metabolomics

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36130451	Morphology, microbiota, and metabolome along the intestinal tract of female turkeys	Janina Rzeznitzeck, Frederic J Hoerr, Ivan Rychlik, Karen Methling, Michael Lalk, Alexandra Rath, Alexandra von Altrock, Silke Rautenschlein	The global turkey industry is confronted with emerging challenges regarding health and welfare. Performance and disease resilience are directly linked to gut health. A clear definition of a healthy gut is a prerequisite to developing new strategies for improved gut health and, thus, general health, welfare and productivity. To date, detailed knowledge about gut health characteristics, especially during the critical fattening period, is still lacking for turkeys. Therefore, the goal of this study...	pmid:36130451 doi:10.1016/j.psj.2022.102046	Wed, 21 Sep 2022 06:00:00 -0400
2	pubmed:36130949	Multi-omic brain and behavioral correlates of cell-free fetal DNA methylation in macaque maternal obesity models	Benjamin I Laufer, Yu Hasegawa, Zhichao Zhang, Casey E Hogrefe, Laura A Del Rosso, Lori Haapanen, Hyeyeon Hwang, Melissa D Bauman, Judy Van de Water, Ameer Y Taha, Carolyn M Slupsky, Mari S Golub, John P Capitanio, Catherine A VandeVoort, Cheryl K Walker, Janine M LaSalle	Maternal obesity during pregnancy is associated with neurodevelopmental disorder (NDD) risk. We utilized integrative multi-omics to examine maternal obesity effects on offspring neurodevelopment in rhesus macaques by comparison to lean controls and two interventions. Differentially methylated regions (DMRs) from longitudinal maternal blood-derived cell-free fetal DNA (cffDNA) significantly overlapped with DMRs from infant brain. The DMRs were enriched for neurodevelopmental functions,...	pmid:36130949 doi:10.1038/s41467-022-33162-7	Wed, 21 Sep 2022 06:00:00 -0400
3	pubmed:36131008	The conservation of human functional variants and their effects across livestock species	Rongrong Zhao, Andrea Talenti, Lingzhao Fang, Shuli Liu, George Liu, Neil P Chue Hong, Albert Tenesa, Musa Hassan, James G D Prendergast	Despite the clear potential of livestock models of human functional variants to provide important insights into the biological mechanisms driving human diseases and traits, their use to date has been limited. Generating such models via genome editing is costly and time consuming, and it is unclear which variants will have conserved effects across species. In this study we address these issues by studying naturally occurring livestock models of human functional variants. We show that orthologues...	pmid:36131008 doi:10.1038/s42003-022-03961-1	Wed, 21 Sep 2022 06:00:00 -0400
4	pubmed:36131046	The serum metabolomic profile of a distinct, inflammatory subtype of acute psychosis	Belinda Lennox, Wenzheng Xiong, Patrick Waters, Alasdair Coles, Peter B Jones, Tianrong Yeo, Jeanne Tan May May, Ksenija Yeeles, Daniel Anthony, Fay Probert	A range of studies suggest that a proportion of psychosis may have an autoimmune basis, but this has not translated through into clinical practice-there is no biochemical test able to accurately identify psychosis resulting from an underlying inflammatory cause. Such a test would be an important step towards identifying who might require different treatments and have the potential to improve outcomes for patients. To identify novel subgroups within patients with acute psychosis we measured the...	pmid:36131046 doi:10.1038/s41380-022-01784-4	Wed, 21 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
5	pubmed:36131087	Identification of -1-pyrroline-5-carboxylate derived biomarkers for hyperprolinemia type II	Jona Merx Rianne E van Outersterp Udo F H Engelke Veronique Hendriks Ron A Wevers Marleen C D G Huigen Huub W A H Waterval Irene M L W Körver-Keularts Jasmin Mecinovi Floris P J T Rutjes Jos Oomens Karlien L M Coene Jonathan Martens Thomas J Boltje	Hyperprolinemia type II (HPII) is an inborn error of metabolism due to genetic variants in ALDH4A1, leading to a deficiency in -1-pyrroline-5-carboxylate (P5C) dehydrogenase. This leads to an accumulation of toxic levels of P5C, an intermediate in proline catabolism. The accumulating P5C spontaneously reacts with, and inactivates, pyridoxal 5'-phosphate, a crucial cofactor for many enzymatic processes, which is thought to be the pathophysiological mechanism for HPII. Here, we describe the use...	pmid:36131087 doi:10.1038/s42003-022-03960-2	Wed, 21 Sep 2022 06:00:00 -0400
6	pubmed:36131643	Advances in the gut microbiome and mood disorders	Sabrina Mörkl Mary I Butler Sonja Lackner	PURPOSE OF REVIEW: The gut microbiome is in constant bidirectional communication with the brain through the microbiota-gut-brain-axis. Mood disorders are among the most common psychiatric disorders and include major depressive disorder and bipolar disorder. The gut microbiome is altered in individuals with mood disorders and has a role in its inflammatory pathophysiology. In this article, we performed a narrative review of clinical studies, randomized controlled trials and meta-analyses...	pmid:36131643 doi:10.1097/YCO.0000000000000829	Thu, 22 Sep 2022 06:00:00 -0400
7	pubmed:36131799	Production of two SARS-CoV-2 neutralizing antibodies with different potencies in *Nicotiana benthamiana*	Rachele Frigerio Carla Marusic Maria Elena Villani Chiara Lico Cristina Capodicasa Emanuele Andreano Ida Paciello Rino Rappuoli Anna Maria Salzano Andrea Scaloni Selene Baschieri Marcello Donini	Monoclonal antibodies are considered to be highly effective therapeutic tools for the treatment of mild to moderate COVID-19 patients. In the present work, we describe the production of two SARS-CoV-2 human IgG1 monoclonal antibodies recognizing the spike protein receptor-binding domain (RBD) and endowed with neutralizing activity (nAbs) in plants. The first one, mAbJ08-MUT, was previously isolated from a COVID-19 convalescent patient and Fc-engineered to prolong the half-life and reduce the...	pmid:36131799 pmc:PMC9484322 doi:10.3389/fpls.2022.956741	Thu, 22 Sep 2022 06:00:00 -0400
8	pubmed:36131915	Early-life stress and dietary fatty acids impact the brain lipid/oxylipin profile into adulthood, basally and in response to LPS	Kitty Reemst Jelle Y Broos Maralinde R Abbink Chiara Cimetti Martin Giera Gijs Kooij Aniko Korosi	Brain lipid dysregulation is a hallmark of depression and Alzheimer's disease, also marked by chronic inflammation. Early-life stress (ELS) and dietary intake of polyunsaturated fatty acids (PUFAs) are risk factors for these pathologies and are known to impact inflammatory processes. However, if these early-life factors alter brain lipid homeostasis on the long-term and thereby contribute to this risk remains to be elucidated. We have recently shown that an early diet enriched in omega()-3...	pmid:36131915 pmc:PMC9484596 doi:10.3389/fimmu.2022.967437	Thu, 22 Sep 2022 06:00:00 -0400
9	pubmed:36132987	Urinary Microbial and Metabolomic Profiles in Kidney Stone Disease	Hong Gao Jiaqiong Lin Fu Xiong Zuhu Yu Shilei Pan Yuxin Huang	CONCLUSIONS: Our study has characterized important profiles and correlations among urinary tract microbiomes and metabolomes in nephrolithiasis patients for the first time. These results shed new light on the pathogenesis of nephrolithiasis and could provide early clinical biomarkers for diagnosing the disease.	pmid:36132987 pmc:PMC9484321 doi:10.3389/fcimb.2022.953392	Thu, 22 Sep 2022 06:00:00 -0400

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10	pubmed:36133639	Possibilities of Liquid Chromatography Mass Spectrometry (LC-MS)-Based Metabolomics and Lipidomics in the Authentication of Meat Products: A Mini Review	Putri Widyanti Harlina Vevi Maritha Ida Musfiroh Syamsul Huda Nandi Sukri Muchtaridi Muchtaridi	The liquid chromatography mass spectrometry (LC-MS)-based metabolomic and lipidomic methodology has great sensitivity and can describe the fingerprint of metabolites and lipids in pork and beef. This approach is commonly used to identify and characterize small molecules such as metabolites and lipids, in meat products with high accuracy. Since the metabolites and lipids can be used as markers for many properties of a food, they can provide further evidence of the foods authenticity claim....	pmid:36133639 pmc:PMC9478982 doi:10.5851/kosfa.2022.e37	Thu, 22 Sep 2022 06:00:00 -0400
11	pubmed:36133908	Machine learning based on metabolomics reveals potential targets and biomarkers for primary Sjogren's syndrome	Kai Wang Ju Li Deqian Meng Zhongyuan Zhang Shanshan Liu	Background: Using machine learning based on metabolomics, this study aimed to construct an effective primary Sjogren's syndrome (pSS) diagnostics model and reveal the potential targets and biomarkers of pSS. Methods: From a total of 39 patients with pSS and 38 healthy controls (HCs), serum specimens were collected. The samples were analyzed by ultra-high-performance liquid chromatography coupled with high-resolution mass spectrometry. Three machine learning algorithms, including the least...	pmid:36133908 pmc:PMC9483105 doi:10.3389/fmolb.2022.913325	Thu, 22 Sep 2022 06:00:00 -0400
12	pubmed:36134031	An integrated metabolome and transcriptome analysis of the *Hibiscus syriacus* L. petals reveal the molecular mechanisms of anthocyanin accumulation	Xiaohong Wang Lihua Li Caixian Liu Minhuan Zhang Yafeng Wen	Hibiscus syriacus L. var. Shigyoku is a new double-flowered bluish-purple variety in China that changes color during flower development from bluish-purple to light purple. There is limited information on the anthocyanin accumulation patterns and associated transcriptome signatures in Shigyoku from D1 (bud) to open flower (D3). Here, we employed a combined transcriptome and metabolome approach to understanding the mechanism of this color change. Our results demonstrate that cyanidins,...	pmid:36134031 pmc:PMC9483124 doi:10.3389/fgene.2022.995748	Thu, 22 Sep 2022 06:00:00 -0400
13	pubmed:36134697	Hyaluronic acids mediate the infiltration, migration, and M2 polarization of macrophages: evaluating metabolic molecular phenotypes in gliomas	Hao Zhang Nan Zhang Ziyu Dai Zeyu Wang Xun Zhang Xisong Liang Liyang Zhang Songshan Feng Wantao Wu Weijie Ye Jian Zhang Peng Luo Zaoqu Liu Quan Cheng Zhixiong Liu	Gliomas cause high mortality around the world. The metabolic pattern of the tumor was previously suggested to be associated with the patient's survival outcome and immune activity. Yet, this relationship in glioma remains unknown. This study systematically evaluated the immune landscape in different phenotypes classified by metabolic-related pathways of 3068 glioma samples and 33 glioblastoma single-cell sequencing samples. Machine learning prediction analysis of microarray with R (pamr) was...	pmid:36134697 doi:10.1002/1878-0261.13315	Thu, 22 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
14	pubmed:36134739	A Photoactivated Sorafenib-Ruthenium(II) Prodrug for Resistant Hepatocellular Carcinoma Therapy through Ferroptosis and Purine Metabolism Disruption	Yidan Lai Nong Lu Shuangling Luo Haobing Wang Pingyu Zhang	The curative effect of sorafenib in hepatocellular carcinoma (HCC) is limited and sorafenib resistance remains a major obstacle for HCC. To overcome this obstacle, a new photoactive sorafenib-Ru(II) complex Ru-Sora has been designed. Upon irradiation (= 465 nm), Ru-Sora rapidly releases sorafenib and generates reactive oxygen species, which can oxidize intracellular substances such as GSH. Cellular experiments show that irradiated Ru-Sora is highly cytotoxic toward Hep-G2 cells, including...	pmid:36134739 doi:10.1021/acs.jmedchem.2c00880	Thu, 22 Sep 2022 06:00:00 -0400
15	pubmed:36135199	Metabolomics as a Prospective Tool for Soybean (*Glycine max*) Crop Improvement	Efficient Ncube Keletso Mohale Noluyolo Nogemane	Global demand for soybean and its products has stimulated research into the production of novel genotypes with higher yields, greater drought and disease tolerance, and shorter growth times. Genetic research may be the most effective way to continue developing high-performing cultivars with desirable agronomic features and improved nutritional content and seed performance. Metabolomics, which predicts the metabolic marker for plant performance under stressful conditions, is rapidly gaining...	pmid:36135199 doi:10.3390/cimb44090287	Thu, 22 Sep 2022 06:00:00 -0400
16	pubmed:36135524	Global Metabolomics of Fireflies (Coleoptera: Lampyridae) Explore Metabolic Adaptation to Fresh Water in Insects	Linyu Yang Zishun Zhao Dan Luo Mingzhong Liang Qilin Zhang	Aquatic insects are well-adapted to freshwater environments, but metabolic mechanisms of such adaptations, particularly to primary environmental factors (e.g., hypoxia, water pressure, dark light, and abundant microbes), are poorly known. Most firefly species (Coleoptera: Lampyridae) are terrestrial, but the larvae of a few species are aquatic. We generated 24 global metabolomic profiles of larvae and adults of Aquatica leii (freshwater) and Lychnuris praetexta (terrestrial) to identify...	pmid:36135524 doi:10.3390/insects13090823	Thu, 22 Sep 2022 06:00:00 -0400
17	pubmed:36135553	Transcriptome and Metabolome Analysis Reveals the Importance of Amino-Acid Metabolism in *Spodoptera Frugiperda* Exposed to Spinetoram	Zupeng Gao Raufa Batool Weifeng Xie Xiaodan Huang Zhenying Wang	Pests are inevitably exposed to sublethal and lethal doses in the agroecosystem following the application of pesticides indispensable to protect food sources. The effect of spinetoram on amino-acid metabolism of fall armyworm, Spodoptera frugiperda (J.E. Smith), was investigated, at the dose of LC(10) and LC(90), by transcriptome and LC-MS/MS analysis. Using statistics-based analysis of both POS and NEG mode, a total of 715,501 metabolites in S. frugiperda were significantly changed after...	pmid:36135553 doi:10.3390/insects13090852	Thu, 22 Sep 2022 06:00:00 -0400
18	pubmed:36135664	Metabolome and Transcriptome Profiling Reveal Carbon Metabolic Flux Changes in *Yarrowia lipolytica* Cells to Rapamycin	Ziyu Liu Junjie Tian Zhengang Miao Wenxing Liang Guangyuan Wang	Yarrowia lipolytica is an oleaginous yeast for the production of oleochemicals and biofuels. Nitrogen deficiency is beneficial to lipids biosynthesis in Y. lipolytica. Target of rapamycin (TOR) regulates the utilization of nutrients, which is inhibited in nitrogen starvation or by rapamycin treatment. However, under nitrogen-rich conditions, the lipids biosynthesis in Y. lipolytica after inhibition of TOR by rapamycin is elusive. Combining metabolomics and transcriptomics analysis, we found that...	pmid:36135664 doi:10.3390/jof8090939	Thu, 22 Sep 2022 06:00:00 -0400

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19	pubmed:36135669	Metabarcoding and Metabolome Analyses Reveal Mechanisms of *Leymus chinensis* Growth Promotion by Fairy Ring of *Leucocalocybe mongolica*	Mingzheng Duan Jia Lu Wenjing Yang Meiling Lu Jibin Wang Suli Li Yiting Chen Lihua Hu Lingqiang Wang	Fairy rings are a unique ecological phenomenon caused by the growth of the fungal mycelium in the soil. Fairy rings formed by Leucocalocybe mongolica (LM) are generally distributed in the Mongolian Plateau, where they promote plant growth without fertilization and alleviate fertilizer use. We previously investigated the soil factors regulating growth promotion in a fairy ring ecosystem; however, the aspects of the plant (Leymus chinensis, LC) that promote growth have not been explored....	pmid:36135669 doi:10.3390/jof8090944	Thu, 22 Sep 2022 06:00:00 -0400
20	pubmed:36135676	Screening of Endophytic Fungi in Locoweed Induced by Heavy-Ion Irradiation and Study on Swainsonine Biosynthesis Pathway	Yanan Mo Zhen Yang Baocheng Hao Feng Cheng Xiangdong Song Xiaofei Shang Haoxia Zhao Ruofeng Shang Xuehong Wang Jianping Liang Shengyi Wang Yu Liu	Swainsonine (SW) is a substance with both animal neurotoxicity and natural anticancer activity produced by the metabolism of endophytic fungus Alternaria section Undifilum oxytropis of locoweed. This paper produced SW by fermentation of the endophytic fungus A. oxytropis of locoweed and obtained the optimal ultrasonic-assisted extraction process of SW by the response surface methodology. Meanwhile, four mutant strains with significant and stable SW-producing properties were screened out after...	pmid:36135676 doi:10.3390/jof8090951	Thu, 22 Sep 2022 06:00:00 -0400
21	pubmed:36135710	Geographically Associated Fungus-Bacterium Interactions Contribute to the Formation of Geography-Dependent Flavor during High-Complexity Spontaneous Fermentation	Yuwei Tan Hai Du Hongxia Zhang Chen Fang Guangyuan Jin Shuang Chen Qun Wu Yan Zhang Menghui Zhang Yan Xu	Fermented foods often have attractive flavor characteristics to meet various human demands. An ever-challenging target is the production of fermented foods with equal flavor profiles outside the product's origin. However, the formation of geography-dependent flavor in high-complexity fermentations remains poorly understood. Here, taking Chinese liquor (baijiu) fermentation as an example, we collected 403 samples from 9 different locations in China across a latitude range of 27°N to 37°N. We...	pmid:36135710 doi:10.1128/spectrum.01844-22	Thu, 22 Sep 2022 06:00:00 -0400
22	pubmed:36135762	Gut and Gill-Associated Microbiota of the Flatfish European Plaice (*Pleuronectes platessa*): Diversity, Metabolome and Bioactivity against Human and Aquaculture Pathogens	Marjan Ghotbi Ole Kelting Martina Blümel Deniz Tasdemir	Similar to other marine holobionts, fish are colonized by complex microbial communities that promote their health and growth. Fish-associated microbiota is emerging as a promising source of bioactive metabolites. Pleuronectes platessa (European plaice, plaice), a flatfish with commercial importance, is common in the Baltic Sea. Here we used a culture-dependent survey followed by molecular identification to identify microbiota associated with the gills and the gastrointestinal tract (GIT) of P....	pmid:36135762 doi:10.3390/md20090573	Thu, 22 Sep 2022 06:00:00 -0400
23	pubmed:36136109	Transcriptome and metabolome analyses reveal the interweaving of immune response and metabolic regulation in pelvic organ prolapse	Xia Yu Ying Chen Li He Hong Liu Zhenglin Yang Yonghong Lin	CONCLUSIONS: Our findings demonstrate that the immune response and metabolic regulatory pathways are intertwined in POP and might provide new therapeutic targets.	pmid:36136109 doi:10.1007/s00192-022-05357-5	Thu, 22 Sep 2022 06:00:00 -0400

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24	pubmed:36136309	Identification of Inflammatory Proteomics Networks of Toll-like Receptor 4 through Immunoprecipitation-Based Chemical Cross-Linking Proteomics	A D A Shahinuzzaman Abu Hena Mostafa Kamal Jayanta K Chakrabarty Aurchie Rahman Saiful M Chowdhury	Toll-like receptor 4 (TLR4) is a receptor on an immune cell that can recognize the invasion of bacteria through their attachment with bacterial lipopolysaccharides (LPS). Hence, LPS is a pro-immune response stimulus. On the other hand, statins are lipid-lowering drugs and can also lower immune cell responses. We used human embryonic kidney (HEK 293) cells engineered to express HA-tagged TLR-4 upon treatment with LPS, statin, and both statin and LPS to understand the effect of pro- and...	pmid:36136309 doi:10.3390/proteomes10030031	Thu, 22 Sep 2022 06:00:00 -0400
25	pubmed:36136311	Viral Biomarker Detection and Validation Using MALDI Mass Spectrometry Imaging (MSI)	Matthew B O'Rourke Ben R Roediger Christopher J Jolly Ben Crossett Matthew P Padula Phillip M Hansbro	(1) Background: MALDI imaging is a technique that still largely depends on time of flight (TOF)-based instrument such as the Bruker UltrafleXtreme. While capable of performing targeted MS/MS, these instruments are unable to perform fragmentation while imaging a tissue section necessitating the reliance of MS1 values for peptide level identifications. With this premise in mind, we have developed a hybrid bioinformatic/image-based method for the identification and validation of viral biomarkers....	pmid:36136311 doi:10.3390/proteomes10030033	Thu, 22 Sep 2022 06:00:00 -0400
26	pubmed:36136458	Embryonic Arsenic Exposure Triggers Long-Term Behavioral Impairment with Metabolite Alterations in Zebrafish	Noraini Abu Bakar Wan Norhamidah Wan Ibrahim Che Azurahanim Che Abdullah Nurul Farhana Ramlan Khozirah Shaari Shamarina Shohaimi Ahmed Mediani Nurrul Shaqinah Nasruddin Cheol-Hee Kim Siti Munirah Mohd Faudzi	Arsenic trioxide (As(2)O(3)) is a ubiquitous heavy metal in the environment. Exposure to this toxin at low concentrations is unremarkable in developing organisms. Nevertheless, understanding the underlying mechanism of its long-term adverse effects remains a challenge. In this study, embryos were initially exposed to As(2)O(3) from gastrulation to hatching under semi-static conditions. Results showed dose-dependent increased mortality, with exposure to 30-40 µM As(2)O(3) significantly reducing...	pmid:36136458 doi:10.3390/toxics10090493	Thu, 22 Sep 2022 06:00:00 -0400
27	pubmed:36136459	A Metabolomic Approach to Assess the Toxicity of the Olive Tree Endophyte *Bacillus* sp. PTA13 Lipopeptides to the Aquatic Macrophyte *Lemna minor* L	Evgenia-Anna Papadopoulou Katerina Giaki Apostolis Angelis Alexios-Leandros Skaltsounis Konstantinos A Aliferis	Pesticides represent a major human input into the ecosystem, posing a serious risk to non-target organisms. Therefore, there is pressure toward the reduction in their use and the discovery of alternative sources of bioactivity. Endophytic microorganisms represent a source of bioactivity, whose potential for plant protection has been recently established. In this context, an olive tree endophytic Bacillus sp. was isolated, exhibiting superior antifungal activity, mainly attributed to its major...	pmid:36136459 doi:10.3390/toxics10090494	Thu, 22 Sep 2022 06:00:00 -0400
28	pubmed:36136671	Serum Amino Acids Imbalance in Canine Chronic Hepatitis: Results in 16 Dogs	Verena Habermaass Eleonora Gori Francesca Abramo Francesco Bartoli Alessio Pierini Chiara Mariti Ilaria Lippi Veronica Marchetti	In humans, chronic liver disease may cause alterations in amino acids (AAs) metabolism, with serum branched-chain AAs (BCAAs) decreasing and aromatic AAs (AAAs) increasing. A reduced Fischer ratio (BCAAs/AAAs) has been found to be associated with hepatic fibrosis and is useful for assessing prognosis in human patients. In veterinary medicine, few studies have been performed, and in contrast to human patients, dogs with different kinds of hepatopathy tend to show both increased AAAs and BCAAs. In...	pmid:36136671 doi:10.3390/vetsci9090455	Thu, 22 Sep 2022 06:00:00 -0400

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29	pubmed:36136944	[The structure of blood gut microbiota markers in athletes and their relationship with the diet](#)	T V Bragina S A Sheveleva E V Elizarova S M Rykova V A Tutelyan	It is known that under conditions of ultra-high physical activity and a specific diet, the state of the microbiota plays a significant role in maintaining the health, metabolic and energy status of athletes. The purpose of the study was to evaluate the composition of blood microbial markers in professional football players and physically active people and their correlation with diets in order to substantiate recommendations for their optimization. Material and methods. In a cross-sectional study...	pmid:36136944 doi:10.33029/0042-8833-2022-91-4-35-46	Thu, 22 Sep 2022 06:00:00 -0400
30	pubmed:36137002	[Primary and metastatic tumors exhibit systems-level differences in dependence on mitochondrial respiratory function](#)	Neal K Bennett Hiroki J Nakaoka Danny Laurent Ross A Okimoto Yoshitaka Sei Andrew E Horvai Trever G Bivona Johanna Ten Hoeve Thomas G Graeber Ken Nakamura Jean L Nakamura	The Warburg effect, aerobic glycolysis, is a hallmark feature of cancer cells grown in culture. However, the relative roles of glycolysis and respiratory metabolism in supporting in vivo tumor growth and processes such as tumor dissemination and metastatic growth remain poorly understood, particularly on a systems level. Using a CRISPRi mini-library enriched for mitochondrial ribosomal protein and respiratory chain genes in multiple human lung cancer cell lines, we analyzed in vivo metabolic...	pmid:36137002 doi:10.1371/journal.pbio.3001753	Thu, 22 Sep 2022 06:00:00 -0400
31	pubmed:36137157	[Untargeted saliva metabolomics by liquid chromatography-Mass spectrometry reveals markers of COVID-19 severity](#)	Cecile F Frampas Katie Longman Matt Spick Holly-May Lewis Catia D S Costa Alex Stewart Deborah Dunn-Walters Danni Greener George Evetts Debra J Skene Drupad Trivedi Andy Pitt Katherine Hollywood Perdita Barran Melanie J Bailey	CONCLUSIONS: In this exploratory work, we found that saliva metabolomics and in particular amino acids can be capable of separating high severity COVID-19 patients from low severity COVID-19 patients. This expands the atlas of COVID-19 metabolic dysregulation and could in future offer the basis of a quick and non-invasive means of sampling patients, intended to supplement existing clinical tests, with the goal of offering timely treatment to patients with potentially poor outcomes.	pmid:36137157 doi:10.1371/journal.pone.0274967	Thu, 22 Sep 2022 06:00:00 -0400
32	pubmed:36137231	[IDSL.UFA Assigns High-Confidence Molecular Formula Annotations for Untargeted LC/HRMS Data Sets in Metabolomics and Exposomics](#)	Sadjad Fakouri Baygi Sanjay K Banerjee Praloy Chakraborty Yashwant Kumar Dinesh Kumar Barupal	Untargeted liquid chromatography/high-resolution mass spectrometry (LC/HRMS) assays in metabolomics and exposomics aim to characterize the small molecule chemical space in a biospecimen. To gain maximum biological insights from these data sets, LC/HRMS peaks should be annotated with chemical and functional information including molecular formula, structure, chemical class, and metabolic pathways. Among these, molecular formulas may be assigned to LC/HRMS peaks through matching theoretical and...	pmid:36137231 doi:10.1021/acs.analchem.2c00563	Thu, 22 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
33	pubmed:36137261	[Biosynthesis of the Isocoumarin Derivatives Fusamarins Is Mediated by the PKS8 Gene Cluster in Fusarium](#)	Anna K Atanasoff-Kardjalieff Bernhard Seidl Katharina Steinert Constantin G Daniliuc Rainer Schuhmacher Hans-Ulrich Humpf Svetlana Kalinina Lena Studt-Reinhold	Fusarium mangiferae causes the mango malformation disease (MMD) on young mango trees and seedlings resulting in economically significant crop losses. Next to this, F. mangiferae produces a vast array of secondary metabolites (SMs), including mycotoxins that may contaminate the harvest. Their production is tightly regulated at the transcriptional level. Here, we show that lack of the H3K9-specific histone methyltransferase, FmKmt1, influences the expression of the F. mangiferae polyketide...	pmid:36137261 doi:10.1002/cbic.202200342	Thu, 22 Sep 2022 06:00:00 -0400