

Jianguo Xia

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/8157942/jianguo-xia-publications-by-year.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

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	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	10.2	1
89	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 , 109370	3.2	0
88	EcoToxXplorer: Leveraging Design Thinking to Develop a Standardized Web-Based Transcriptomics Analytics Platform for Diverse Users. <i>Environmental Toxicology and Chemistry</i> , 2021 ,	3.8	1
87	Comparative analysis of transcriptomic points-of-departure (tPODs) and apical responses in embryo-larval fathead minnows exposed to fluoxetine.. <i>Environmental Pollution</i> , 2021 , 295, 118667	9.3	1
86	Development of a Comprehensive Toxicity Pathway Model for 17 β Ethinylestradiol in Early Life Stage Fathead Minnows (). <i>Environmental Science & Technology</i> , 2021 , 55, 5024-5036	10.3	8
85	Ultrafast functional profiling of RNA-seq data for nonmodel organisms. <i>Genome Research</i> , 2021 , 31, 713-720	37.0	2
84	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	4.5	1
83	OmicsAnalyst: a comprehensive web-based platform for visual analytics of multi-omics data. <i>Nucleic Acids Research</i> , 2021 , 49, W476-W482	20.1	4
82	MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights. <i>Nucleic Acids Research</i> , 2021 , 49, W388-W396	20.1	393
81	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	10.3	5
80	FastBMD: an online tool for rapid benchmark dose-response analysis of transcriptomics data. <i>Bioinformatics</i> , 2021 , 37, 1035-1036	7.2	7
79	A Practical Guide to Metabolomics Software Development. <i>Analytical Chemistry</i> , 2021 , 93, 1912-1923	7.8	10
78	Comprehensive Meta-Analysis of COVID-19 Global Metabolomics Datasets. <i>Metabolites</i> , 2021 , 11,	5.6	36
77	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	3.8	0
76	MetaboAnalystR 3.0: Toward an Optimized Workflow for Global Metabolomics. <i>Metabolites</i> , 2020 , 10,	5.6	182
75	miRNet 2.0: network-based visual analytics for miRNA functional analysis and systems biology. <i>Nucleic Acids Research</i> , 2020 , 48, W244-W251	20.1	147
74	EcoToxModules: Custom Gene Sets to Organize and Analyze Toxicogenomics Data from Ecological Species. <i>Environmental Science & Technology</i> , 2020 , 54, 4376-4387	10.3	5

73	Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data. <i>Nature Protocols</i> , 2020 , 15, 799-821	18.8	346
72	Comprehensive phenotyping and transcriptome profiling to study nanotoxicity in. <i>PeerJ</i> , 2020 , 8, e8684	3.1	7
71	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	1.4	59
70	Network-Based Approaches for Multi-omics Integration. <i>Methods in Molecular Biology</i> , 2020 , 2104, 469-487	1.7	13
69	EcoToxChip: A next-generation toxicogenomics tool for chemical prioritization and environmental management. <i>Environmental Toxicology and Chemistry</i> , 2019 , 38, 279-288	3.8	26
68	MetaboAnalystR 2.0: From Raw Spectra to Biological Insights. <i>Metabolites</i> , 2019 , 9,	5.6	167
67	NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. <i>Nucleic Acids Research</i> , 2019 , 47, W234-W241	20.1	491
66	Metabolome Analysis		0
65	Using MetaboAnalyst 4.0 for Comprehensive and Integrative Metabolomics Data Analysis. <i>Current Protocols in Bioinformatics</i> , 2019 , 68, e86	24.2	928
64	T1000: a reduced gene set prioritized for toxicogenomic studies. <i>PeerJ</i> , 2019 , 7, e7975	3.1	8
63	Intestinal dysbiosis compromises alveolar macrophage immunity to Mycobacterium tuberculosis. <i>Mucosal Immunology</i> , 2019 , 12, 772-783	9.2	32
62	Using OmicsNet for Network Integration and 3D Visualization. <i>Current Protocols in Bioinformatics</i> , 2019 , 65, e69	24.2	27
61	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	4.4	21
60	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	4.9	11
59	MetaboAnalystR: an R package for flexible and reproducible analysis of metabolomics data. <i>Bioinformatics</i> , 2018 , 34, 4313-4314	7.2	274
58	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	4.6	44
57	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	20.1	78
56	Xeno-miRNet: a comprehensive database and analytics platform to explore xeno-miRNAs and their potential targets. <i>PeerJ</i> , 2018 , 6, e5650	3.1	24

55	miRNet-Functional Analysis and Visual Exploration of miRNA-Target Interactions in a Network Context. <i>Methods in Molecular Biology</i> , 2018 , 1819, 215-233	1.4	95
54	Metabolomics investigation of dietary effects on flesh quality in grass carp (<i>Ctenopharyngodon idellus</i>). <i>GigaScience</i> , 2018 , 7,	7.6	20
53	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. <i>Nucleic Acids Research</i> , 2018 , 46, W486-W494	20.1	2157
52	Computational Strategies for Biological Interpretation of Metabolomics Data. <i>Advances in Experimental Medicine and Biology</i> , 2017 , 965, 191-206	3.6	5
51	MicrobiomeAnalyst: a web-based tool for comprehensive statistical, visual and meta-analysis of microbiome data. <i>Nucleic Acids Research</i> , 2017 , 45, W180-W188	20.1	706
50	Bioinformatics Tools for the Interpretation of Metabolomics Data. <i>Current Pharmacology Reports</i> , 2017 , 3, 374-383	5.5	28
49	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	4	21
48	Transcript analysis in two alfalfa salt tolerance selected breeding populations relative to a non-tolerant population. <i>Genome</i> , 2017 , 60, 104-127	2.4	9
47	Computational Approaches for Integrative Analysis of the Metabolome and Microbiome. <i>Metabolites</i> , 2017 , 7,	5.6	55
46	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	5.3	11
45	miRNet - dissecting miRNA-target interactions and functional associations through network-based visual analysis. <i>Nucleic Acids Research</i> , 2016 , 44, W135-41	20.1	265
44	The Effect of In Vitro Cultivation on the Transcriptome of Adult <i>Brugia malayi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004311	4.8	15
43	Comprehensive Transcriptome Meta-analysis to Characterize Host Immune Responses in Helminth Infections. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004624	4.8	13
42	The Effects of Ivermectin on <i>Brugia malayi</i> Females In Vitro: A Transcriptomic Approach. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004929	4.8	17
41	Using MetaboAnalyst 3.0 for Comprehensive Metabolomics Data Analysis. <i>Current Protocols in Bioinformatics</i> , 2016 , 55, 14.10.1-14.10.91	24.2	957
40	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	4	11
39	Conditional-ready mouse embryonic stem cell derived macrophages enable the study of essential genes in macrophage function. <i>Scientific Reports</i> , 2015 , 5, 8908	4.9	15
38	NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data. <i>Nature Protocols</i> , 2015 , 10, 823-44	18.8	459

37	Disruption of histone methylation in developing sperm impairs offspring health transgenerationally. <i>Science</i> , 2015 , 350, aab2006	33.3	317
36	MetaboAnalyst 3.0--making metabolomics more meaningful. <i>Nucleic Acids Research</i> , 2015 , 43, W251-7	20.1	2067
35	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, 4457-69	5.6	35
34	An Endotoxin Tolerance Signature Predicts Sepsis and Organ Dysfunction at Initial Clinical Presentation. <i>EBioMedicine</i> , 2014 , 1, 64-71	8.8	84
33	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	2.9	2
32	NetworkAnalyst--integrative approaches for protein-protein interaction network analysis and visual exploration. <i>Nucleic Acids Research</i> , 2014 , 42, W167-74	20.1	254
31	Pathways of Toxicity. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2014 , 31, 53-61	4.3	59
30	Translational biomarker discovery in clinical metabolomics: an introductory tutorial. <i>Metabolomics</i> , 2013 , 9, 280-299	4.7	594
29	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	5.3	12
28	HMDB 3.0--The Human Metabolome Database in 2013. <i>Nucleic Acids Research</i> , 2013 , 41, D801-7	20.1	2210
27	Metabolomic analysis for first-trimester Down syndrome prediction. <i>American Journal of Obstetrics and Gynecology</i> , 2013 , 208, 371.e1-8	6.4	36
26	First-trimester metabolomic detection of late-onset preeclampsia. <i>American Journal of Obstetrics and Gynecology</i> , 2013 , 208, 58.e1-7	6.4	55
25	INVEX--a web-based tool for integrative visualization of expression data. <i>Bioinformatics</i> , 2013 , 29, 3232-4.2	4.2	42
24	INMEX--a web-based tool for integrative meta-analysis of expression data. <i>Nucleic Acids Research</i> , 2013 , 41, W63-70	20.1	119
23	Metabolomic analysis of cold acclimation of Arctic <i>Mesorhizobium</i> sp. strain N33. <i>PLoS ONE</i> , 2013 , 8, e84801	3.7	12
22	MetaboAnalyst 2.0--a comprehensive server for metabolomic data analysis. <i>Nucleic Acids Research</i> , 2012 , 40, W127-33	20.1	935
21	METAGENassist: a comprehensive web server for comparative metagenomics. <i>Nucleic Acids Research</i> , 2012 , 40, W88-95	20.1	267
20	Metabolomics and first-trimester prediction of early-onset preeclampsia. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2012 , 25, 1840-7	2	85

19	Metabolomic data processing, analysis, and interpretation using MetaboAnalyst. <i>Current Protocols in Bioinformatics</i> , 2011 , Chapter 14, Unit 14.10	24.2	124
18	Web-based inference of biological patterns, functions and pathways from metabolomic data using MetaboAnalyst. <i>Nature Protocols</i> , 2011 , 6, 743-60	18.8	718
17	Expression of duck CCL19 and CCL21 and CCR7 receptor in lymphoid and influenza-infected tissues. <i>Molecular Immunology</i> , 2011 , 48, 1950-7	4.3	21
16	The human serum metabolome. <i>PLoS ONE</i> , 2011 , 6, e16957	3.7	1118
15	Learning to predict cancer-associated skeletal muscle wasting from 1H-NMR profiles of urinary metabolites. <i>Metabolomics</i> , 2011 , 7, 25-34	4.7	38
14	MetATT: a web-based metabolomics tool for analyzing time-series and two-factor datasets. <i>Bioinformatics</i> , 2011 , 27, 2455-6	7.2	52
13	MSEA: a web-based tool to identify biologically meaningful patterns in quantitative metabolomic data. <i>Nucleic Acids Research</i> , 2010 , 38, W71-7	20.1	412
12	MetPA: a web-based metabolomics tool for pathway analysis and visualization. <i>Bioinformatics</i> , 2010 , 26, 2342-4	7.2	447
11	SMPDB: The Small Molecule Pathway Database. <i>Nucleic Acids Research</i> , 2010 , 38, D480-7	20.1	213
10	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	4.7	125
9	Spatiotemporal integration of molecular and anatomical data in virtual reality using semantic mapping. <i>International Journal of Nanomedicine</i> , 2009 , 4, 79-89	7.3	2
8	HMDB: a knowledgebase for the human metabolome. <i>Nucleic Acids Research</i> , 2009 , 37, D603-10	20.1	1431
7	MetaboAnalyst: a web server for metabolomic data analysis and interpretation. <i>Nucleic Acids Research</i> , 2009 , 37, W652-60	20.1	1202
6	MetaboMiner--semi-automated identification of metabolites from 2D NMR spectra of complex biofluids. <i>BMC Bioinformatics</i> , 2008 , 9, 507	3.6	150
5	The duck toll like receptor 7: genomic organization, expression and function. <i>Molecular Immunology</i> , 2008 , 45, 2055-61	4.3	61
4	Dendritic cell inhibitory and activating immunoreceptors (DCIR and DCAR) in duck: Genomic organization and expression. <i>Molecular Immunology</i> , 2008 , 45, 3942-6	4.3	7
3	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	1.9	14
2	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, 272-85	3.2	21

1 Using MetaboAnalyst 5.0 for LC-MS/MS spectra processing, multi-omics integration and covariate adjustment of global metabolomics data. *Nature Protocols*, 18.8 27