

Shuzhao Li

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

64

papers

6,884

citations

30

h-index

73

g-index

73

ext. papers

10,021

ext. citations

10

avg. IF

6.25

L-index

#	Paper	IF	Citations
64	MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights. <i>Nucleic Acids Research</i> , 2021 , 49, W388-W396	20.1	393
63	A Practical Guide to Metabolomics Software Development. <i>Analytical Chemistry</i> , 2021 , 93, 1912-1923	7.8	10
62	Large scale enzyme based xenobiotic identification for exposomics. <i>Nature Communications</i> , 2021 , 12, 5418	17.4	4
61	Clinical recovery of <i>Macaca fascicularis</i> infected with <i>Plasmodium knowlesi</i> . <i>Malaria Journal</i> , 2021 , 20, 486	3.6	1
60	MetaboAnalystR 3.0: Toward an Optimized Workflow for Global Metabolomics. <i>Metabolites</i> , 2020 , 10,	5.6	182
59	Cloud-based archived metabolomics data: A resource for in-source fragmentation/annotation, meta-analysis and systems biology. <i>Analytical Science Advances</i> , 2020 , 1, 70-80	1.1	1
58	Early Pregnancy Serum Metabolite Profiles Associated with Hypertensive Disorders of Pregnancy in African American Women: A Pilot Study. <i>Journal of Pregnancy</i> , 2020 , 2020, 1515321	2.5	4
57	Metabolites and metabolic pathways associated with glucocorticoid resistance in pregnant African-American women. <i>Comprehensive Psychoneuroendocrinology</i> , 2020 , 1-2, 100001-100001	1.1	3
56	Reprint of "Metabolome Wide Association Study of Serum Poly and Perfluoroalkyl Substances (PFASs) in Pregnancy and Early Postpartum". <i>Reproductive Toxicology</i> , 2020 , 92, 120-128	3.4	3
55	Tryptophan catabolism reflects disease activity in human tuberculosis. <i>JCI Insight</i> , 2020 , 5,	9.9	19
54	A Bioinformatics Primer to Data Science, with Examples for Metabolomics. <i>Methods in Molecular Biology</i> , 2020 , 2104, 245-263	1.4	1
53	Transcriptomic and Metabolic Responses to a Live-Attenuated Vaccine. <i>Vaccines</i> , 2020 , 8,	5.3	5
52	Addressing the batch effect issue for LC/MS metabolomics data in data preprocessing. <i>Scientific Reports</i> , 2020 , 10, 13856	4.9	9
51	Metabolome Wide Association Study of serum DDT and DDE in Pregnancy and Early Postpartum. <i>Reproductive Toxicology</i> , 2020 , 92, 129-137	3.4	13
50	Regulating colonic dendritic cells by commensal glycosylated large surface layer protein A to sustain gut homeostasis against pathogenic inflammation. <i>Mucosal Immunology</i> , 2020 , 13, 34-46	9.2	5
49	Understanding mixed environmental exposures using metabolomics via a hierarchical community network model in a cohort of California women in 1960s. <i>Reproductive Toxicology</i> , 2020 , 92, 57-65	3.4	14
48	The Essential Toolbox of Data Science: Python, R, Git, and Docker. <i>Methods in Molecular Biology</i> , 2020 , 2104, 265-311	1.4	7

47	Pathway Analysis for Targeted and Untargeted Metabolomics. <i>Methods in Molecular Biology</i> , 2020 , 2104, 387-400	1.4	13
46	Network-Based Approaches for Multi-omics Integration. <i>Methods in Molecular Biology</i> , 2020 , 2104, 469-487		13
45	Antibiotics-Driven Gut Microbiome Perturbation Alters Immunity to Vaccines in Humans. <i>Cell</i> , 2019 , 178, 1313-1328.e13	56.2	205
44	Metabolic perturbations in classic galactosemia beyond the Leloir pathway: Insights from an untargeted metabolomic study. <i>Journal of Inherited Metabolic Disease</i> , 2019 , 42, 254-263	5.4	5
43	The Effect of Anticoagulants, Temperature, and Time on the Human Plasma Metabolome and Lipidome from Healthy Donors as Determined by Liquid Chromatography-Mass Spectrometry. <i>Biomolecules</i> , 2019 , 9,	5.9	20
42	Metabolome Wide Association Study of Serum Poly and Perfluoroalkyl Substances (PFASs) in Pregnancy and Early Postpartum. <i>Reproductive Toxicology</i> , 2019 , 87, 70-78	3.4	11
41	Distinct amino acid and lipid perturbations characterize acute versus chronic malaria. <i>JCI Insight</i> , 2019 , 4,	9.9	23
40	Neonatal intestinal immune regulation by the commensal bacterium, P. UF1. <i>Mucosal Immunology</i> , 2019 , 12, 434-444	9.2	12
39	Integrative metabolomics and transcriptomics signatures of clinical tolerance to Plasmodium vivax reveal activation of innate cell immunity and T cell signaling. <i>Redox Biology</i> , 2018 , 17, 158-170	11.3	43
38	Integrative analysis of transcriptomic and metabolomic data via sparse canonical correlation analysis with incorporation of biological information. <i>Biometrics</i> , 2018 , 74, 300-312	1.8	13
37	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. <i>Nucleic Acids Research</i> , 2018 , 46, W486-W494	20.1	2157
36	Plasma metabolomics in adults with cystic fibrosis during a pulmonary exacerbation: A pilot randomized study of high-dose vitamin D administration. <i>Metabolism: Clinical and Experimental</i> , 2017 , 70, 31-41	12.7	30
35	Metabolic Phenotypes of Response to Vaccination in Humans. <i>Cell</i> , 2017 , 169, 862-877.e17	56.2	157
34	Bioinformatics Tools for the Interpretation of Metabolomics Data. <i>Current Pharmacology Reports</i> , 2017 , 3, 374-383	5.5	28
33	Metabolome-wide association study of peripheral parasitemia in Plasmodium vivax malaria. <i>International Journal of Medical Microbiology</i> , 2017 , 307, 533-541	3.7	22
32	One Step Forward for Reducing False Positive and False Negative Compound Identifications from Mass Spectrometry Metabolomics Data: New Algorithms for Constructing Extracted Ion Chromatograms and Detecting Chromatographic Peaks. <i>Analytical Chemistry</i> , 2017 , 89, 8696-8703	7.8	137
31	Detailed Investigation and Comparison of the XCMS and MZmine 2 Chromatogram Construction and Chromatographic Peak Detection Methods for Preprocessing Mass Spectrometry Metabolomics Data. <i>Analytical Chemistry</i> , 2017 , 89, 8689-8695	7.8	86
30	Low-level maternal exposure to nicotine associates with significant metabolic perturbations in second-trimester amniotic fluid. <i>Environment International</i> , 2017 , 107, 227-234	12.9	12

29	mTOR regulates metabolic adaptation of APCs in the lung and controls the outcome of allergic inflammation. <i>Science</i> , 2017 , 357, 1014-1021	33.3	68
28	Commensal Propionibacterium strain UF1 mitigates intestinal inflammation via Th17 cell regulation. <i>Journal of Clinical Investigation</i> , 2017 , 127, 3970-3986	15.9	42
27	Computational Metabolomics: A Framework for the Million Metabolome. <i>Chemical Research in Toxicology</i> , 2016 , 29, 1956-1975	4	130
26	Training in metabolomics research. I. Designing the experiment, collecting and extracting samples and generating metabolomics data. <i>Journal of Mass Spectrometry</i> , 2016 , 51, 461-75	2.2	45
25	Training in metabolomics research. II. Processing and statistical analysis of metabolomics data, metabolite identification, pathway analysis, applications of metabolomics and its future. <i>Journal of Mass Spectrometry</i> , 2016 , 51, 535-548	2.2	37
24	Correlation of the lung microbiota with metabolic profiles in bronchoalveolar lavage fluid in HIV infection. <i>Microbiome</i> , 2016 , 4, 3	16.6	62
23	Blood transcriptomics and metabolomics for personalized medicine. <i>Computational and Structural Biotechnology Journal</i> , 2016 , 14, 1-7	6.8	52
22	The amino acid sensor GCN2 controls gut inflammation by inhibiting inflammasome activation. <i>Nature</i> , 2016 , 531, 523-527	50.4	152
21	Amino Acid Metabolism is Altered in Adolescents with Nonalcoholic Fatty Liver Disease-An Untargeted, High Resolution Metabolomics Study. <i>Journal of Pediatrics</i> , 2016 , 172, 14-19.e5	3.6	53
20	High-Resolution Metabolomics: Review of the Field and Implications for Nursing Science and the Study of Preterm Birth. <i>Biological Research for Nursing</i> , 2016 , 18, 12-22	2.6	20
19	Low-dose oral cadmium increases airway reactivity and lung neuronal gene expression in mice. <i>Physiological Reports</i> , 2016 , 4, e12821	2.6	21
18	Pathway and network analysis for high-throughput metabolomics 2015 , 112-124		
17	Molecular signatures of antibody responses derived from a systems biology study of five human vaccines. <i>Nature Immunology</i> , 2014 , 15, 195-204	19.1	429
16	Vaccine activation of the nutrient sensor GCN2 in dendritic cells enhances antigen presentation. <i>Science</i> , 2014 , 343, 313-317	33.3	154
15	Effects of age, sex, and genotype on high-sensitivity metabolomic profiles in the fruit fly, <i>Drosophila melanogaster</i> . <i>Aging Cell</i> , 2014 , 13, 596-604	9.9	86
14	Autophagy is essential for effector CD8(+) T cell survival and memory formation. <i>Nature Immunology</i> , 2014 , 15, 1152-61	19.1	271
13	Systems biological approaches to measure and understand vaccine immunity in humans. <i>Seminars in Immunology</i> , 2013 , 25, 209-18	10.7	46
12	Hybrid feature detection and information accumulation using high-resolution LC-MS metabolomics data. <i>Journal of Proteome Research</i> , 2013 , 12, 1419-27	5.6	62

11	Predicting network activity from high throughput metabolomics. <i>PLoS Computational Biology</i> , 2013 , 9, e1003123	5	431
10	Detailed mitochondrial phenotyping by high resolution metabolomics. <i>PLoS ONE</i> , 2012 , 7, e33020	3.7	40
9	Systems vaccinology: learning to compute the behavior of vaccine induced immunity. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2012 , 4, 193-205	6.6	65
8	An open-ended plea for the development of a global database of HIV vaccine responses. <i>Current Opinion in HIV and AIDS</i> , 2012 , 7, 10-6	4.2	1
7	Systems biology of vaccination for seasonal influenza in humans. <i>Nature Immunology</i> , 2011 , 12, 786-95	19.1	589
6	Linking probe thermodynamics to microarray quantification. <i>Physical Biology</i> , 2010 , 7, 048001; discussion 048002	3	3
5	Constructing a fish metabolic network model. <i>Genome Biology</i> , 2010 , 11, R115	18.3	39
4	Systems vaccinology. <i>Immunity</i> , 2010 , 33, 516-29	32.3	283
3	A microarray screen for direct targets of Zic1 identifies an aquaporin gene, aqp-3b, expressed in the neural folds. <i>Developmental Dynamics</i> , 2009 , 238, 1179-94	2.9	14
2	A competitive hybridization model predicts probe signal intensity on high density DNA microarrays. <i>Nucleic Acids Research</i> , 2008 , 36, 6585-91	20.1	18
1	The Xfeb gene is directly upregulated by Zic1 during early neural development. <i>Developmental Dynamics</i> , 2006 , 235, 2817-27	2.9	6