

# Shuzhao Li

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

11,952  
citations

156536

32  
h-index

116156

66  
g-index

73  
all docs

73  
docs citations

73  
times ranked

20991  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluating Co-occurrence as a Criterion for Identification of Undocumented Xenobiotic Exposures in Human Metabolomics. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
2	A Practical Guide to Metabolomics Software Development. <i>Analytical Chemistry</i> , 2021, 93, 1912-1923.	3.2	30
3	Enzyme-Based Chemical Identification for Metabolomics. <i>FASEB Journal</i> , 2021, 35, .	0.2	2
4	Pooling Strategies to Improve Throughput of High Resolution Mass Spectrometry-Based Analysis of Xenobiotic Metabolites Generated from Huh7 Human Hepatoma Cell Lines Transduced with P450 Enzymes. <i>FASEB Journal</i> , 2021, 35, .	0.2	0
5	MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights. <i>Nucleic Acids Research</i> , 2021, 49, W388-W396.	6.5	2,221
6	Large scale enzyme based xenobiotic identification for exposomics. <i>Nature Communications</i> , 2021, 12, 5418.	5.8	18
7	Clinical recovery of <i>Macaca fascicularis</i> infected with <i>Plasmodium knowlesi</i> . <i>Malaria Journal</i> , 2021, 20, 486.	0.8	8
8	Metabolome Wide Association Study of serum DDT and DDE in Pregnancy and Early Postpartum. <i>Reproductive Toxicology</i> , 2020, 92, 129-137.	1.3	25
9	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.	2.7	15
10	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.	1.3	26
11	Transcriptomic and Metabolic Responses to a Live-Attenuated <i>Francisella tularensis</i> Vaccine. <i>Vaccines</i> , 2020, 8, 412.	2.1	17
12	Addressing the batch effect issue for LC/MS metabolomics data in data preprocessing. <i>Scientific Reports</i> , 2020, 10, 13856.	1.6	28
13	MetaboAnalystR 3.0: Toward an Optimized Workflow for Global Metabolomics. <i>Metabolites</i> , 2020, 10, 186.	1.3	359
14	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.	1.2	3
15	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, 1-13.	1.1	8
16	Metabolites and metabolic pathways associated with glucocorticoid resistance in pregnant African-American women. <i>Comprehensive Psychoneuroendocrinology</i> , 2020, 1-2, 100001.	0.7	5
17	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.	1.3	7
18	The Essential Toolbox of Data Science: Python, R, Git, and Docker. <i>Methods in Molecular Biology</i> , 2020, 2104, 265-311.	0.4	11

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19	Pathway Analysis for Targeted and Untargeted Metabolomics. <i>Methods in Molecular Biology</i> , 2020, 2104, 387-400.	0.4	35
20	Network-Based Approaches for Multi-omics Integration. <i>Methods in Molecular Biology</i> , 2020, 2104, 469-487.	0.4	38
21	Tryptophan catabolism reflects disease activity in human tuberculosis. <i>JCI Insight</i> , 2020, 5, .	2.3	44
22	A Bioinformatics Primer to Data Science, with Examples for Metabolomics. <i>Methods in Molecular Biology</i> , 2020, 2104, 245-263.	0.4	6
23	Distinct amino acid and lipid perturbations characterize acute versus chronic malaria. <i>JCI Insight</i> , 2019, 4, .	2.3	46
24	Antibiotics-Driven Gut Microbiome Perturbation Alters Immunity to Vaccines in Humans. <i>Cell</i> , 2019, 178, 1313-1328.e13.	13.5	402
25	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.	1.7	10
26	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, 200.	1.8	33
27	Metabolome Wide Association Study of Serum Poly and Perfluoroalkyl Substances (PFASs) in Pregnancy and Early Postpartum. <i>Reproductive Toxicology</i> , 2019, 87, 70-78.	1.3	30
28	Neonatal intestinal immune regulation by the commensal bacterium, <i>P. UF1</i> . <i>Mucosal Immunology</i> , 2019, 12, 434-444.	2.7	17
29	Integrative metabolomics and transcriptomics signatures of clinical tolerance to <i>Plasmodium vivax</i> reveal activation of innate cell immunity and T cell signaling. <i>Redox Biology</i> , 2018, 17, 158-170.	3.9	59
30	Integrative Analysis of Transcriptomic and Metabolomic Data via Sparse Canonical Correlation Analysis with Incorporation of Biological Information. <i>Biometrics</i> , 2018, 74, 300-312.	0.8	19
31	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. <i>Nucleic Acids Research</i> , 2018, 46, W486-W494.	6.5	3,199
32	Metabolomics, Complex Exposures, and Multi-Omics Integration. <i>ISEE Conference Abstracts</i> , 2018, 2018, .	0.0	0
33	Plasma metabolomics in adults with cystic fibrosis during a pulmonary exacerbation: A pilot randomized study of high-dose vitamin D 3 administration. <i>Metabolism: Clinical and Experimental</i> , 2017, 70, 31-41.	1.5	50
34	Metabolic Phenotypes of Response to Vaccination in Humans. <i>Cell</i> , 2017, 169, 862-877.e17.	13.5	234
35	Bioinformatics Tools for the Interpretation of Metabolomics Data. <i>Current Pharmacology Reports</i> , 2017, 3, 374-383.	1.5	34
36	Metabolome-wide association study of peripheral parasitemia in <i>Plasmodium vivax</i> malaria. <i>International Journal of Medical Microbiology</i> , 2017, 307, 533-541.	1.5	25

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37	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.	3.2	275
38	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.	3.2	146
39	Low-level maternal exposure to nicotine associates with significant metabolic perturbations in second-trimester amniotic fluid. <i>Environment International</i> , 2017, 107, 227-234.	4.8	15
40	mTOR regulates metabolic adaptation of APCs in the lung and controls the outcome of allergic inflammation. <i>Science</i> , 2017, 357, 1014-1021.	6.0	98
41	Commensal <i>Propionibacterium</i> strain UF1 mitigates intestinal inflammation via Th17 cell regulation. <i>Journal of Clinical Investigation</i> , 2017, 127, 3970-3986.	3.9	67
42	Low-dose oral cadmium increases airway reactivity and lung neuronal gene expression in mice. <i>Physiological Reports</i> , 2016, 4, e12821.	0.7	30
43	Computational Metabolomics: A Framework for the Million Metabolome. <i>Chemical Research in Toxicology</i> , 2016, 29, 1956-1975.	1.7	191
44	Training in metabolomics research. I. Designing the experiment, collecting and extracting samples and generating metabolomics data. <i>Journal of Mass Spectrometry</i> , 2016, 51, 461-475.	0.7	64
45	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.	0.7	49
46	Correlation of the lung microbiota with metabolic profiles in bronchoalveolar lavage fluid in HIV infection. <i>Microbiome</i> , 2016, 4, 3.	4.9	83
47	Blood transcriptomics and metabolomics for personalized medicine. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 1-7.	1.9	73
48	The amino acid sensor GCN2 controls gut inflammation by inhibiting inflammasome activation. <i>Nature</i> , 2016, 531, 523-527.	13.7	221
49	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.	0.9	73
50	High-Resolution Metabolomics. <i>Biological Research for Nursing</i> , 2016, 18, 12-22.	1.0	26
51	Autophagy is essential for effector CD8+ T cell survival and memory formation. <i>Nature Immunology</i> , 2014, 15, 1152-1161.	7.0	367
52	Molecular signatures of antibody responses derived from a systems biology study of five human vaccines. <i>Nature Immunology</i> , 2014, 15, 195-204.	7.0	672
53	Vaccine Activation of the Nutrient Sensor GCN2 in Dendritic Cells Enhances Antigen Presentation. <i>Science</i> , 2014, 343, 313-317.	6.0	181
54	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.	3.0	107

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55	Systems biological approaches to measure and understand vaccine immunity in humans. <i>Seminars in Immunology</i> , 2013, 25, 209-218.	2.7	58
56	Hybrid Feature Detection and Information Accumulation Using High-Resolution LC-MS Metabolomics Data. <i>Journal of Proteome Research</i> , 2013, 12, 1419-1427.	1.8	81
57	Predicting Network Activity from High Throughput Metabolomics. <i>PLoS Computational Biology</i> , 2013, 9, e1003123.	1.5	697
58	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, 10-16.	1.5	1
59	Detailed Mitochondrial Phenotyping by High Resolution Metabolomics. <i>PLoS ONE</i> , 2012, 7, e33020.	1.1	44
60	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	78
61	Systems biology of vaccination for seasonal influenza in humans. <i>Nature Immunology</i> , 2011, 12, 786-795.	7.0	749
62	Systems Vaccinology. <i>Immunity</i> , 2010, 33, 516-529.	6.6	343
63	Linking probe thermodynamics to microarray quantification. <i>Physical Biology</i> , 2010, 7, 048001.	0.8	3
64	Constructing a fish metabolic network model. <i>Genome Biology</i> , 2010, 11, R115.	13.9	47
65	A microarray screen for direct targets of Zic1 identifies an aquaporin gene, <i>aqp3b</i> , expressed in the neural folds. <i>Developmental Dynamics</i> , 2009, 238, 1179-1194.	0.8	17
66	A competitive hybridization model predicts probe signal intensity on high density DNA microarrays. <i>Nucleic Acids Research</i> , 2008, 36, 6585-6591.	6.5	19
67	The Xfeb gene is directly upregulated by Zic1 during early neural development. <i>Developmental Dynamics</i> , 2006, 235, 2817-2827.	0.8	7