



高分辨质谱系统

代谢/脂质组学发表文章目录(第一卷)



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代谢组学

一、疾病代谢组学

1. Farnesoid X Receptor Regulation of the NLRP3 Inflammasome Underlies Cholestasis-Associated Sepsis. *Cell Metab* 2017, doi:10.1016/j.cmet.2017.03.007 影响因子: 20.565
2. A large-scale, multi-center serum metabolite biomarkers identification study for the early detection of hepatocellular carcinoma. *HEPATOLOGY* 2017, doi: 10.1002/hep.29561 影响因子: 14.079
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4. Polo-like kinase 1 coordinates biosynthesis during cell cycle progression by directly activating pentose phosphate pathway. *Nat Commun* 2017, DOI: 10.1038/s41467-017-01647-5 影响因子: 12.124
5. Polyunsaturated fatty acids metabolism, purine metabolism and inosine as potential independent diagnostic biomarkers for major depressive disorder in children and adolescents. *Mol Psych* 2018, Doi:10.1038/s41380-018-0047-z 影响因子: 11.64
6. Hominoid-specific enzyme GLUD2 promotes growth of IDH1R132H glioma. *PNAS* 2014, doi:10.1073/pnas.1409653111 影响因子: 9.661
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8. Impaired pentose phosphate pathway in the development of 3D MCF-7 cells mediated intracellular redox disturbance and multi-cellular resistance without drug induction. *Redox Biology* 2018, Doi:10.1016/j.re-

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10. Integration of Metabolomics and Transcriptomics Reveals Major Metabolic Pathways and Potential Biomarker Involved in Prostate Cancer. *Mol Cell Proteomics* 2016, Doi: 10.1074/mcp.M115.052381 影响因子: 5.232
11. Identification of SPOP related metabolic pathways in prostate cancer. *Oncotarget* 2017, Vol. 8, (No. 61), pp: 103032-103046 影响因子: 5.168
12. Repression of intestinal transporters and FXR-FGF15 signaling explains bile acids dysregulation in experimental colitis associated colon cancer. *Oncotarget* 2017, Vol. 8, (No. 38), pp: 63665-63679 影响因子: 5.168
13. Untargeted serum metabolomics study of psoriasis vulgaris based on ultra-performance liquid chromatography coupled to mass spectrometry. *Oncotarget* 2017, Vol. 8, (No. 56), pp: 95931-95944 影响因子: 5.168
14. Vitamin C Deficiency Activates the Purine Nucleotide Cycle in Zebrafish. *JBC* 2011, Doi: 10.1074/jbc.M111.316018 影响因子: 4.25
15. Serum Monounsaturated Triacylglycerol Predicts Steatohepatitis in Patients with Non-alcoholic Fatty Liver Disease and Chronic Hepatitis B. *Sci Rep* 2017, Doi:10.1038/s41598-017-11278-x 影响因子: 4.122
16. Arteriovenous Blood Metabolomics: A Readout of Intra-Tissue Metabostasis. *Sci Rep* 2015, Doi: 10.1038/srep12757 影响因子: 4.122
17. Serum Metabolomics Study and Eicosanoid Analysis of Childhood Atopic Dermatitis Based on Liquid Chromatography-Mass Spectrometry. *J Proteome Res* 2014, Doi:10.1021/pr5007069 影响因子: 3.95
18. Untargeted Mass Spectrometry-Based Metabolomic Profiling of Pleural

- Effusions: Fatty Acids as Novel Cancer Biomarkers for Malignant Pleural Effusions. *J Proteome Res* 2014, Doi:10.1021/pr5003774 影响因子: 3.95
19. Discovery and Validation of Plasma Biomarkers for Major Depressive Disorder Classification Based on Liquid Chromatography-Mass Spectrometry. *J Proteome Res* 2015, DOI: 10.1021/acs.jproteome.5b00144 影响因子: 3.95
 20. Comparative Metabolomics Analysis of Cervicitis in Human Patients and a Phenol Mucilage-Induced Rat Model Using Liquid Chromatography Tandem Mass Spectrometry. *Front Pharmacol* 2018, Doi: 10.3389/fphar.2018.00282 影响因子: 3.83
 21. Serum metabolomics for early diagnosis of esophageal squamous cell carcinoma by UHPLC-QTOF/MS. *Metabolomics* 2016, DOI 10.1007/s11306-016-1050-5 影响因子: 3.511
 22. Combined obeticholic acid and apoptosis inhibitor treatment alleviates liver fibrosis. *Acta Pharm Sin B* 2018, Doi: 10.1016/j.apsb.2018.11.004 影响因子: 3.223
 23. Mass-Spectrometric Detection of Omega-Oxidation Products of Aliphatic Fatty Acids in Exhaled Breath. *Anal Chem* 2017, DOI: 10.1021/acs.anal-chem.7b02092 影响因子: 6.32
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 27. changes of the plasma metabolome of newly born piglets subjected to

postnatal hypoxia and resuscitation with air. *Pediatric Res* 2016, <https://www.nature.com/articles/pr201666> 影响因子: 2.882

28. Characterization of The Human Tear Metabolome by LC MS/MS. *J Proteome Res* 2011, doi:10.1021/pr2004874 影响因子: 3.95
29. Discovering Regulated Metabolite Families in Untargeted Metabolomics Studies. *Anal Chem* 2016, DOI: 10.1021/acs.analchem.6b01569 影响因子: 6.32

二、中药代谢组学

1. Assessment of Peeling of Astragalus Roots using ¹H NMR and UPLC-MS-based Metabolite Profiling. *J Agric Food Chem* 2013, DOI: 10.1021/jf4026103 影响因子: 3.412
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3. Metabolic Pathway Extension Approach for Metabolomic Biomarker Identification. *Anal Chem* 2017, DOI: 10.1021/acs.analchem.6b03757 影响因子: 6.32
4. Transcriptome Profiling of Two Ornamental and Medicinal Papaver Herb-snt. *J Mol Sci* 2018, doi:10.3390/ijms19103192 影响因子: 3.687
5. Analysis of Chemical Variations between Crude and Salt-Processed *Aemannarhenae rhizoma* Using Ultra-High-Performance Liquid Chromatography–Mass Spectrometry Methods. *Molecules* 2018, doi:10.3390/molecules23010023 影响因子: 3.098
6. Transcriptional Profiles of Secondary Metabolite Biosynthesis Genes and Cytochromes in the Leaves of Four Papaver Species. *Data* 2018, doi:10.3390/data3040055

7. Saffron authentication based on liquid chromatography high resolution tandem mass spectrometry and multivariate data analysis. Food Chem 2016, doi: 10.1016/j.foodchem.2016.01.003 影响因子: 4.946
8. Integrative analysis of proteomics and metabolomics of anaphylactoid reaction induced by Xuesaitong injection. J Chromatogr A 2015, doi:10.1016/j.chroma.2015.09.019 影响因子: 3.716
9. Identification and differentiation of major component sin three different “Sheng-ma” crude drug species by UPLC/Q-TOF-MS. Acta Pharm Sin B 2017, doi:10.1016/j.apsb.2016.11.002 影响因子: 3.223
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12. Metabolomics Strategy Using High Resolution Mass Spectrometry Reveals Novel Biomarkers and Pain-Relief Effect of Traditional Chinese Medicine Prescription Wu-Zhu-Yu Decoction Acting on Headache Modelling Rats. Molecules 2017, doi:10.3390/molecules22122110 影响因子: 3.098
13. A metabolomic strategy based on integrating headspace gas chromatography-mass spectrometry and liquid chromatography-mass spectrometry to differentiate the five cultivars of Chrysanthemum flower. RSC advance 2018, doi:10.1039/c7ra13503c 影响因子: 2.93

三、食品代谢组学

1. Arabinoxylan Attenuates Type 2 Diabetes by Improvement of Carbohydrate, Lipid, and Amino Acid Metabolism. Mol Nutr Food Res 2018, DOI:

10.1002/mnfr.201800222 影响因子: 5.151

2. Untargeted Metabolomic Screen Reveals Changes in Human Plasma Metabolite Profiles Following Consumption of Fresh Broccoli Sprouts. *Mol Nutr Food Res* 2018, DOI: 10.1002/mnfr.201700665 影响因子: 5.151
3. Untargeted metabolomics of fresh and heat treatment Tiger nut (*Cyperus esculentus* L.) milks reveals further insight into food quality and nutrition. *J Chromatogr A* 2017, doi:10.1016/j.chroma.2017.07.071 影响因子: 3.71
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5. Liquid chromatography–mass spectrometry-based metabolomics for authenticity assessment of fruit juices. *Metabolomics* 2011, DOI: 10.1007/s11306-011-0371-7 影响因子: 3.511
6. Ultrafast polyphenol metabolomics of red wines using microLC-MS/MS. *J Agric Food Chem* 2016, DOI: 10.1021/acs.jafc.5b04890 影响因子: 3.412
7. Metabolomic Approach for the Authentication of Berry Fruit Juice by Liquid Chromatography Quadrupole Time-of-Flight Mass Spectrometry Coupled to Chemometrics. *J Agric Food Chem* 2018, DOI: 10.1021/acs.jafc.8b01682 影响因子: 3.412
8. Metabolic fingerprinting based on high-resolution tandem mass spectrometry: a reliable tool for wine authentication? *Anal Bioanal Chem* 2014, 10.1007/s00216-014-7864-y 影响因子: 3.2
9. Metabolomics Study on the Toxicity of *Annona squamosa* by Ultrapformance Liquid-Chromatography High-Definition Mass Spectrometry Coupled with Pattern Recognition Approach and Metabolic Pathways Analysis. *J Ethnopharmacol* 2016, doi:10.1016/j.jep.2016.03.006 影响因子: 3.115

四、植物代谢组学

1. A systematic simulation of the effect of salicylic acid on sphingolipid 1 metabolism. *Front Plant Sci* 2014, doi: 10.1101/011676 影响因子: 3.678
2. Comparative Analysis of Phenolic Compound Characterization and Their Biosynthesis Genes between Two Diverse Bread Wheat (*Triticum aestivum*) Varieties Differing for Chapatti (Unleavened Flat Bread) Quality. *Front Plant Sci* 2016, doi: 10.3389/fpls.2016.01870 影响因子: 3.678
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4. Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights. *Nat Commun* 2014, DOI: 10.1038/ncomms4438 影响因子: 12.124
5. Rewiring of the Fruit Metabolome in Tomato Breeding. *Cell* 2018, doi:10.1016/j.cell.2017.12.019 影响因子: 30.41
6. A systematic simulation of the effect of salicylic acid on sphingolipid metabolism. *Front Plant Sci* 2015, doi:10.3389/fpls.2015.00186 影响因子: 3.678

五、环境代谢组学 (环境毒理)

1. Monoethylhexyl Phthalate Elicits an Inflammatory Response in Adipocytes Characterized by Alterations in Lipid and Cytokine Pathways. *Environ Health Perspec* 2017, doi:10.1289/EHP464. 影响因子: 8.309
2. Use of Metallomics and Metabolomics to Assess Metal Pollution in Doñana National Park (SW Spain). *Environ Sci Technol* 2014, doi:10.1021/es4057938 影响因子: 6.198
3. Metabolomic analysis to define and compare the effects of PAHs and oxygenated PAHs in developing zebrafish. *Environ Res* 2015, doi:10.1016/j.

envres.2015.05.009 影响因子: 4.732

4. Stereoselective bioaccumulation of chiral PCB 91 in earthworm and its metabolomic and lipidomic responses. *Environ Pollut* 2018, doi:10.1016/j.envpol.2018.03.060 影响因子: 4.358
5. Effects of low-levels of three hexabromocyclododecane diastereomers on the metabolic profiles of pak choi leaves using high-throughput untargeted metabolomics approach. *Environ Pollut* 2018, doi:10.1016/j.envpol.2018.07.062 影响因子: 4.358
6. Correlations in the elemental and metabolic profiles of the lichen *Dirinaria picta* after road traffic exposure. *Metallomics* 2017, DOI: 10.1039/c7mt00207f 影响因子: 4.069
7. UHPLC-Q-TOF/MS based plasma metabolomics revealed the metabolic perturbations by manganese exposure in rat models. *Metallomics* 2017, DOI: 10.1039/C7MT00007C 影响因子: 4.069
8. Nonylphenol Toxicity Evaluation and Discovery of Biomarkers in Rat Urine by a Metabolomics Strategy through HPLC-QTOF-MS. *Inter J Env Res Pub Heal* 2016, doi:10.3390/ijerph13050501 影响因子: 2.145

六、微生物代谢组学 (发酵)

1. Elucidation of the biosynthesis of carnosic acid and its reconstitution in yeast. *Nat Commun* 2016, DOI: 10.1038/ncomms12942 影响因子: 12.124
2. Perturbations of tyrosine metabolism promote the indolepyruvate pathway via tryptophan in host and microbiome. *Mol Genet Metab* 2015, doi: 10.1016/j.ymgme.2015.01.005 影响因子: 3.774
3. Synthetic multispecies microbial communities reveals shifts in secondary metabolism and facilitates cryptic natural product discovery. *Environ Micro-*

biol 2017, DOI: 10.1111/1462-2920.13858 影响因子: 4.974

4. TiO₂-Assisted Laser Desorption/Ionization Mass Spectrometry for Rapid Profiling of Candidate Metabolite Biomarkers from Antimicrobial-Resistant Bacteria. *Anal Chem* 2018, DOI: 10.1021/acs.analchem.7b04565 影响因子: 6.32
5. Prediction and quantification of bioactive microbiota metabolites in the mouse gut. *Nat Commun* 2014, DOI: 10.1038/ncomms6492 影响因子: 12.124

七、代谢组学方法学

1. Metabolomic spectral libraries for data-independent SWATH liquid chromatography mass spectrometry acquisition. *Anal Bioanal Chem* 2018, doi:10.1007/s00216-018-0860-x 影响因子: 3.2
2. Optimization of large-scale pseudotargeted metabolomics method based on liquid chromatography-mass spectrometry. *J Chromatogr A* 2016, doi:10.1016/j.chroma.2016.01.078 影响因子: 3.71
3. An alignment algorithm for LC-MS-based metabolomics dataset assisted by MS/MS. *Chim Acta* 2017, doi: 10.1016/j.aca.2017.07.058 影响因子: 5.12
4. Integrated Quantification and Identification of Aldehydes and Ketones in Biological Samples. *Anal Chem* 2014, doi:10.1021/ac500810r 影响因子: 6.32
5. MetDIA: Targeted Metabolite Extraction of Multiplexed MS/MS Spectra Generated by Data-Independent Acquisition. *Anal Chem* 2016, 影响因子: 6.32
6. Customized consensus spectral library building for untargeted quantitative metabolomics analysis using data independent acquisition mass spectrom-

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7. A Comprehensive Strategy to Construct In-house Database for Accurate and Batch Identification of Small Molecular Metabolites. *Anal Chem* 2018, DOI: 10.1021/acs.analchem.8b01482 影响因子: 6.32
 8. MRM-Ion Pair Finder: a systematic approach to transform nontargeted mode to pseudo-targeted mode for metabolomics study based on liquid chromatography-mass spectrometry. *Anal Chem* 2015, DOI: 10.1021/acs.analchem.5b00615 影响因子: 6.32
 9. Facile Synthesis of Boronate-Decorated Polyethyleneimine-Grafted Hybrid Magnetic Nanoparticles for the Highly Selective Enrichment of Modified Nucleosides and Ribosylated Metabolites. *Anal Chem* 2013, doi:10.1021/ac402979w 影响因子: 6.32
 10. Autonomous Metabolomics for Rapid Metabolite Identification in Global Profiling. *Anal Chem* 2015, DOI: 10.1021/ac5025649 影响因子: 6.32
 11. MS-DIAL: data-independent MS/MS deconvolution for comprehensive metabolome analysis. *Nature method* 2015, doi:10.1038/nmeth.33932 影响因子: 9.886

脂质组学

一、疾病脂质组学

1. The cold-induced lipokine 12,13-diHOME promotes fatty acid transport into brown adipose tissue. *Nat Med* 2017, doi:10.1038/nm.4297. 影响因子 32.621
2. SF-1 expression in the hypothalamus is required for beneficial metabolic effects of exercise. *Life* 2016, DOI: 10.7554/eLife.18206.001 影响因子: 7.616
3. A high fat diet rich in saturated and mono-unsaturated fatty acids induces disturbance of thyroid lipid profile and hypothyroxinemia in male rats. *Mol Nutr Food Res* 2018, doi:10.1002/mnfr.201700599. 影响因子: 5.151
4. Altered Lipid Metabolism in Recovered SARS Patients Twelve Years after Infection. *Sci Rep* 2017, Doi:10.1038/s41598-017-09536-z 影响因子: 4.122
5. Integration of lipidomics and transcriptomics unravels aberrant lipid metabolism and defines cholesteryl oleate as potential biomarker of prostate cancer. *Sci Rep* 2016, DOI: 10.1038/srep20984 影响因子: 4.122
6. Plasma Lipidomics Investigation of Hemodialysis Effects by Using Liquid Chromatography-Mass Spectrometry. *J Proteome Res* 2016, DOI: 10.1021/acs.jproteome.6b00170 影响因子: 3.95
7. Altered levels of serum sphingomyelin and ceramide containing distinct acyl chains in young obese adults. *Nutr Diabetes* 2014, doi:10.1038/nutd.2014.38 影响因子: 3.534
8. Absolute quantitative lipidomics reveals lipidome-wide alterations in aging brain. *Metabolomics* 2018, Doi:10.1007/s11306-017-1304-x 影响因子: 3.511
9. Plasma lipidomics reveals potential lipid markers of major depressive disorder.

- der. Anal Bioanal Chem 2016, DOI 10.1007/s00216-016-9768-5 影响因子: 3.2
10. Early lipid changes in acute kidney injury using SWATH lipidomics coupled with MALDI tissue imaging. Am J Physiol Ren Physiol 2016, DOI: 10.1152/ajprenal.00100.2016 影响因子: 3.164
 11. Novel function of vitamin E in regulation of zebrafish (Danio rerio) brain lysophospholipids discovered using lipidomics. J Lipid Res 2015, DOI 10.1194/jlr.M058941 影响因子: 4.81
 12. Comparative Lipidomics of Caenorhabditis elegans Metabolic Disease Models by SWATH Non-Targeted Tandem Mass Spectrometry. Metabolites 2015, doi: 10.3390/metabo5040677
 13. Hyperoxidation of ether-linked phospholipids accelerates neutrophil extracellular trap formation. Sci Rep 2017, DOI:10.1038/s41598-017-15668-z 影响因子: 4.122
 14. Lipidomics Suggests a New Role for Ceramide Synthase in Phagocytosis. ACS Chem Biol 2018, DOI: 10.1021/acscchembio.8b00438 影响因子: 4.592
 15. Novel approach in LC-MS/MS using MRM to generate a full profile of acyl-CoAs: discovery of acyl-dephospho-CoAs. J Lipid Res 2014, doi: 10.1194/jlr.D045112 影响因子: 4.81
 16. The lipid profile of brown adipose tissue is sex-specific in mice. Biochim Biophys Acta 2014, doi:10.1016/j.bbalip.2014.08.003 影响因子: 5.018
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 18. Transformation-Associated Changes in Sphingolipid Metabolism Sensitize Cells to Lysosomal Cell Death Induced by Inhibitors of Acid Sphingomyelinase. Cancer Cell 2013, <http://dx.doi.org/10.1016/j.ccr.2013.08.003> 影响因子: 27.047

二、植物/食品脂质组学

1. High-mass-resolution MALDI Mass spectrometry imaging reveals detailed spatial distribution of metabolite and lipids in roots of barley seedling in response to salinity stress . *Metabolomics* 2018, doi:10.1007/s11306-018-1359-3 影响因子: 3.511
2. Lipidomics and RNA-Seq Study of Lipid Regulation in *Aphis gossypii* parasitized by *Lysiphlebia japonica*. *Sci Rep* 2017, DOI:10.1038/s41598-017-01546-1 影响因子: 4.122
3. Profiling of Omega-Polyunsaturated Fatty Acids and Their Oxidized Products in Salmon after Different Cooking Methods. *Antioxidants* 2018, doi:10.3390/antiox7080096 影响因子: 6.53

三、脂质组学方法学

1. Retention Time Prediction Improves Identification in Nontargeted Lipidomics Approaches *Anal Chem* 2015, DOI: 10.1021/acs.analchem.5b01139 影响因子: 6.32
2. Novel approach in LC-MS/MS using MRM to generate a full profile of acyl-CoAs: discovery of acyl-dephospho-CoAs. *J Lipid Res* 2013, DOI 10.1194/jlr.D045112 影响因子: 4.81
3. A novel stop-flow two-dimensional liquid chromatography–mass spectrometry method for lipid analysis. *J Chromatogr A* 2013, doi:10.1016/j.chroma.2013.10.069 影响因子: 3.71
4. Post acquisition data processing techniques for lipid analysis by quadrupole time-of-flight mass spectrometry. *J Chromatogr B* 2012, <http://dx.doi.org/10.1016/j.jchromb.2012.08.001> 影响因子: 2.441

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