Jianguo Xia

List of Publications by Year
in descending order

98	33,474	46918	37111
papers	citations	47	96
		h-index	g-index

104	104	104	44084
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	EcoToxXplorer: Leveraging Design Thinking to Develop a Standardized Web‐Based Transcriptomics Analytics Platform for Diverse Users. Environmental Toxicology and Chemistry, 2022, 41, 21-29.	2.2	6
2	Characterizing toxicity pathways of fluoxetine to predict adverse outcomes in adult fathead minnows (Pimephales promelas). Science of the Total Environment, 2022, 817, 152747.	3.9	5
3	Comparative analysis of transcriptomic points-of-departure (tPODs) and apical responses in embryo-larval fathead minnows exposed to fluoxetine. Environmental Pollution, 2022, 295, 118667.	3.7	10
4	Oxidative stress suppression in C. elegans by peptides from dogfish skin via regulation of transcription factors DAF-16 and HSF-1. Food and Function, 2022, 13, 716-724.	2.1	3
5	Native Microbiome Members of C. elegans Act Synergistically in Biosynthesis of Pyridoxal 5′-Phosphate. Metabolites, 2022, 12, 172.	1.3	2
6	TrpNet: Understanding Tryptophan Metabolism across Gut Microbiome. Metabolites, 2022, 12, 10.	1.3	11
7	OmicsNet 2.0: a web-based platform for multi-omics integration and network visual analytics. Nucleic Acids Research, 2022, 50, W527-W533.	6.5	58
8	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, 258, 109370.	1.3	3
9	mGWAS-Explorer: Linking SNPs, Genes, Metabolites, and Diseases for Functional Insights. Metabolites, 2022, 12, 526.	1.3	5
10	Using MetaboAnalyst 5.0 for LC–HRMS spectra processing, multi-omics integration and covariate adjustment of global metabolomics data. Nature Protocols, 2022, 17, 1735-1761.	5.5	556
11	FastBMD: an online tool for rapid benchmark dose–response analysis of transcriptomics data. Bioinformatics, 2021, 37, 1035-1036.	1.8	19
12	A Practical Guide to Metabolomics Software Development. Analytical Chemistry, 2021, 93, 1912-1923.	3.2	30
13	Comprehensive Meta-Analysis of COVID-19 Global Metabolomics Datasets. Metabolites, 2021, 11, 44.	1.3	72
14	Development of a Comprehensive Toxicity Pathway Model for 17α-Ethinylestradiol in Early Life Stage Fathead Minnows (<i>Pimephales promelas</i>). Environmental Science & Technology, 2021, 55, 5024-5036.	4.6	13
15	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. Genome Research, 2021, 31, 713-720.	2.4	15
16	The symbiotic relationship between Caenorhabditis elegans and members of its microbiome contributes to worm fitness and lifespan extension. BMC Genomics, 2021, 22, 364.	1.2	12
17	OmicsAnalyst: a comprehensive web-based platform for visual analytics of multi-omics data. Nucleic Acids Research, 2021, 49, W476-W482.	6.5	39
18	MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights. Nucleic Acids Research, 2021, 49, W388-W396.	6.5	2,221

#	Article	IF	Citations
19	Assessing the Toxicity of 17Î±-Ethinylestradiol in Rainbow Trout Using a 4-Day Transcriptomics Benchmark Dose (BMD) Embryo Assay. Environmental Science & Technology, 2021, 55, 10608-10618.	4.6	14
20	Using Transcriptomics and Metabolomics to Understand Species Differences in Sensitivity to Chlorpyrifos in Japanese Quail and Doubleâ€Crested Cormorant Embryos. Environmental Toxicology and Chemistry, 2021, 40, 3019-3033.	2.2	11
21	Targeted Metabolomics to Assess Exposure to Environmental Chemicals of Concern in Japanese Quail at Two Life Stages. Metabolites, 2021, 11, 850.	1.3	3
22	MetaboAnalystR 3.0: Toward an Optimized Workflow for Global Metabolomics. Metabolites, 2020, 10, 186.	1.3	359
23	miRNet 2.0: network-based visual analytics for miRNA functional analysis and systems biology. Nucleic Acids Research, 2020, 48, W244-W251.	6.5	461
24	EcoToxModules: Custom Gene Sets to Organize and Analyze Toxicogenomics Data from Ecological Species. Environmental Science & Technology, 2020, 54, 4376-4387.	4.6	16
25	Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data. Nature Protocols, 2020, 15, 799-821.	5.5	1,019
26	Using MetaboAnalyst 4.0 for Metabolomics Data Analysis, Interpretation, and Integration with Other Omics Data. Methods in Molecular Biology, 2020, 2104, 337-360.	0.4	117
27	Network-Based Approaches for Multi-omics Integration. Methods in Molecular Biology, 2020, 2104, 469-487.	0.4	38
28	Comprehensive phenotyping and transcriptome profiling to study nanotoxicity in *C. elegans*. PeerJ, 2020, 8, e8684.	0.9	12
29	Metabolome Analysis. , 2019, , 396-409.		3
30	Using MetaboAnalyst 4.0 for Comprehensive and Integrative Metabolomics Data Analysis. Current Protocols in Bioinformatics, 2019, 68, e86.	25.8	1,644
31	EcoToxChip: A nextâ€generation toxicogenomics tool for chemical prioritization and environmental management. Environmental Toxicology and Chemistry, 2019, 38, 279-288.	2.2	47
32	MetaboAnalystR 2.0: From Raw Spectra to Biological Insights. Metabolites, 2019, 9, 57.	1.3	252
33	NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. Nucleic Acids Research, 2019, 47, W234-W241.	6.5	1,191
34	Intestinal dysbiosis compromises alveolar macrophage immunity to Mycobacterium tuberculosis. Mucosal Immunology, 2019, 12, 772-783.	2.7	65
35	Using OmicsNet for Network Integration and 3D Visualization. Current Protocols in Bioinformatics, 2019, 65, e69.	25.8	44
36	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.	1.7	36

#	Article	IF	Citations
37	T1000: a reduced gene set prioritized for toxicogenomic studies. PeerJ, 2019, 7, e7975.	0.9	15
38	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.	1.6	15
39	miRNetâ€"Functional Analysis and Visual Exploration of miRNAâ€"Target Interactions in a Network Context. Methods in Molecular Biology, 2018, 1819, 215-233.	0.4	198
40	Metabolomics investigation of dietary effects on flesh quality in grass carp (Ctenopharyngodon) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 6	3.3	35
41	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. Nucleic Acids Research, 2018, 46, W486-W494.	6.5	3,199
42	MetaboAnalystR: an R package for flexible and reproducible analysis of metabolomics data. Bioinformatics, 2018, 34, 4313-4314.	1.8	542
43	Diet Affects Muscle Quality and Growth Traits of Grass Carp (Ctenopharyngodon idellus): A Comparison Between Grass and Artificial Feed. Frontiers in Physiology, 2018, 9, 283.	1.3	81
44	OmicsNet: a web-based tool for creation and visual analysis of biological networks in 3D space. Nucleic Acids Research, 2018, 46, W514-W522.	6.5	126
45	Xeno-miRNet: a comprehensive database and analytics platform to explore xeno-miRNAs and their potential targets. PeerJ, 2018, 6, e5650.	0.9	35
46	Computational Strategies for Biological Interpretation of Metabolomics Data. Advances in Experimental Medicine and Biology, 2017, 965, 191-206.	0.8	8
47	MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. Nucleic Acids Research, 2017, 45, W180-W188.	6.5	1,359
48	Bioinformatics Tools for the Interpretation of Metabolomics Data. Current Pharmacology Reports, 2017, 3, 374-383.	1.5	34
49	Transcript analysis in two alfalfa salt tolerance selected breeding populations relative to a non-tolerant population. Genome, 2017, 60, 104-127.	0.9	12
50	Computational Approaches for Integrative Analysis of the Metabolome and Microbiome. Metabolites, 2017, 7, 62.	1.3	78
51	Genetic profiles of ten Dirofilaria immitis isolates susceptible or resistant to macrocyclic lactone heartworm preventives. Parasites and Vectors, 2017, 10, 504.	1.0	33
52	The Effects of Ivermectin on Brugia malayi Females In Vitro: A Transcriptomic Approach. PLoS Neglected Tropical Diseases, 2016, 10, e0004929.	1.3	26
53	Using MetaboAnalyst 3.0 for Comprehensive Metabolomics Data Analysis. Current Protocols in Bioinformatics, 2016, 55, 14.10.1-14.10.91.	25.8	1,293
54	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.	1.4	15

#	Article	IF	Citations
55	Effect of atmospheric carbon dioxide levels and nitrate fertilization on glucosinolate biosynthesis in mechanically damaged Arabidopsis plants. BMC Plant Biology, 2016, 16, 68.	1.6	16
56	miRNet - dissecting miRNA-target interactions and functional associations through network-based visual analysis. Nucleic Acids Research, 2016, 44, W135-W141.	6.5	371
57	The Effect of In Vitro Cultivation on the Transcriptome of Adult Brugia malayi. PLoS Neglected Tropical Diseases, 2016, 10, e0004311.	1.3	22
58	Comprehensive Transcriptome Meta-analysis to Characterize Host Immune Responses in Helminth Infections. PLoS Neglected Tropical Diseases, 2016, 10, e0004624.	1.3	30
59	Metabolomic Analysis for First Trimester Down Syndrome Prediction. Obstetric Anesthesia Digest, 2015, 35, 35-36.	0.0	0
60	MetaboAnalyst 3.0â€"making metabolomics more meaningful. Nucleic Acids Research, 2015, 43, W251-W257.	6.5	2,493
61	Conditional-ready mouse embryonic stem cell derived macrophages enable the study of essential genes in macrophage function. Scientific Reports, 2015, 5, 8908.	1.6	16
62	NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data. Nature Protocols, 2015, 10, 823-844.	5.5	779
63	Disruption of histone methylation in developing sperm impairs offspring health transgenerationally. Science, 2015, 350, aab2006.	6.0	426
64	An Endotoxin Tolerance Signature Predicts Sepsis and Organ Dysfunction at Initial Clinical Presentation. EBioMedicine, 2014, 1, 64-71.	2.7	140
65	Increased IL-8 production in human bronchial epithelial cells after exposure to azithromycin-pretreated<i>Pseudomonas aeruginosa in vitro</i>. FEMS Microbiology Letters, 2014, 355, 43-50.	0.7	2
66	NetworkAnalyst - integrative approaches for proteinâ€"protein interaction network analysis and visual exploration. Nucleic Acids Research, 2014, 42, W167-W174.	6.5	398
67	Development of Isotope Labeling Liquid Chromatography Mass Spectrometry for Mouse Urine Metabolomics: Quantitative Metabolomic Study of Transgenic Mice Related to Alzheimerâ€™s Disease. Journal of Proteome Research, 2014, 13, 4457-4469.	1.8	48
68	Pathways of Toxicity. ALTEX: Alternatives To Animal Experimentation, 2014, 31, 53-61.	0.9	75
69	Translational biomarker discovery in clinical metabolomics: an introductory tutorial. Metabolomics, 2013, 9, 280-299.	1.4	765
70	Differential metabolite profiles and salinity tolerance between two genetically related brown-seeded and yellow-seeded Brassica carinata lines. Plant Science, 2013, 198, 17-26.	1.7	13
71	Metabolomic analysis for first-trimester Down syndrome prediction. American Journal of Obstetrics and Gynecology, 2013, 208, 371.e1-371.e8.	0.7	39
72	597: Metabolomic prediction of trisomy 18 first trimester pregnancies. American Journal of Obstetrics and Gynecology, 2013, 208, S255.	0.7	1

#	Article	IF	Citations
73	First-trimester metabolomic detection of late-onset preeclampsia. American Journal of Obstetrics and Gynecology, 2013, 208, 58.e1-58.e7.	0.7	60
74	INVEXâ€"a web-based tool for integrative visualization of expression data. Bioinformatics, 2013, 29, 3232-3234.	1.8	62
75	INMEXâ€"a web-based tool for integrative meta-analysis of expression data. Nucleic Acids Research, 2013, 41, W63-W70.	6.5	162
76	Metabolomic Analysis of Cold Acclimation of Arctic Mesorhizobium sp. Strain N33. PLoS ONE, 2013, 8, e84801.	1.1	13
77	METAGENassist: a comprehensive web server for comparative metagenomics. Nucleic Acids Research, 2012, 40, W88-W95.	6.5	345
78	Metabolomics and first-trimester prediction of early-onset preeclampsia. Journal of Maternal-Fetal and Neonatal Medicine, 2012, 25, 1840-1847.	0.7	101
79	HMDB 3.0â€"The Human Metabolome Database in 2013. Nucleic Acids Research, 2012, 41, D801-D807.	6.5	2,564
80	MetaboAnalyst 2.0--a comprehensive server for metabolomic data analysis. Nucleic Acids Research, 2012, 40, W127-W133.	6.5	1,058
81	Metabolomic Data Processing, Analysis, and Interpretation Using MetaboAnalyst. Current Protocols in Bioinformatics, 2011, 34, Unit 14.10.	25.8	190
82	Web-based inference of biological patterns, functions and pathways from metabolomic data using MetaboAnalyst. Nature Protocols, 2011, 6, 743-760.	5.5	976
83	Expression of duck CCL19 and CCL21 and CCR7 receptor in lymphoid and influenza-infected tissues. Molecular Immunology, 2011, 48, 1950-1957.	1.0	23
84	The Human Serum Metabolome. PLoS ONE, 2011, 6, e16957.	1.1	1,378
85	Learning to predict cancer-associated skeletal muscle wasting from 1H-NMR profiles of urinary metabolites. Metabolomics, 2011, 7, 25-34.	1.4	51
86	MetATT: a web-based metabolomics tool for analyzing time-series and two-factor datasets. Bioinformatics, 2011, 27, 2455-2456.	1.8	60
87	Metabolomics reveals unhealthy alterations in rumen metabolism with increased proportion of cereal grain in the diet of dairy cows. Metabolomics, 2010, 6, 583-594.	1.4	174
88	MSEA: a web-based tool to identify biologically meaningful patterns in quantitative metabolomic data. Nucleic Acids Research, 2010, 38, W71-W77.	6.5	582
89	MetPA: a web-based metabolomics tool for pathway analysis and visualization. Bioinformatics, 2010, 26, 2342-2344.	1.8	624
90	SMPDB: The Small Molecule Pathway Database. Nucleic Acids Research, 2010, 38, D480-D487.	6.5	290

#	Article	IF	Citations
91	Spatiotemporal integration of molecular and anatomical data in virtual reality using semantic mapping. International Journal of Nanomedicine, 2009, 4, 79.	3.3	4
92	HMDB: a knowledgebase for the human metabolome. Nucleic Acids Research, 2009, 37, D603-D610.	6.5	1,649
93	MetaboAnalyst: a web server for metabolomic data analysis and interpretation. Nucleic Acids Research, 2009, 37, W652-W660.	6.5	1,674
94	MetaboMiner â€" semi-automated identification of metabolites from 2D NMR spectra of complex biofluids. BMC Bioinformatics, 2008, 9, 507.	1.2	168
95	The duck toll like receptor 7: Genomic organization, expression and function. Molecular Immunology, 2008, 45, 2055-2061.	1.0	67
96	Dendritic cell inhibitory and activating immunoreceptors (DCIR and DCAR) in duck: Genomic organization and expression. Molecular Immunology, 2008, 45, 3942-3946.	1.0	8
97	Genomics of antiviral defenses in the duck, a natural host of influenza and hepatitis B viruses. Cytogenetic and Genome Research, 2007, 117, 195-206.	0.6	15
98	Immune gene discovery by expressed sequence tag analysis of spleen in the duck (Anas platyrhynchos). Developmental and Comparative Immunology, 2007, 31, 272-285.	1.0	23