Recent patents in metabolomics and metabolic engineering

Patent number	Description	Assignee	Inventor	Date
US 9,944,659	Boron-containing diacylhydrazines having a specific formula I and the pharmaceutically acceptable salts and solvates thereof, as set forth in the specification. Also, the use of boron-containing diacylhydrazines in ecdysone receptor-based inducible gene expression systems. Useful for applications such as gene therapy, treatment of disease, large-scale production of proteins and antibodies, cell-based screening assays, functional genomics, proteomics, metabolomics, and regulation of traits in transgenic organisms, where control of gene expression levels is desirable.	Intrexon (Blacksburg, VA, USA)	James RA, Chellappan SK, Hormann RE	4/17/2018
US 9,646,139	Statistically significant methods for metabolomics data analysis that incorporate the structure information of metabolites. Understanding of disease pathogenesis and drug effects, as well as prediction of variation in drug response can be achieved by analyzing quantitative data measuring metabolomics biomarker profiles from biological samples. The comprising methods may include retrieving information of metabolites' chemical structures, converting them into structural data, and integrating the structural data into analysis of metabolite concentration data to improve the evaluation of metabolites and to better identify metabolomics signatures.	Zhu H, Luo M	Zhu H, Luo M	5/9/2017
US 9,598,355	Diacylhydrazine ligands and chiral diacylhydrazine ligands for use with ecdysone receptor-based inducible gene expression systems. Useful for applications such as gene therapy, large-scale production of proteins and antibodies, cell-based screening assays, functional genomics, proteomics, metabolomics, and regulation of traits in transgenic organisms, where control of gene expression levels is desirable.	Intrexon (Blacksburg, VA, USA)	Hormann R, Li B	3/21/2017
US 9,594,880	Methods for quantification of metabolite concentrations in metabolomics studies, which addresses the difficulties in quantification through 1D peak integrals due to significant peak overlaps in metabolomics samples.	Florida State University Research Foundation (Tallahassee, FL, USA)	Bruschweiler R, Bingol K	3/14/2017
US 8,940,497	A multidimensional profiling strategy that combines activity-based proteomics and metabolomics was used to determine that an active protein, which is a previously uncharacterized enzyme highly elevated in aggressive cancer cells, serves as a central node in an ether-lipid-signaling network that bridges platelet-activating factor and the lysophospholipids.	The Scripps Research Institute (La Jolla, CA, USA)	Cravatt BF, Chiang KP, Niessen S, Saghatelian A	1/27/2015
US 8,703,424	Biomarker profiles of metabolites and methods for screening chemical compounds including pharmaceutical agents, lead and candidate drug compounds and other chemicals using human stem-like cells (hSLCs) or lineage-specific cells produced therefrom. Useful for testing toxicity, particularly developmental toxicity and detecting teratogenic effects of such chemical compounds, specifically, a more predictive developmental toxicity model, based on an *in vitro* method that utilizes both hSLCs and metabolomics to discover biomarkers of developmental toxicity.	Stemina Biomarker Discovery (Madison, WI, USA)	West PR, Weir-Hauptman AM, Smith AM, Donley ELR	4/22/2014
US 7,847,245	A shotgun metabolomics approach using MALDI-tandem mass spectrometry developed for the rapid analysis of cellular metabolites. Through the use of neutral organic solvents to inactivate endogenous enzyme activities, multiplexed extraction conditions and combinatorial alterations in matrix stereoelectronic composition and analyte interactions, multiple suites of metabolites were directly ionized and quantitated directly from biologic extracts without the need for prior chromatographic separation.	Platomics (Chesterfield, MO, USA)	Gross RW, Sun G, Han X	12/7/2010
US 7,804,062	A method of obtaining pure component mass spectra or pure peak elution profiles from mass spectra of a mixture of components, involving estimating number of components in the mixture, filtering noise, and extracting individual component mass spectra or pure peak elution profiles using blind entropy minimization with direct optimization. The method may be applied to deconvolution of pure GC/MS spectra of overlapping or partially overlapping isotopologues or other compounds, separation of overlapping or partially overlapping compounds in proteomics or metabolomics mass spectrometry applications.	National Research Council of Canada (Ottawa, Ontario, Canada)	Meija J, Mester Z	9/28/2010

Source: United States Patent and Trademark Office (http://www.uspto.gov).