Xia Yang

List of Publications by Year in descending order

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101	9,750	42	93
papers	citations	h-index	g-index
115	115	115	17120 citing authors
all docs	docs citations	times ranked	

#	Article	IF	Citations
1	IAPP-induced beta cell stress recapitulates the islet transcriptome in type 2 diabetes. Diabetologia, 2022, 65, 173-187.	2.9	19
2	Relative contributions of sex hormones, sex chromosomes, and gonads to sex differences in tissue gene regulation. Genome Research, 2022, , .	2.4	23
3	PharmOmics: A species- and tissue-specific drug signature database and gene-network-based drug repositioning tool. IScience, 2022, 25, 104052.	1.9	8
4	Bioinformatics network analyses of growth differentiation factor 11. Open Life Sciences, 2022, 17, 426-437.	0.6	0
5	Single-Cell Study of Two Rat Models of Pulmonary Arterial Hypertension Reveals Connections to Human Pathobiology and Drug Repositioning. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 1006-1022.	2.5	36
6	Systems toxicogenomics of prenatal low-dose BPA exposure on liver metabolic pathways, gut microbiota, and metabolic health in mice. Environment International, 2021, 146, 106260.	4.8	42
7	Estrogen receptor alpha in the brain mediates tamoxifen-induced changes in physiology in mice. ELife, 2021, 10, .	2.8	17
8	Mergeomics 2.0: a web server for multi-omics data integration to elucidate disease networks and predict therapeutics. Nucleic Acids Research, 2021, 49, W375-W387.	6.5	46
9	Transcription Factor MAFF (MAF Basic Leucine Zipper Transcription Factor F) Regulates an Atherosclerosis Relevant Network Connecting Inflammation and Cholesterol Metabolism. Circulation, 2021, 143, 1809-1823.	1.6	28
10	Joint cell segmentation and cell type annotation for spatial transcriptomics. Molecular Systems Biology, 2021, 17, e10108.	3.2	46
11	Disparate Metabolomic Responses to Fructose Consumption between Different Mouse Strains and the Role of Gut Microbiota. Metabolites, 2021, 11, 342.	1.3	7
12	Conservation and divergence of vulnerability and responses to stressors between human and mouse astrocytes. Nature Communications, 2021, 12, 3958.	5.8	94
13	The 2020 FASEB virtual Catalyst Conference on Integrative Approach for Complex Diseases Prevention and Management and Beyond, December 16, 2020. FASEB Journal, 2021, 35, e21500.	0.2	O
14	Found in translationâ€"core network preservation across liver diseases and species. Cell Reports Medicine, 2021, 2, 100347.	3.3	1
15	Unveiling the Pathogenesis of Psychiatric Disorders Using Network Models. Genes, 2021, 12, 1101.	1.0	10
16	Gene networks and pathways for plasma lipid traits via multitissue multiomics systems analysis. Journal of Lipid Research, 2021, 62, 100019.	2.0	9
17	Differential metabolic and multi-tissue transcriptomic responses to fructose consumption among genetically diverse mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2020, 1866, 165569.	1.8	21
18	Multiâ€Tissue Multiâ€Omics Nutrigenomics Indicates Contextâ€Specific Effects of Docosahexaenoic Acid on Rat Brain. Molecular Nutrition and Food Research, 2020, 64, e2000788.	1.5	2

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19	MethylResolverâ€"a method for deconvoluting bulk DNA methylation profiles into known and unknown cell contents. Communications Biology, 2020, 3, 422.	2.0	33
20	Omegaâ€3 fatty acids increase OXPHOS energy for immune therapy of Alzheimer disease patients. FASEB Journal, 2020, 34, 9982-9994.	0.2	6
21	Oral 15-Hydroxyeicosatetraenoic Acid Induces Pulmonary Hypertension in Mice by Triggering T Cell–Dependent Endothelial Cell Apoptosis. Hypertension, 2020, 76, 985-996.	1.3	15
22	Host Genetic Background and Gut Microbiota Contribute to Differential Metabolic Responses to Fructose Consumption in Mice. Journal of Nutrition, 2020, 150, 2716-2728.	1.3	15
23	Single-cell RNA-seq analysis of the brainstem of mutant SOD1 mice reveals perturbed cell types and pathways of amyotrophic lateral sclerosis. Neurobiology of Disease, 2020, 141, 104877.	2.1	48
24	Therapeutic IDOL Reduction Ameliorates Amyloidosis and Improves Cognitive Function in APP/PS1 Mice. Molecular and Cellular Biology, 2020, 40, .	1.1	8
25	Liver ChREBP Protects Against Fructose-Induced Glycogenic Hepatotoxicity by Regulating L-Type Pyruvate Kinase. Diabetes, 2020, 69, 591-602.	0.3	32
26	Hypothalamic oestrogen receptor alpha establishes a sexually dimorphic regulatory node of energy expenditure. Nature Metabolism, 2020, 2, 351-363.	5.1	61
27	Multitissue Multiomics Systems Biology to Dissect Complex Diseases. Trends in Molecular Medicine, 2020, 26, 718-728.	3.5	39
28	Systems genetics applications in metabolism research. Nature Metabolism, 2019, 1, 1038-1050.	5.1	35
29	Network modeling of single-cell omics data: challenges, opportunities, and progresses. Emerging Topics in Life Sciences, 2019, 3, 379-398.	1.1	48
30	Diesel exhaust particles dysregulate multiple immunological pathways in murine macrophages: Lessons from microarray and scRNA-seq technologies. Archives of Biochemistry and Biophysics, 2019, 678, 108116.	1.4	10
31	Prenatal Bisphenol A Exposure in Mice Induces Multitissue Multiomics Disruptions Linking to Cardiometabolic Disorders. Endocrinology, 2019, 160, 409-429.	1.4	35
32	Targeting BCAA Catabolism to Treat Obesity-Associated Insulin Resistance. Diabetes, 2019, 68, 1730-1746.	0.3	201
33	Brain Trauma Disrupts Hepatic Lipid Metabolism: Blame It on Fructose?. Molecular Nutrition and Food Research, 2019, 63, e1801054.	1.5	12
34	Integrative Genomics Analysis Unravels Tissue-Specific Pathways, Networks, and Key Regulators of Blood Pressure Regulation. Frontiers in Cardiovascular Medicine, 2019, 6, 21.	1.1	15
35	Network Modeling Approaches and Applications to Unravelling Non-Alcoholic Fatty Liver Disease. Genes, 2019, 10, 966.	1.0	26
36	IDOL regulates systemic energy balance through control of neuronal VLDLR expression. Nature Metabolism, 2019, 1, 1089-1100.	5.1	12

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37	Novel Treatment of Hypertension by Specifically Targeting E2F for Restoration of Endothelial Dihydrofolate Reductase and eNOS Function Under Oxidative Stress. Hypertension, 2019, 73, 179-189.	1.3	22
38	Multi-omics integration reveals molecular networks and regulators of psoriasis. BMC Systems Biology, 2019, 13 , 8 .	3.0	37
39	Single cell analysis reveals immune cell–adipocyte crosstalk regulating the transcription of thermogenic adipocytes. ELife, 2019, 8, .	2.8	110
40	Novel Treatment of Hypertension by Specifically Targeting E2F for Restoration of Endothelial Dihydrofolate Reductase and eNOS Function Under Oxidative Stress. FASEB Journal, 2019, 33, 835.15.	0.2	0
41	Integration of Multi-omics Data from Mouse Diversity Panel Highlights Mitochondrial Dysfunction in Non-alcoholic Fatty Liver Disease. Cell Systems, 2018, 6, 103-115.e7.	2.9	124
42	Maternal High-Protein and Low-Protein Diets Perturb Hypothalamus and Liver Transcriptome and Metabolic Homeostasis in Adult Mouse Offspring. Frontiers in Genetics, 2018, 9, 642.	1.1	6
43	Biglycan gene connects metabolic dysfunction with brain disorder. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 3679-3687.	1.8	18
44	Single cell molecular alterations reveal target cells and pathways of concussive brain injury. Nature Communications, 2018, 9, 3894.	5.8	113
45	Tissue-specific pathways and networks underlying sexual dimorphism in non-alcoholic fatty liver disease. Biology of Sex Differences, 2018, 9, 46.	1.8	65
46	<i>JCAD</i> , a Gene at the 10p11 Coronary Artery Disease Locus, Regulates Hippo Signaling in Endothelial Cells. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 1711-1722.	1.1	36
47	The Memory of Environmental Chemical Exposure in C.Âelegans Is Dependent on the Jumonji Demethylases jmjd-2 and jmjd-3/utx-1. Cell Reports, 2018, 23, 2392-2404.	2.9	53
48	System biology approach intersecting diet and cell metabolism with pathogenesis of brain disorders. Progress in Neurobiology, 2018, 169, 76-90.	2.8	11
49	Co-regulatory networks of human serum proteins link genetics to disease. Science, 2018, 361, 769-773.	6.0	375
50	Shared mechanisms among neurodegenerative diseases: from genetic factors to gene networks. Journal of Genetics, 2018, 97, 795-806.	0.4	50
51	Translating GWAS Findings to Novel Therapeutic Targets for Coronary Artery Disease. Frontiers in Cardiovascular Medicine, 2018, 5, 56.	1.1	21
52	Innate Immune Cells Are Regulated by Axl in Hypertensive Kidney. American Journal of Pathology, 2018, 188, 1794-1806.	1.9	6
53	GM-CSF driven myeloid cells in adipose tissue link weight gain and insulin resistance via formation of 2-aminoadipate. Scientific Reports, 2018, 8, 11485.	1.6	18
54	Oxidized phospholipids regulate amino acid metabolism through MTHFD2 to facilitate nucleotide release in endothelial cells. Nature Communications, 2018, 9, 2292.	5.8	44

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55	The Genetic Architecture of Dietâ€Induced Hepatic Fibrosis in Mice. Hepatology, 2018, 68, 2182-2196.	3.6	51
56	Host Genetic Background and Gut Microbiota Contribute to Differential Metabolic Responses to High Fructose Consumption in Mice. Diabetes, 2018, 67, .	0.3	3
57	Shared mechanisms among neurodegenerative diseases: from genetic factors to gene networks. Journal of Genetics, 2018, 97, 795-806.	0.4	20
58	Traumatic Brain Injury Induces Genome-Wide Transcriptomic, Methylomic, and Network Perturbations in Brain and Blood Predicting Neurological Disorders. EBioMedicine, 2017, 16, 184-194.	2.7	88
59	Applications and Limitations of Mouse Models for Understanding Human Atherosclerosis. Cell Metabolism, 2017, 25, 248-261.	7.2	161
60	Extended Multiplexing of Tandem Mass Tags (TMT) Labeling Reveals Age and High Fat Diet Specific Proteome Changes in Mouse Epididymal Adipose Tissue. Molecular and Cellular Proteomics, 2017, 16, 873-890.	2.5	240
61	Multidimensional Integrative Genomics Approaches to Dissecting Cardiovascular Disease. Frontiers in Cardiovascular Medicine, 2017, 4, 8.	1.1	25
62	Shared genetic regulatory networks for cardiovascular disease and type 2 diabetes in multiple populations of diverse ethnicities in the United States. PLoS Genetics, 2017, 13, e1007040.	1.5	82
63	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. EBioMedicine, 2016, 7, 157-166.	2.7	59
64	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. BMC Genomics, 2016, 17, 874.	1.2	106
65	Mergeomics: a web server for identifying pathological pathways, networks, and key regulators via multidimensional data integration. BMC Genomics, 2016, 17, 722.	1.2	59
66	Molecular and genetic inflammation networks in major human diseases. Molecular BioSystems, 2016, 12, 2318-2341.	2.9	49
67	Network-Based Identification and Prioritization of Key Regulators of Coronary Artery Disease Loci. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 928-941.	1.1	66
68	Exposure to the BPA-Substitute Bisphenol S Causes Unique Alterations of Germline Function. PLoS Genetics, 2016, 12, e1006223.	1.5	80
69	Abstract 58: Network-based Identification and Prioritization of Key Regulators of Coronary Artery Disease Loci. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, .	1.1	0
70	Identification and validation of N-acetyltransferase 2 as an insulin sensitivity gene. Journal of Clinical Investigation, 2015, 125, 1739-1751.	3.9	94
71	Dissecting the Roles of MicroRNAs in Coronary Heart Disease via Integrative Genomic Analyses. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1011-1021.	1.1	53
72	A systems genetics study of swine illustrates mechanisms underlying human phenotypic traits. BMC Genomics, 2015, 16, 88.	1.2	28

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73	Nutritional systems biology of type 2 diabetes. Genes and Nutrition, 2015, 10, 481.	1.2	26
74	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	1.5	107
75	Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. PLoS Genetics, 2015, 11, e1005202.	1.5	41
76	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. Molecular Systems Biology, 2015, 11, 799.	3.2	102
77	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2207-2217.	1.1	101
78	Abstract 18836: Integrative Pathway Analysis of Genome-wide Association Studies of Carotid Plaque Phenotypes. Circulation, 2015, 132, .	1.6	0
79	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. Diabetes, 2014, 63, 2158-2171.	0.3	297
80	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. PLoS Genetics, 2014, 10, e1004502.	1.5	192
81	Shared Molecular Pathways and Gene Networks for Cardiovascular Disease and Type 2 Diabetes Mellitus in Women Across Diverse Ethnicities. Circulation: Cardiovascular Genetics, 2014, 7, 911-919.	5.1	48
82	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. Molecular Systems Biology, 2014, 10, 743.	3.2	182
83	The pathogenesis of obesity from a genomic and systems biology perspective. Yale Journal of Biology and Medicine, 2014, 87, 113-26.	0.2	20
84	Systems Biology Approaches and Applications in Obesity, Diabetes, and Cardiovascular Diseases. Current Cardiovascular Risk Reports, 2013, 7, 73-83.	0.8	49
85	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1427-1434.	1.1	157
86	Integrative Analysis of a Cross-Loci Regulation Network Identifies App as a Gene Regulating Insulin Secretion from Pancreatic Islets. PLoS Genetics, 2012, 8, e1003107.	1.5	76
87	Integrating Genetic Association, Genetics of Gene Expression, and Single Nucleotide Polymorphism Set Analysis to Identify Susceptibility Loci for Type 2 Diabetes Mellitus. American Journal of Epidemiology, 2012, 176, 423-430.	1.6	31
88	Systems analysis of eleven rodent disease models reveals an inflammatome signature and key drivers. Molecular Systems Biology, 2012, 8, 594.	3.2	134
89	Functional Genomics- and Network-driven Systems Biology Approaches for Pharmacogenomics and Toxicogenomics. Current Drug Metabolism, 2012, 13, 952-967.	0.7	9
90	Use of Functional Genomics to Identify Candidate Genes Underlying Human Genetic Association Studies of Vascular Diseases. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 216-222.	1.1	22

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91	Integrative genomics strategies to elucidate the complexity of drug response. Pharmacogenomics, 2011, 12, 1695-1715.	0.6	28
92	Integrating Pathway Analysis and Genetics of Gene Expression for Genome-wide Association Studies. American Journal of Human Genetics, 2010, 86, 581-591.	2.6	224
93	Systematic genetic and genomic analysis of cytochrome P450 enzyme activities in human liver. Genome Research, 2010, 20, 1020-1036.	2.4	231
94	Liver and Adipose Expression Associated SNPs Are Enriched for Association to Type 2 Diabetes. PLoS Genetics, 2010, 6, e1000932.	1.5	161
95	ldentification and validation of genes affecting aortic lesions in mice. Journal of Clinical Investigation, 2010, 120, 2414-2422.	3.9	49
96	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. Nature Genetics, 2009, 41, 415-423.	9.4	257
97	Variations in DNA elucidate molecular networks that cause disease. Nature, 2008, 452, 429-435.	13.7	840
98	Mapping the Genetic Architecture of Gene Expression in Human Liver. PLoS Biology, 2008, 6, e107.	2.6	872
99	Dosage compensation is less effective in birds than in mammals. Journal of Biology, 2007, 6, 2.	2.7	304
100	Tissue-specific expression and regulation of sexually dimorphic genes in mice. Genome Research, 2006, 16, 995-1004.	2.4	785
101	An integrative genomics approach to infer causal associations between gene expression and disease. Nature Genetics, 2005, 37, 710-717.	9.4	967