

Jianguo Xia

List of Publications by Year in descending order

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| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. <i>Nucleic Acids Research</i> , 2018, 46, W486-W494. | 6.5 | 3,199 |
| 2 | HMDB 3.0—The Human Metabolome Database in 2013. <i>Nucleic Acids Research</i> , 2012, 41, D801-D807. | 6.5 | 2,564 |
| 3 | MetaboAnalyst 3.0—making metabolomics more meaningful. <i>Nucleic Acids Research</i> , 2015, 43, W251-W257. | 6.5 | 2,493 |
| 4 | 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 |
| 5 | MetaboAnalyst: a web server for metabolomic data analysis and interpretation. <i>Nucleic Acids Research</i> , 2009, 37, W652-W660. | 6.5 | 1,674 |
| 6 | HMDB: a knowledgebase for the human metabolome. <i>Nucleic Acids Research</i> , 2009, 37, D603-D610. | 6.5 | 1,649 |
| 7 | Using MetaboAnalyst 4.0 for Comprehensive and Integrative Metabolomics Data Analysis. <i>Current Protocols in Bioinformatics</i> , 2019, 68, e86. | 25.8 | 1,644 |
| 8 | The Human Serum Metabolome. <i>PLoS ONE</i> , 2011, 6, e16957. | 1.1 | 1,378 |
| 9 | MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. <i>Nucleic Acids Research</i> , 2017, 45, W180-W188. | 6.5 | 1,359 |
| 10 | Using MetaboAnalyst 3.0 for Comprehensive Metabolomics Data Analysis. <i>Current Protocols in Bioinformatics</i> , 2016, 55, 14.10.1-14.10.91. | 25.8 | 1,293 |
| 11 | NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. <i>Nucleic Acids Research</i> , 2019, 47, W234-W241. | 6.5 | 1,191 |
| 12 | MetaboAnalyst 2.0—a comprehensive server for metabolomic data analysis. <i>Nucleic Acids Research</i> , 2012, 40, W127-W133. | 6.5 | 1,058 |
| 13 | Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data. <i>Nature Protocols</i> , 2020, 15, 799-821. | 5.5 | 1,019 |
| 14 | Web-based inference of biological patterns, functions and pathways from metabolomic data using MetaboAnalyst. <i>Nature Protocols</i> , 2011, 6, 743-760. | 5.5 | 976 |
| 15 | NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data. <i>Nature Protocols</i> , 2015, 10, 823-844. | 5.5 | 779 |
| 16 | Translational biomarker discovery in clinical metabolomics: an introductory tutorial. <i>Metabolomics</i> , 2013, 9, 280-299. | 1.4 | 765 |
| 17 | MetPA: a web-based metabolomics tool for pathway analysis and visualization. <i>Bioinformatics</i> , 2010, 26, 2342-2344. | 1.8 | 624 |
| 18 | MSEA: a web-based tool to identify biologically meaningful patterns in quantitative metabolomic data. <i>Nucleic Acids Research</i> , 2010, 38, W71-W77. | 6.5 | 582 |

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|----|---|------|-----------|
| 19 | Using MetaboAnalyst 5.0 for LC-MS/MS spectra processing, multi-omics integration and covariate adjustment of global metabolomics data. <i>Nature Protocols</i> , 2022, 17, 1735-1761. | 5.5 | 556 |
| 20 | MetaboAnalystR: an R package for flexible and reproducible analysis of metabolomics data. <i>Bioinformatics</i> , 2018, 34, 4313-4314. | 1.8 | 542 |
| 21 | miRNet 2.0: network-based visual analytics for miRNA functional analysis and systems biology. <i>Nucleic Acids Research</i> , 2020, 48, W244-W251. | 6.5 | 461 |
| 22 | Disruption of histone methylation in developing sperm impairs offspring health transgenerationally. <i>Science</i> , 2015, 350, aab2006. | 6.0 | 426 |
| 23 | NetworkAnalyst - integrative approaches for protein-protein interaction network analysis and visual exploration. <i>Nucleic Acids Research</i> , 2014, 42, W167-W174. | 6.5 | 398 |
| 24 | miRNet - dissecting miRNA-target interactions and functional associations through network-based visual analysis. <i>Nucleic Acids Research</i> , 2016, 44, W135-W141. | 6.5 | 371 |
| 25 | MetaboAnalystR 3.0: Toward an Optimized Workflow for Global Metabolomics. <i>Metabolites</i> , 2020, 10, 186. | 1.3 | 359 |
| 26 | METAGENassist: a comprehensive web server for comparative metagenomics. <i>Nucleic Acids Research</i> , 2012, 40, W88-W95. | 6.5 | 345 |
| 27 | SMPDB: The Small Molecule Pathway Database. <i>Nucleic Acids Research</i> , 2010, 38, D480-D487. | 6.5 | 290 |
| 28 | MetaboAnalystR 2.0: From Raw Spectra to Biological Insights. <i>Metabolites</i> , 2019, 9, 57. | 1.3 | 252 |
| 29 | miRNet-Functional Analysis and Visual Exploration of miRNA-Target Interactions in a Network Context. <i>Methods in Molecular Biology</i> , 2018, 1819, 215-233. | 0.4 | 198 |
| 30 | Metabolomic Data Processing, Analysis, and Interpretation Using MetaboAnalyst. <i>Current Protocols in Bioinformatics</i> , 2011, 34, Unit 14.10. | 25.8 | 190 |
| 31 | Metabolomics reveals unhealthy alterations in rumen metabolism with increased proportion of cereal grain in the diet of dairy cows. <i>Metabolomics</i> , 2010, 6, 583-594. | 1.4 | 174 |
| 32 | MetaboMiner - semi-automated identification of metabolites from 2D NMR spectra of complex biofluids. <i>BMC Bioinformatics</i> , 2008, 9, 507. | 1.2 | 168 |
| 33 | INMEX - a web-based tool for integrative meta-analysis of expression data. <i>Nucleic Acids Research</i> , 2013, 41, W63-W70. | 6.5 | 162 |
| 34 | An Endotoxin Tolerance Signature Predicts Sepsis and Organ Dysfunction at Initial Clinical Presentation. <i>EBioMedicine</i> , 2014, 1, 64-71. | 2.7 | 140 |
| 35 | OmicsNet: A web-based tool for creation and visual analysis of biological networks in 3D space. <i>Nucleic Acids Research</i> , 2018, 46, W514-W522. | 6.5 | 126 |
| 36 | Using MetaboAnalyst 4.0 for Metabolomics Data Analysis, Interpretation, and Integration with Other Omics Data. <i>Methods in Molecular Biology</i> , 2020, 2104, 337-360. | 0.4 | 117 |

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|----|--|------|-----------|
| 37 | Metabolomics and first-trimester prediction of early-onset preeclampsia. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2012, 25, 1840-1847. | 0.7 | 101 |
| 38 | Diet Affects Muscle Quality and Growth Traits of Grass Carp (<i>Ctenopharyngodon idellus</i>): A Comparison Between Grass and Artificial Feed. <i>Frontiers in Physiology</i> , 2018, 9, 283. | 1.3 | 81 |
| 39 | Computational Approaches for Integrative Analysis of the Metabolome and Microbiome. <i>Metabolites</i> , 2017, 7, 62. | 1.3 | 78 |
| 40 | Pathways of Toxicity. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2014, 31, 53-61. | 0.9 | 75 |
| 41 | Comprehensive Meta-Analysis of COVID-19 Global Metabolomics Datasets. <i>Metabolites</i> , 2021, 11, 44. | 1.3 | 72 |
| 42 | The duck toll like receptor 7: Genomic organization, expression and function. <i>Molecular Immunology</i> , 2008, 45, 2055-2061. | 1.0 | 67 |
| 43 | Intestinal dysbiosis compromises alveolar macrophage immunity to <i>Mycobacterium tuberculosis</i> . <i>Mucosal Immunology</i> , 2019, 12, 772-783. | 2.7 | 65 |
| 44 | INVEX—a web-based tool for integrative visualization of expression data. <i>Bioinformatics</i> , 2013, 29, 3232-3234. | 1.8 | 62 |
| 45 | MetATT: a web-based metabolomics tool for analyzing time-series and two-factor datasets. <i>Bioinformatics</i> , 2011, 27, 2455-2456. | 1.8 | 60 |
| 46 | First-trimester metabolomic detection of late-onset preeclampsia. <i>American Journal of Obstetrics and Gynecology</i> , 2013, 208, 58.e1-58.e7. | 0.7 | 60 |
| 47 | OmicsNet 2.0: a web-based platform for multi-omics integration and network visual analytics. <i>Nucleic Acids Research</i> , 2022, 50, W527-W533. | 6.5 | 58 |
| 48 | Learning to predict cancer-associated skeletal muscle wasting from 1H-NMR profiles of urinary metabolites. <i>Metabolomics</i> , 2011, 7, 25-34. | 1.4 | 51 |
| 49 | Development of Isotope Labeling Liquid Chromatography Mass Spectrometry for Mouse Urine Metabolomics: Quantitative Metabolomic Study of Transgenic Mice Related to Alzheimer's Disease. <i>Journal of Proteome Research</i> , 2014, 13, 4457-4469. | 1.8 | 48 |
| 50 | EcoToxChip: A next-generation toxicogenomics tool for chemical prioritization and environmental management. <i>Environmental Toxicology and Chemistry</i> , 2019, 38, 279-288. | 2.2 | 47 |
| 51 | Using OmicsNet for Network Integration and 3D Visualization. <i>Current Protocols in Bioinformatics</i> , 2019, 65, e69. | 25.8 | 44 |
| 52 | Metabolomic analysis for first-trimester Down syndrome prediction. <i>American Journal of Obstetrics and Gynecology</i> , 2013, 208, 371.e1-371.e8. | 0.7 | 39 |
| 53 | OmicsAnalyst: a comprehensive web-based platform for visual analytics of multi-omics data. <i>Nucleic Acids Research</i> , 2021, 49, W476-W482. | 6.5 | 39 |
| 54 | Network-Based Approaches for Multi-omics Integration. <i>Methods in Molecular Biology</i> , 2020, 2104, 469-487. | 0.4 | 38 |

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|----|---|-----|-----------|
| 55 | Transcriptome and physiological analysis reveal alterations in muscle metabolisms and immune responses of grass carp (<i>Ctenopharyngodon idellus</i>) cultured at different stocking densities. <i>Aquaculture</i> , 2019, 503, 186-197. | 1.7 | 36 |
| 56 | Metabolomics investigation of dietary effects on flesh quality in grass carp (<i>Ctenopharyngodon</i>) Tj ETQq0 0 0 rgBT/Overlock, 10 Tf 50 7 | 3.3 | 35 |
| 57 | Xeno-miRNet: a comprehensive database and analytics platform to explore xeno-miRNAs and their potential targets. <i>PeerJ</i> , 2018, 6, e5650. | 0.9 | 35 |
| 58 | Bioinformatics Tools for the Interpretation of Metabolomics Data. <i>Current Pharmacology Reports</i> , 2017, 3, 374-383. | 1.5 | 34 |
| 59 | Genetic profiles of ten <i>Dirofilaria immitis</i> isolates susceptible or resistant to macrocyclic lactone heartworm preventives. <i>Parasites and Vectors</i> , 2017, 10, 504. | 1.0 | 33 |
| 60 | A Practical Guide to Metabolomics Software Development. <i>Analytical Chemistry</i> , 2021, 93, 1912-1923. | 3.2 | 30 |
| 61 | Comprehensive Transcriptome Meta-analysis to Characterize Host Immune Responses in Helminth Infections. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004624. | 1.3 | 30 |
| 62 | The Effects of Ivermectin on <i>Brugia malayi</i> Females In Vitro: A Transcriptomic Approach. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004929. | 1.3 | 26 |
| 63 | Immune gene discovery by expressed sequence tag analysis of spleen in the duck (<i>Anas platyrhynchos</i>). <i>Developmental and Comparative Immunology</i> , 2007, 31, 272-285. | 1.0 | 23 |
| 64 | Expression of duck CCL19 and CCL21 and CCR7 receptor in lymphoid and influenza-infected tissues. <i>Molecular Immunology</i> , 2011, 48, 1950-1957. | 1.0 | 23 |
| 65 | The Effect of In Vitro Cultivation on the Transcriptome of Adult <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004311. | 1.3 | 22 |
| 66 | FastBMD: an online tool for rapid benchmark dose response analysis of transcriptomics data. <i>Bioinformatics</i> , 2021, 37, 1035-1036. | 1.8 | 19 |
| 67 | Conditional-ready mouse embryonic stem cell derived macrophages enable the study of essential genes in macrophage function. <i>Scientific Reports</i> , 2015, 5, 8908. | 1.6 | 16 |
| 68 | Effect of atmospheric carbon dioxide levels and nitrate fertilization on glucosinolate biosynthesis in mechanically damaged <i>Arabidopsis</i> plants. <i>BMC Plant Biology</i> , 2016, 16, 68. | 1.6 | 16 |
| 69 | EcoToxModules: Custom Gene Sets to Organize and Analyze Toxicogenomics Data from Ecological Species. <i>Environmental Science & Technology</i> , 2020, 54, 4376-4387. | 4.6 | 16 |
| 70 | Genomics of antiviral defenses in the duck, a natural host of influenza and hepatitis B viruses. <i>Cytogenetic and Genome Research</i> , 2007, 117, 195-206. | 0.6 | 15 |
| 71 | Profiling the macrofilaricidal effects of flubendazole on adult female <i>Brugia malayi</i> using RNAseq. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2016, 6, 288-296. | 1.4 | 15 |
| 72 | Loss of disease tolerance during <i>Citrobacter rodentium</i> infection is associated with impaired epithelial differentiation and hyperactivation of T cell responses. <i>Scientific Reports</i> , 2018, 8, 847. | 1.6 | 15 |

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|----|--|-----|-----------|
| 73 | Ultrafast functional profiling of RNA-seq data for nonmodel organisms. <i>Genome Research</i> , 2021, 31, 713-720. | 2.4 | 15 |
| 74 | T1000: a reduced gene set prioritized for toxicogenomic studies. <i>PeerJ</i> , 2019, 7, e7975. | 0.9 | 15 |
| 75 | Assessing the Toxicity of 17 β -Ethinylestradiol in Rainbow Trout Using a 4-Day Transcriptomics Benchmark Dose (BMD) Embryo Assay. <i>Environmental Science & Technology</i> , 2021, 55, 10608-10618. | 4.6 | 14 |
| 76 | Differential metabolite profiles and salinity tolerance between two genetically related brown-seeded and yellow-seeded <i>Brassica carinata</i> lines. <i>Plant Science</i> , 2013, 198, 17-26. | 1.7 | 13 |
| 77 | Metabolomic Analysis of Cold Acclimation of Arctic <i>Mesorhizobium</i> sp. Strain N33. <i>PLoS ONE</i> , 2013, 8, e84801. | 1.1 | 13 |
| 78 | Development of a Comprehensive Toxicity Pathway Model for 17 β -Ethinylestradiol in Early Life Stage Fathead Minnows (<i>Pimephales promelas</i>). <i>Environmental Science & Technology</i> , 2021, 55, 5024-5036. | 4.6 | 13 |
| 79 | Transcript analysis in two alfalfa salt tolerance selected breeding populations relative to a non-tolerant population. <i>Genome</i> , 2017, 60, 104-127. | 0.9 | 12 |
| 80 | The symbiotic relationship between <i>Caenorhabditis elegans</i> and members of its microbiome contributes to worm fitness and lifespan extension. <i>BMC Genomics</i> , 2021, 22, 364. | 1.2 | 12 |
| 81 | Comprehensive phenotyping and transcriptome profiling to study nanotoxicity in <i>C. elegans</i> . <i>PeerJ</i> , 2020, 8, e8684. | 0.9 | 12 |
| 82 | Using Transcriptomics and Metabolomics to Understand Species Differences in Sensitivity to Chlorpyrifos in Japanese Quail and Double-crested Cormorant Embryos. <i>Environmental Toxicology and Chemistry</i> , 2021, 40, 3019-3033. | 2.2 | 11 |
| 83 | TrpNet: Understanding Tryptophan Metabolism across Gut Microbiome. <i>Metabolites</i> , 2022, 12, 10. | 1.3 | 11 |
| 84 | Comparative analysis of transcriptomic points-of-departure (tPODs) and apical responses in embryo-larval fathead minnows exposed to fluoxetine. <i>Environmental Pollution</i> , 2022, 295, 118667. | 3.7 | 10 |
| 85 | Dendritic cell inhibitory and activating immunoreceptors (DCIR and DCAR) in duck: Genomic organization and expression. <i>Molecular Immunology</i> , 2008, 45, 3942-3946. | 1.0 | 8 |
| 86 | Computational Strategies for Biological Interpretation of Metabolomics Data. <i>Advances in Experimental Medicine and Biology</i> , 2017, 965, 191-206. | 0.8 | 8 |
| 87 | EcoToxExplorer: Leveraging Design Thinking to Develop a Standardized Web-based Transcriptomics Analytics Platform for Diverse Users. <i>Environmental Toxicology and Chemistry</i> , 2022, 41, 21-29. | 2.2 | 6 |
| 88 | Characterizing toxicity pathways of fluoxetine to predict adverse outcomes in adult fathead minnows (<i>Pimephales promelas</i>). <i>Science of the Total Environment</i> , 2022, 817, 152747. | 3.9 | 5 |
| 89 | mGWAS-Explorer: Linking SNPs, Genes, Metabolites, and Diseases for Functional Insights. <i>Metabolites</i> , 2022, 12, 526. | 1.3 | 5 |
| 90 | Spatiotemporal integration of molecular and anatomical data in virtual reality using semantic mapping. <i>International Journal of Nanomedicine</i> , 2009, 4, 79. | 3.3 | 4 |

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|----|--|-----|-----------|
| 91 | Metabolome Analysis. , 2019, , 396-409. | | 3 |
| 92 | Oxidative stress suppression in <i>C. elegans</i> by peptides from dogfish skin via regulation of transcription factors DAF-16 and HSF-1. <i>Food and Function</i> , 2022, 13, 716-724. | 2.1 | 3 |
| 93 | Targeted Metabolomics to Assess Exposure to Environmental Chemicals of Concern in Japanese Quail at Two Life Stages. <i>Metabolites</i> , 2021, 11, 850. | 1.3 | 3 |
| 94 | Consideration of metabolomics and transcriptomics data in the context of using avian embryos for toxicity testing. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2022, 258, 109370. | 1.3 | 3 |
| 95 | Increased IL-8 production in human bronchial epithelial cells after exposure to azithromycin-pretreated <i>Pseudomonas aeruginosa</i> in vitro. <i>FEMS Microbiology Letters</i> , 2014, 355, 43-50. | 0.7 | 2 |
| 96 | Native Microbiome Members of <i>C. elegans</i> Act Synergistically in Biosynthesis of Pyridoxal 5-Phosphate. <i>Metabolites</i> , 2022, 12, 172. | 1.3 | 2 |
| 97 | 597: Metabolomic prediction of trisomy 18 first trimester pregnancies. <i>American Journal of Obstetrics and Gynecology</i> , 2013, 208, S255. | 0.7 | 1 |
| 98 | Metabolomic Analysis for First Trimester Down Syndrome Prediction. <i>Obstetric Anesthesia Digest</i> , 2015, 35, 35-36. | 0.0 | 0 |