Jianguo Xia

List of Publications by Citations

90 papers	21,592 citations	42 h-index	104 g-index
104 ext. papers	28,819 ext. citations	9.2 avg, IF	7.69 L-index

#	Paper	IF	Citations
90	HMDB 3.0--The Human Metabolome Database in 2013. *Nucleic Acids Research*, **2013**, 41, D801-7	20.1	2210
89	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. *Nucleic Acids Research*, **2018**, 46, W486-W494	20.1	2157
88	MetaboAnalyst 3.0--making metabolomics more meaningful. *Nucleic Acids Research*, **2015**, 43, W251-7	20.1	2067
87	HMDB: a knowledgebase for the human metabolome. *Nucleic Acids Research*, **2009**, 37, D603-10	20.1	1431
86	MetaboAnalyst: a web server for metabolomic data analysis and interpretation. *Nucleic Acids Research*, **2009**, 37, W652-60	20.1	1202
85	The human serum metabolome. *PLoS ONE*, **2011**, 6, e16957	3.7	1118
84	Using MetaboAnalyst 3.0 for Comprehensive Metabolomics Data Analysis. *Current Protocols in Bioinformatics*, **2016**, 55, 14.10.1-14.10.91	24.2	957
83	MetaboAnalyst 2.0--a comprehensive server for metabolomic data analysis. *Nucleic Acids Research*, **2012**, 40, W127-33	20.1	935
82	Using MetaboAnalyst 4.0 for Comprehensive and Integrative Metabolomics Data Analysis. *Current Protocols in Bioinformatics*, **2019**, 68, e86	24.2	928
81	Web-based inference of biological patterns, functions and pathways from metabolomic data using MetaboAnalyst. *Nature Protocols*, **2011**, 6, 743-60	18.8	718
80	MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. *Nucleic Acids Research*, **2017**, 45, W180-W188	20.1	706
79	Translational biomarker discovery in clinical metabolomics: an introductory tutorial. *Metabolomics*, **2013**, 9, 280-299	4.7	594
78	NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. *Nucleic Acids Research*, **2019**, 47, W234-W241	20.1	491
77	NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data. *Nature Protocols*, **2015**, 10, 823-44	18.8	459
76	MetPA: a web-based metabolomics tool for pathway analysis and visualization. *Bioinformatics*, **2010**, 26, 2342-4	7.2	447
75	MSEA: a web-based tool to identify biologically meaningful patterns in quantitative metabolomic data. *Nucleic Acids Research*, **2010**, 38, W71-7	20.1	412
74	MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights. *Nucleic Acids Research*, **2021**, 49, W388-W396	20.1	393

73	Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data. *Nature Protocols*, **2020**, 15, 799-821	18.8	346
72	Disruption of histone methylation in developing sperm impairs offspring health transgenerationally. *Science*, **2015**, 350, aab2006	33.3	317
71	MetaboAnalystR: an R package for flexible and reproducible analysis of metabolomics data. *Bioinformatics*, **2018**, 34, 4313-4314	7.2	274
70	METAGENassist: a comprehensive web server for comparative metagenomics. *Nucleic Acids Research*, **2012**, 40, W88-95	20.1	267
69	miRNet - dissecting miRNA-target interactions and functional associations through network-based visual analysis. *Nucleic Acids Research*, **2016**, 44, W135-41	20.1	265
68	NetworkAnalyst--integrative approaches for protein-protein interaction network analysis and visual exploration. *Nucleic Acids Research*, **2014**, 42, W167-74	20.1	254
67	SMPDB: The Small Molecule Pathway Database. *Nucleic Acids Research*, **2010**, 38, D480-7	20.1	213
66	MetaboAnalystR 3.0: Toward an Optimized Workflow for Global Metabolomics. *Metabolites*, **2020**, 10,	5.6	182
65	MetaboAnalystR 2.0: From Raw Spectra to Biological Insights. *Metabolites*, **2019**, 9,	5.6	167
64	MetaboMiner--semi-automated identification of metabolites from 2D NMR spectra of complex biofluids. *BMC Bioinformatics*, **2008**, 9, 507	3.6	150
63	miRNet 2.0: network-based visual analytics for miRNA functional analysis and systems biology. *Nucleic Acids Research*, **2020**, 48, W244-W251	20.1	147
62	Metabolomics reveals unhealthy alterations in rumen metabolism with increased proportion of cereal grain in the diet of dairy cows. *Metabolomics*, **2010**, 6, 583-594	4.7	125
61	Metabolomic data processing, analysis, and interpretation using MetaboAnalyst. *Current Protocols in Bioinformatics*, **2011**, Chapter 14, Unit 14.10	24.2	124
60	INMEX--a web-based tool for integrative meta-analysis of expression data. *Nucleic Acids Research*, **2013**, 41, W63-70	20.1	119
59	miRNet-Functional Analysis and Visual Exploration of miRNA-Target Interactions in a Network Context. *Methods in Molecular Biology*, **2018**, 1819, 215-233	1.4	95
58	Metabolomics and first-trimester prediction of early-onset preeclampsia. *Journal of Maternal-Fetal and Neonatal Medicine*, **2012**, 25, 1840-7	2	85
57	An Endotoxin Tolerance Signature Predicts Sepsis and Organ Dysfunction at Initial Clinical Presentation. *EBioMedicine*, **2014**, 1, 64-71	8.8	84
56	OmicsNet:□a web-based tool for creation and visual analysis of biological networks in 3D space. *Nucleic Acids Research*, **2018**, 46, W514-W522	20.1	78

55	The duck toll like receptor 7: genomic organization, expression and function. *Molecular Immunology* , **2008**, 45, 2055-61	4.3	61
54	Pathways of Toxicity. *ALTEX: Alternatives To Animal Experimentation*, **2014**, 31, 53-61	4.3	59
53	Using MetaboAnalyst 4.0 for Metabolomics Data Analysis, Interpretation, and Integration with Other Omics Data. *Methods in Molecular Biology*, **2020**, 2104, 337-360	1.4	59
52	Computational Approaches for Integrative Analysis of the Metabolome and Microbiome. *Metabolites*, **2017**, 7,	5.6	55
51	First-trimester metabolomic detection of late-onset preeclampsia. *American Journal of Obstetrics and Gynecology*, **2013**, 208, 58.e1-7	6.4	55
50	MetATT: a web-based metabolomics tool for analyzing time-series and two-factor datasets. *Bioinformatics*, **2011**, 27, 2455-6	7.2	52
49	Diet Affects Muscle Quality and Growth Traits of Grass Carp (): A Comparison Between Grass and Artificial Feed. *Frontiers in Physiology*, **2018**, 9, 283	4.6	44
48	INVEX--a web-based tool for integrative visualization of expression data. *Bioinformatics*, **2013**, 29, 3232-4	7.2	42
47	Learning to predict cancer-associated skeletal muscle wasting from 1H-NMR profiles of urinary metabolites. *Metabolomics*, **2011**, 7, 25-34	4.7	38
46	Metabolomic analysis for first-trimester Down syndrome prediction. *American Journal of Obstetrics and Gynecology*, **2013**, 208, 371.e1-8	6.4	36
45	Comprehensive Meta-Analysis of COVID-19 Global Metabolomics Datasets. *Metabolites*, **2021**, 11,	5.6	36
44	Development of isotope labeling liquid chromatography mass spectrometry for mouse urine metabolomics: quantitative metabolomic study of transgenic mice related to Alzheimer's disease. *Journal of Proteome Research*, **2014**, 13, 4457-69	5.6	35
43	Intestinal dysbiosis compromises alveolar macrophage immunity to Mycobacterium tuberculosis. *Mucosal Immunology*, **2019**, 12, 772-783	9.2	32
42	Bioinformatics Tools for the Interpretation of Metabolomics Data. *Current Pharmacology Reports*, **2017**, 3, 374-383	5.5	28
41	Using OmicsNet for Network Integration and 3D Visualization. *Current Protocols in Bioinformatics*, **2019**, 65, e69	24.2	27
40	Using MetaboAnalyst 5.0 for LC□HRMS spectra processing, multi-omics integration and covariate adjustment of global metabolomics data. *Nature Protocols*,	18.8	27
39	EcoToxChip: A next-generation toxicogenomics tool for chemical prioritization and environmental management. *Environmental Toxicology and Chemistry*, **2019**, 38, 279-288	3.8	26
38	Xeno-miRNet: a comprehensive database and analytics platform to explore xeno-miRNAs and their potential targets. *PeerJ*, **2018**, 6, e5650	3.1	24

37	Genetic profiles of ten Dirofilaria immitis isolates susceptible or resistant to macrocyclic lactone heartworm preventives. *Parasites and Vectors*, **2017**, 10, 504	4	21
36	Expression of duck CCL19 and CCL21 and CCR7 receptor in lymphoid and influenza-infected tissues. *Molecular Immunology*, **2011**, 48, 1950-7	4.3	21
35	Immune gene discovery by expressed sequence tag analysis of spleen in the duck (Anas platyrhynchos). *Developmental and Comparative Immunology*, **2007**, 31, 272-85	3.2	21
34	Transcriptome and physiological analysis reveal alterations in muscle metabolisms and immune responses of grass carp (Ctenopharyngodon idellus) cultured at different stocking densities. *Aquaculture*, **2019**, 503, 186-197	4.4	21
33	Metabolomics investigation of dietary effects on flesh quality in grass carp (Ctenopharyngodon idellus). *GigaScience*, **2018**, 7,	7.6	20
32	The Effects of Ivermectin on Brugia malayi Females In Vitro: A Transcriptomic Approach. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004929	4.8	17
31	Conditional-ready mouse embryonic stem cell derived macrophages enable the study of essential genes in macrophage function. *Scientific Reports*, **2015**, 5, 8908	4.9	15
30	The Effect of In Vitro Cultivation on the Transcriptome of Adult Brugia malayi. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004311	4.8	15
29	Genomics of antiviral defenses in the duck, a natural host of influenza and hepatitis B viruses. *Cytogenetic and Genome Research*, **2007**, 117, 195-206	1.9	14
28	Comprehensive Transcriptome Meta-analysis to Characterize Host Immune Responses in Helminth Infections. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004624	4.8	13
27	Network-Based Approaches for Multi-omics Integration. *Methods in Molecular Biology*, **2020**, 2104, 469-487	1.4	13
26	Differential metabolite profiles and salinity tolerance between two genetically related brown-seeded and yellow-seeded Brassica carinata lines. *Plant Science*, **2013**, 198, 17-26	5.3	12
25	Metabolomic analysis of cold acclimation of Arctic Mesorhizobium sp. strain N33. *PLoS ONE*, **2013**, 8, e84801	3.7	12
24	Loss of disease tolerance during Citrobacter rodentium infection is associated with impaired epithelial differentiation and hyperactivation of T cell responses. *Scientific Reports*, **2018**, 8, 847	4.9	11
23	Effect of atmospheric carbon dioxide levels and nitrate fertilization on glucosinolate biosynthesis in mechanically damaged Arabidopsis plants. *BMC Plant Biology*, **2016**, 16, 68	5.3	11
22	Profiling the macrofilaricidal effects of flubendazole on adult female Brugia malayi using RNAseq. *International Journal for Parasitology: Drugs and Drug Resistance*, **2016**, 6, 288-296	4	11
21	A Practical Guide to Metabolomics Software Development. *Analytical Chemistry*, **2021**, 93, 1912-1923	7.8	10
20	Transcript analysis in two alfalfa salt tolerance selected breeding populations relative to a non-tolerant population. *Genome*, **2017**, 60, 104-127	2.4	9

19	T1000: a reduced gene set prioritized for toxicogenomic studies. *PeerJ*, **2019**, 7, e7975	3.1	8
18	Development of a Comprehensive Toxicity Pathway Model for 17Ethinylestradiol in Early Life Stage Fathead Minnows (). *Environmental Science & Technology*, **2021**, 55, 5024-5036	10.3	8
17	Dendritic cell inhibitory and activating immunoreceptors (DCIR and DCAR) in duck: Genomic organization and expression. *Molecular Immunology*, **2008**, 45, 3942-6	4.3	7
16	Comprehensive phenotyping and transcriptome profiling to study nanotoxicity in. *PeerJ*, **2020**, 8, e8684	3.1	7
15	FastBMD: an online tool for rapid benchmark dose-response analysis of transcriptomics data. *Bioinformatics*, **2021**, 37, 1035-1036	7.2	7
14	Computational Strategies for Biological Interpretation of Metabolomics Data. *Advances in Experimental Medicine and Biology*, **2017**, 965, 191-206	3.6	5
13	EcoToxModules: Custom Gene Sets to Organize and Analyze Toxicogenomics Data from Ecological Species. *Environmental Science & Technology*, **2020**, 54, 4376-4387	10.3	5
12	Assessing the Toxicity of 17Ethinylestradiol in Rainbow Trout Using a 4-Day Transcriptomics Benchmark Dose (BMD) Embryo Assay. *Environmental Science & Technology*, **2021**, 55, 10608-10618	10.3	5
11	OmicsAnalyst: a comprehensive web-based platform for visual analytics of multi-omics data. *Nucleic Acids Research*, **2021**, 49, W476-W482	20.1	4
10	Increased IL-8 production in human bronchial epithelial cells after exposure to azithromycin-pretreated Pseudomonas aeruginosa in vitro. *FEMS Microbiology Letters*, **2014**, 355, 43-50	2.9	2
9	Spatiotemporal integration of molecular and anatomical data in virtual reality using semantic mapping. *International Journal of Nanomedicine*, **2009**, 4, 79-89	7.3	2
8	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. *Genome Research*, **2021**, 31, 713-720	7.7	2
7	EcoToxXplorer: Leveraging Design Thinking to Develop a Standardized Web-Based Transcriptomics Analytics Platform for Diverse Users. *Environmental Toxicology and Chemistry*, **2021**,	3.8	1
6	Characterizing toxicity pathways of fluoxetine to predict adverse outcomes in adult fathead minnows (Pimephales promelas).. *Science of the Total Environment*, **2022**, 817, 152747	10.2	1
5	Comparative analysis of transcriptomic points-of-departure (tPODs) and apical responses in embryo-larval fathead minnows exposed to fluoxetine.. *Environmental Pollution*, **2021**, 295, 118667	9.3	1
4	The symbiotic relationship between Caenorhabditis elegans and members of its microbiome contributes to worm fitness and lifespan extension. *BMC Genomics*, **2021**, 22, 364	4.5	1
3	Metabolome Analysis **2019**, 396-409		0
2	Using Transcriptomics and Metabolomics to Understand Species Differences in Sensitivity to Chlorpyrifos in Japanese Quail and Double-Crested Cormorant Embryos. *Environmental Toxicology and Chemistry*, **2021**, 40, 3019-3033	3.8	0

1	Consideration of metabolomics and transcriptomics data in the context of using avian embryos for toxicity testing.. *Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology*, **2022**, 109370	3.2	0