metabolomics

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36095861	The pathophysiology of major depressive disorder through the lens of systems biology: Network analysis of the psycho-immune-neuroendocrine physiome	Nicolas J C Stapelberg Tuan A Bui Verena Mansour Susannah Johnson Grace Branjerdporn Sam Adhikary Kevin Ashton Nevin Taylor John P Headrick	CONCLUSION: The identified hubs have a high degree of connection and are known to play roles in the progression from health to MDD. These nodes represent strategic targets for therapeutic intervention or prevention. Future work is required to build a weighted and dynamic simulation of the network PINE.	pmid:36095861 doi:10.1016/j.jneuroim.2022.577959	Mon, 12 Sep 2022 06:00:00 -0400
2	pubmed:36096204	Exacerbation-prone pediatric asthma is associated with arginine, lysine, methionine pathway alterations	Kirsten A Cottrill Susan T Stephenson Ahmad F Mohammad Susan O Kim Nael A McCarty Rishikesan Kamaleswaran Anne M Fitzpatrick Joshua D Chandler	CONCLUSIONS: Several plasma metabolites are perturbed in children with exacerbation-prone asthma and are largely related to arginine, lysine, and methionine pathways. While validation is needed, plasma metabolites may be potential biomarkers for exacerbation-prone asthma in children.	pmid:36096204 doi:10.1016/j.jaci.2022.07.027	Mon, 12 Sep 2022 06:00:00 -0400
3	pubmed:36096239	Integrating Epigenetics and Metabolomics to Advance Treatments for Pulmonary Arterial Hypertension	A Dushani C U Ranasinghe Margaret A Schwarz	Pulmonary arterial hypertension (PAH) is a devastating vascular disease with multiple etiologies. Emerging evidence supports a fundamental role for epigenetic machinery and metabolism in the initiation and progression of PAH. Here, we summarize emerging epigenetic mechanisms that have been identified as contributors to PAH evolution, specifically, DNA methylation, histone modifications, and microRNAs. Furthermore, the interplay between epigenetics with metabolism is explored while new crosstalk	pmid:36096239 doi:10.1016/j.bcp.2022.115245	Mon, 12 Sep 2022 06:00:00 -0400
4	pubmed:36096433	Effect of dietary Spirulina (Arthrospira platensis) on the intestinal function of postweaned piglet: An approach combining proteomics, metabolomics and histological studies	Cátia F Martins David M Ribeiro Manolis Matzapetakis Mário A Pinho Josipa Kuleš Anita Horvati Nicolas Guillemin Peter David Eckersall João P B Freire André M de Almeida José A M Prates	The effect of dietary Spirulina (Arthrospira platensis) and CAZyme supplementation was assessed on the gut of weaned piglets, using an integrated NMR-metabolomics approach combined with Tandem Mass Tag labelled proteomics. Thirty weaned male piglets were assigned to one of the three following diets (n = 10): cereal and soybean meal basal diet (Control), basal diet with 10% Spirulina inclusion (SP) and SP diet supplemented with 0.01% lysozyme (SP + L). The experiment lasted 4 weeks and, upon	pmid:36096433 doi:10.1016/j.jprot.2022.104726	Mon, 12 Sep 2022 06:00:00 -0400
5	pubmed:36096642	Identification of HLA-E Binding Mycobacterium tuberculosis-Derived Epitopes through Improved Prediction Models	Paula Ruibal Kees L M C Franken Krista E van Meijgaarden Marjolein van Wolfswinkel Ian Derksen Ferenc A Scheeren George M C Janssen Peter A van Veelen Charlotte Sarfas Andrew D White Sally A Sharpe Fabrizio Palmieri Linda Petrone Delia Goletti Thomas Abeel Tom H M Ottenhoff Simone A Joosten	Tuberculosis (TB) remains one of the deadliest infectious diseases worldwide, posing great social and economic burden to affected countries. Novel vaccine approaches are needed to increase protective immunity against the causative agent Mycobacterium tuberculosis (Mtb) and to reduce the development of active TB disease in latently infected individuals. Donor-unrestricted T cell responses represent such novel potential vaccine targets. HLA-E-restricted T cell responses have been shown to play an	pmid:36096642 doi:10.4049/jimmunol.2200122	Mon, 12 Sep 2022 06:00:00 -0400

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6	pubmed:36097154	Polyvinyl chloride degradation by a bacterium isolated from the gut of insect larvae	Zhe Zhang Haoran Peng Dongchen Yang Guoqing Zhang Jinlin Zhang Feng Ju	Evidence for microbial degradation of polyvinyl chloride (PVC) has previously been reported, but little is known about the degrading strains and enzymes. Here, we isolate a PVC-degrading bacterium from the gut of insect larvae and shed light on the PVC degradation pathway using a multiomic approach. We show that the larvae of an insect pest, Spodoptera frugiperda, can survive by feeding on PVC film, and this is associated with enrichment of Enterococcus, Klebsiella and other bacteria in the	pmid:36097154 doi:10.1038/s41467-022-32903-y	Tue, 13 Sep 2022 06:00:00 -0400
7	pubmed:36097248	Combining Machine Learning with Metabolomic and Embryologic Data Improves Embryo Implantation Prediction	Aswathi Cheredath Shubhashree Uppangala Asha C S Ameya Jijo Vani Lakshmi R Pratap Kumar David Joseph Nagana Gowda G A Guruprasad Kalthur Satish Kumar Adiga	This study investigated whether combining metabolomic and embryologic data with machine learning (ML) models improve the prediction of embryo implantation potential. In this prospective cohort study, infertile couples (n=56) undergoing day-5 single blastocyst transfer between February 2019 and August 2021 were included. After day-5 single blastocyst transfer, spent culture medium (SCM) was subjected to metabolite analysis using nuclear magnetic resonance (NMR) spectroscopy. Derived metabolite	pmid:36097248 doi:10.1007/s43032-022-01071-1	Tue, 13 Sep 2022 06:00:00 -0400
8	pubmed:36097390	Fumarate mitigates disruption induced by fenpropathrin in the silkworm Bombyx mori (Lepidoptera): A metabolomics study	Xue-Yang Wang Zi-Qin Zhao Cheng-Xian Song Zhi-Hao Su Mu-Wang Li Yang-Chun Wu Byung Rae Jin Ming-Jie Deng	The silkworm Bombyx mori L. is a model organism of the order Lepidoptera. Understanding the mechanism of pesticide resistance in silkworms is valuable for Lepidopteran pest control. In this study, comparative metabolomics was used to analyze the metabolites of two silkworm strains with different pesticide resistance levels at 6, 12, and 24 h after feeding with fenpropathrin. Twenty-six of 27 metabolites showed significant differences after fenpropathrin treatment and were classified into six	pmid:36097390 doi:10.1111/1744-7917.13114	Tue, 13 Sep 2022 06:00:00 -0400
9	pubmed:36097398	Serum metabolomics using UPLC Q- Exactive MS/MS reveals the mechanism of improved effects of exercise training on COPD rats	Yan Du Jing Wu Yange Tian Lanxi Zhang Peng Zhao Jiansheng Li	Exercise training is the cornerstone component of pulmonary rehabilitation, which possesses the symptom-reducing, psychosocial, and health economic benefits for chronic obstructive pulmonary disease (COPD) patients. However, the potential mechanisms of action remain poorly understood. In this study, serum metabolomics based on UPLC Q-Exactive MS/MS was conducted to explore the metabolic changes of COPD rats, and the effects of exercise training on the improvement of COPD was further	pmid:36097398 doi:10.1002/bmc.5507	Tue, 13 Sep 2022 06:00:00 -0400
10	pubmed:36097410	Overall metabolic network analysis of urine in hyperlipidemic rats treated with Bidens bipinnata L	Shu-Jiao Li Yu-Qing Wang Guo Zhuang Xu Jiang Xiao-Yu Wang Dong Shui	Hyperlipidemia has been highlighted to be one of the most prominent and global chronic condition nowadays. Bidens bipinnata L. (BBL), a folk medicine in contemporary China, has the efficacy in treatment of hyperlipidemia (HLP) in China. Although some physiological and pathological function parameters of the hyperlipidemia have been investigated, little information about the changes of small metabolites in biofluids has been reported. In present study, global metabolic profiling with high	pmid:36097410 doi:10.1002/bmc.5509	Tue, 13 Sep 2022 06:00:00 -0400