER) to the cell surface, where it serves as a ligand for LDL-receptor-related protein 1 (LRP1, also known as CD91) expressed by dendritic cells (DCs). Surface-exposed CALR facilitates tumor...	pmid:36064229 doi:10.1016/bs.mcb.2021.12.027	Mon, 05 Sep 2022 06:00:00 -0400
9	pubmed:36064294	Assessing food authenticity through protein and metabolic markers	Barbara Prandi Laura Righetti Augusta Caligiani Tullia Tedeschi Martina Cirlini Gianni Galaverna Stefano Sforza	This chapter aims to address an issue of ancient origins, but more and more topical in a globalized world in which consumers and stakeholders are increasingly aware: the authenticity of food. Foods are systems that can also be very complex, and verifying the correspondence between what is declared and the actual characteristics of the product is often a challenging issue. The complexity of the question we want to answer (is the food authentic?) means that the answer is equally articulated and...	pmid:36064294 doi:10.1016/bs.afnr.2022.04.010	Mon, 05 Sep 2022 06:00:00 -0400
10	pubmed:36064406	Prostate cancer in omics era	Nasrin Gholami Amin Haghpourast Iraj Alipourfard Majid Nazari	Recent advances in omics technology have prompted extraordinary attempts to define the molecular changes underlying the onset and progression of a variety of complex human diseases, including cancer. Since the advent of sequencing technology, cancer biology has become increasingly reliant on the generation and integration of data generated at these levels. The availability of multi-omic data has transformed medicine and biology by enabling integrated systems-level approaches. Multivariate...	pmid:36064406 doi:10.1186/s12935-022-02691-y	Mon, 05 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
11	pubmed:36064959	The role of NMR-based circulating metabolic biomarkers in development and risk prediction of new onset type 2 diabetes	Fiona Bragg Christiana Kartsonaki Yu Guo Michael Holmes Huaidong Du Canqing Yu Pei Pei Ling Yang Donghui Jin Yiping Chen Dan Schmidt Daniel Avery Jun Lv Junshi Chen Robert Clarke Michael R Hill Liming Li Iona Y Millwood Zhengming Chen	Associations of circulating metabolic biomarkers with type 2 diabetes (T2D) and their added value for risk prediction are uncertain among Chinese adults. A case-cohort study included 882 T2D cases diagnosed during 8-years' follow-up and a subcohort of 789 participants. NMR-metabolomic profiling quantified 225 plasma biomarkers in stored samples taken at recruitment into the study. Cox regression yielded adjusted hazard ratios (HRs) for T2D associated with individual biomarkers, with a set of...	pmid:36064959 doi:10.1038/s41598-022-19159-8	Tue, 06 Sep 2022 06:00:00 -0400
12	pubmed:36065182	Quantitative modeling of human liver reveals dysregulation of glycosphingolipid pathways in nonalcoholic fatty liver disease	Partho Sen Olivier Govaere Tim Sinioja Aidan McGlinchey Dawei Geng Vlad Ratziu Elisabetta Bugianesi Jörn M Schattenberg Antonio Vidal-Puig Michael Allison Simon Cockell Ann K Daly Tuulia Hyötyläinen Quentin M Anstee Matej Oreši	Nonalcoholic fatty liver disease (NAFLD) is an increasingly prevalent disease that is associated with multiple metabolic disturbances, yet the metabolic pathways underlying its progression are poorly understood. Here, we studied metabolic pathways of the human liver across the full histological spectrum of NAFLD. We analyzed whole liver tissue transcriptomics and serum metabolomics data obtained from a large, prospectively enrolled cohort of 206 histologically characterized patients derived from...	pmid:36065182 pmc:PMC9440293 doi:10.1016/j.jisci.2022.104949	Tue, 06 Sep 2022 06:00:00 -0400
13	pubmed:36065196	Spirulina polysaccharide induces the metabolic shifts and gut microbiota change of lung cancer in mice	Yingfang Lu Bo Peng Yuqi Lin Qianmin Lin Xuewei Xia Saiyi Zhong Lianxiang Luo Riming Huang	A polysaccharide obtained from Spirulina (PSP) and its effect on lung cancer in mice was investigated. Our results indicate that the tumor volume and weight of the lung cancer-bearing mice treated with PSP decreased significantly. Metabolite analysis showed that 27 differential accumulated metabolites (DAMs) changed significantly, in which 24 DAMs increased while 3 DAMs decreased. KEGG enrichment results showed that these differential metabolites were enriched significantly in the high-affinity...	pmid:36065196 pmc:PMC9440268 doi:10.1016/j.crfs.2022.08.010	Tue, 06 Sep 2022 06:00:00 -0400
14	pubmed:36065322	Serum metabolomic abnormalities in survivors of non-severe COVID-19	Fang Li Lei Fu Xiaoxiong Liu Xin-An Liu Yong Liang Yueguang Lv Zhiyi Yang Ang Guo Zhiyu Chen Wenbo Li Fan Pan Qian Luo	Metabolic reprogramming is a distinctive characteristic of SARS-CoV-2 infection, which refers to metabolic changes in hosts triggered by viruses for their survival and spread. It is current urgent to understand the metabolic health status of COVID-19 survivors and its association with long-term health consequences of infection, especially for the predominant non-severe patients. Herein, we show systemic metabolic signatures of survivors of non-severe COVID-19 from Wuhan, China at six months...	pmid:36065322 pmc:PMC9433334 doi:10.1016/j.heliyon.2022.e10473	Tue, 06 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
15	pubmed:36065328	Itaconic acid production is regulated by LaeA in Aspergillus pseudoterreus	Kyle R Pomraning Ziyu Dai Nathalie Munoz Young-Mo Kim Yuqian Gao Shuang Deng Teresa Lemmon Marie S Swita Jeremy D Zucker Joonhoon Kim Stephen J Mondo Ellen Panisko Meagan C Burnet Bobbie-Jo M Webb-Robertson Beth Hofstad Scott E Baker Kristin E Burnum-Johnson Jon K Magnuson Agile BioFoundry	The global regulator LaeA controls secondary metabolism in diverse Aspergillus species. Here we explored its role in regulation of itaconic acid production in Aspergillus pseudoterreus. To understand its role in regulating metabolism, we deleted and overexpressed laeA, and assessed the transcriptome, proteome, and secreted metabolome prior to and during initiation of phosphate limitation induced itaconic acid production. We found that secondary metabolite clusters, including the itaconic acid...	pmid:36065328 pmc:PMC9440423 doi:10.1016/j.mec.2022.e00203	Tue, 06 Sep 2022 06:00:00 -0400
16	pubmed:36065601	Advances in mass spectrometry imaging for spatial cancer metabolomics	Xin Ma Facundo M Fernández	Mass spectrometry (MS) has become a central technique in cancer research. The ability to analyze various types of biomolecules in complex biological matrices makes it well suited for understanding biochemical alterations associated with disease progression. Different biological samples, including serum, urine, saliva, and tissues have been successfully analyzed using mass spectrometry. In particular, spatial metabolomics using MS imaging (MSI) allows the direct visualization of metabolite...	pmid:36065601 doi:10.1002/mas.21804	Tue, 06 Sep 2022 06:00:00 -0400
17	pubmed:36065819	Metabolomic fingerprint of Hamamelis virginiana L. gallotannins by suspect screening analysis with UHPLC-qToF and their semiquantitative evaluation	Michela Burico Giada Fodaroni Enrico Flamini Nicola Ascani Giacomo Proietti Sara Tamimi Claudio Marzio Quintiero Luca Massa Mattia Gianni Luisa Mattoli	The evolution of the regulatory framework for medical devices in the EU (Reg 2017/745) has opened the study of complex systems emerging properties. This makes necessary to identify new analytical approaches able of characterizing complex natural substrates as completely as possible. Therefore, omics approaches and advanced analytical methods for the determination of metabolite classes appear to be at the forefront to meet this need. In this perspective, a new approach based on the suspect...	pmid:36065819 doi:10.1002/jms.4878	Tue, 06 Sep 2022 06:00:00 -0400
18	pubmed:36066093	Optical photothermal infrared spectroscopy can differentiate equine osteoarthritic plasma extracellular vesicles from healthy controls	Emily J Clarke Cassio Lima James R Anderson Catarina Castanheira Alison Beckett Victoria James Jacob Hyett Royston Goodacre Mandy J Peffers	Equine osteoarthritis is a chronic degenerative disease of the articular joint, characterised by cartilage degradation resulting in pain and reduced mobility and thus is a prominent equine welfare concern. Diagnosis is usually at a late stage through clinical examination and radiographic imaging, whilst treatment is symptomatic not curative. Extracellular vesicles are nanoparticles that are involved in intercellular communication. The objective of this study was to investigate the feasibility of...	pmid:36066093 doi:10.1039/d2ay00779g	Tue, 06 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
19	pubmed:36066309	PhRHMs play important roles in leaf and flower development and anthocyanin synthesis in petunia	Lina Sang Guoju Chen Jiahao Cao Juanxu Liu Yixun Yu	Anthocyanins, vital metabolites in plants, are formed by anthocyanidins combined with various monosaccharides, including glucose, rhamnose, and arabinose. Rhamnose contributes greatly to the glycosylation of anthocyanidins. There are two kinds of rhamnose synthase (RS): rhamnose biosynthesis (RHM) and nucleotide-rhamnose synthase/epimerase-reductase (UER1). Nevertheless, no RS isoform was reported to be involved in anthocyanin synthesis. Here, three homologous PhRHM genes, namely PhRHM1, PhRHM2,...	pmid:36066309 doi:10.1111/ppl.13773	Tue, 06 Sep 2022 06:00:00 -0400
20	pubmed:36067040	Functional Assessment of Homozygous ALDH18A1 Variants Reveals Alterations in Amino Acid and Antioxidant Metabolism	Maxwell B Colonna Tonya Moss Sneha Mokashi Sujata Srikanth Julie R Jones Jackson R Foley Cindy Skinner Angie Lichty Anthony Kocur Tim Wood Tracy Murray Stewart Robert A Casero Heather Flanagan-Steet Arthur S Edison Michael J Lyons Richard Steet	Mono- and biallelic variants in ALDH18A1 cause a spectrum of human disorders associated with cutaneous and neurological findings that overlap with both cutis laxa and spastic paraplegia. ALDH18A1 encodes the bifunctional enzyme pyrroline-5-carboxylate synthetase (P5CS) that plays a role in the de novo biosynthesis of proline and ornithine. Here we characterize a previously unreported homozygous ALDH18A1 variant (p.Thr331Pro) in four affected probands from two unrelated families, and demonstrate...	pmid:36067040 doi:10.1093/hmg/ddac226	Tue, 06 Sep 2022 06:00:00 -0400
21	pubmed:36067168	Spatially resolved characterization of tissue metabolic compartments in fasted and high-fat diet livers	Sylwia A Stopka Jiska van der Reest Walid M Abdelmoula Daniela F Ruiz Shakchhi Joshi Alison E Ringel Marcia C Haigis Nathalie Y R Agar	Cells adapt their metabolism to physiological stimuli, and metabolic heterogeneity exists between cell types, within tissues, and subcellular compartments. The liver plays an essential role in maintaining whole-body metabolic homeostasis and is structurally defined by metabolic zones. These zones are well-understood on the transcriptomic level, but have not been comprehensively characterized on the metabolomic level. Mass spectrometry imaging (MSI) can be used to map hundreds of metabolites...	pmid:36067168 doi:10.1371/journal.pone.0261803	Tue, 06 Sep 2022 06:00:00 -0400
22	pubmed:36067206	NMR-based metabolomic analysis identifies RON-DEK--catenin dependent metabolic pathways and a gene signature that stratifies breast cancer patient survival	Sara Vicente-Muñoz Brian G Hunt Taylor E Lange Susanne I Wells Susan E Waltz	CONCLUSIONS: The RON-DEK--catenin axis regulates the numerous metabolic pathways with significant associations to breast cancer patient outcomes.	pmid:36067206 doi:10.1371/journal.pone.0274128	Tue, 06 Sep 2022 06:00:00 -0400
23	pubmed:36067333	c-di-AMP signaling is required for bile salt resistance, osmotolerance, and long-term host colonization by <i>Clostridioides difficile</i>	Marine Oberkampff Audrey Hamiot Pamela Altamirano-Silva Paula Bellés-Sancho Yannick D N Tremblay Nicholas DiBenedetto Roland Seifert Olga Soutourina Lynn Bry Bruno Dupuy Johann Peltier	To colonize the host and cause disease, the human enteropathogen <i>Clostridioides difficile</i> must sense, respond, and adapt to the harsh environment of the gastrointestinal tract. We showed that the production and degradation of cyclic diadenosine monophosphate (c-di-AMP) were necessary during different phases of <i>C. difficile</i> growth, environmental adaptation, and infection. The production of this nucleotide second messenger was essential for growth because it controlled the uptake of potassium and...	pmid:36067333 doi:10.1126/scisignal.abn8171	Tue, 06 Sep 2022 06:00:00 -0400