

# Jiang Qian

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2622477/publications.pdf>

Version: 2024-02-01

114  
papers

7,814  
citations

61857

43  
h-index

62479

80  
g-index

126  
all docs

126  
docs citations

126  
times ranked

12871  
citing authors

#	ARTICLE	IF	CITATIONS
1	Increased LCN2 (lipocalin 2) in the RPE decreases autophagy and activates inflammasome-ferroptosis processes in a mouse model of dry AMD. <i>Autophagy</i> , 2023, 19, 92-111.	4.3	41
2	scEnhancer: a single-cell enhancer resource with annotation across hundreds of tissue/cell types in three species. <i>Nucleic Acids Research</i> , 2022, 50, D371-D379.	6.5	16
3	Aqueous proteins help predict the response of patients with neovascular age-related macular degeneration to anti-VEGF therapy. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	9
4	Cell-specific cis-regulatory elements and mechanisms of non-coding genetic disease in human retina and retinal organoids. <i>Developmental Cell</i> , 2022, 57, 820-836.e6.	3.1	37
5	LRLoop: a method to predict feedback loops in cell-cell communication. <i>Bioinformatics</i> , 2022, 38, 4117-4126.	1.8	9
6	Role of glia in optic nerve. <i>Progress in Retinal and Eye Research</i> , 2021, 81, 100886.	7.3	23
7	Identification of Novel Serological Autoantibodies in Takayasu Arteritis Patients Using HuProt Arrays. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100036.	2.5	13
8	Proteome Landscape of Epithelial-to-Mesenchymal Transition (EMT) of Retinal Pigment Epithelium Shares Commonalities With Malignancy-Associated EMT. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100131.	2.5	12
9	Temperature and species-dependent regulation of browning in retrobulbar fat. <i>Scientific Reports</i> , 2021, 11, 3094.	1.6	1
10	An Integrated Systems Biology Approach Identifies the Proteasome as A Critical Host Machinery for ZIKV and DENV Replication. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 108-122.	3.0	7
11	An all-to-all approach to the identification of sequence-specific readers for epigenetic DNA modifications on cytosine. <i>Nature Communications</i> , 2021, 12, 795.	5.8	22
12	Factors Associated With a Patient's Decision to Select a Cost-effective vs the Most Effective Therapy for Their Own Eye Disease. <i>JAMA Network Open</i> , 2021, 4, e2037880.	2.8	6
13	Î²A1-crystallin regulates glucose metabolism and mitochondrial function in mouse retinal astrocytes by modulating PTP1B activity. <i>Communications Biology</i> , 2021, 4, 248.	2.0	10
14	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	7.7	189
15	Transcriptome Landscape of Epithelial to Mesenchymal Transition of Human Stem Cell-Derived RPE. , 2021, 62, 1.		12
16	Polycomb Group Protein Ezh2 Supports Mammalian Axon Regeneration in Peripheral and Central Nervous System. <i>FASEB Journal</i> , 2021, 35, .	0.2	1
17	Control of neurogenic competence in mammalian hypothalamic tanycytes. <i>Science Advances</i> , 2021, 7, .	4.7	36
18	Large-scale phenotypic drug screen identifies neuroprotectants in zebrafish and mouse models of retinitis pigmentosa. <i>ELife</i> , 2021, 10, .	2.8	15

#	ARTICLE	IF	CITATIONS
19	Î²A3/A1-crystallin regulates apical polarity and EGFR endocytosis in retinal pigmented epithelial cells. <i>Communications Biology</i> , 2021, 4, 850.	2.0	13
20	Primary angle closure glaucoma is characterized by altered extracellular matrix homeostasis in the iris. <i>Proteomics - Clinical Applications</i> , 2021, 15, 2000094.	0.8	3
21	Human retinal organoids release extracellular vesicles that regulate gene expression in target human retinal progenitor cells. <i>Scientific Reports</i> , 2021, 11, 21128.	1.6	18
22	Gene regulatory networks controlling temporal patterning, neurogenesis, and cell-fate specification in mammalian retina. <i>Cell Reports</i> , 2021, 37, 109994.	2.9	52
23	EnhancerAtlas 2.0: an updated resource with enhancer annotation in 586 tissue/cell types across nine species. <i>Nucleic Acids Research</i> , 2020, 48, D58-D64.	6.5	142
24	Gene regulatory networks controlling vertebrate retinal regeneration. <i>Science</i> , 2020, 370, .	6.0	248
25	Glycoproteomics-based signatures for tumor subtyping and clinical outcome prediction of high-grade serous ovarian cancer. <i>Nature Communications</i> , 2020, 11, 6139.	5.8	72
26	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276.	2.9	83
27	Knocking Out Non-muscle Myosin II in Retinal Ganglion Cells Promotes Long-Distance Optic Nerve Regeneration. <i>Cell Reports</i> , 2020, 31, 107537.	2.9	33
28	Retinal pigment epithelium transcriptome analysis in chronic smoking reveals a suppressed innate immune response and activation of differentiation pathways. <i>Free Radical Biology and Medicine</i> , 2020, 156, 176-189.	1.3	4
29	Investigating cone photoreceptor development using patient-derived NRL null retinal organoids. <i>Communications Biology</i> , 2020, 3, 82.	2.0	62
30	Integration of IgA and IgG Autoantigens Improves Performance of Biomarker Panels for Early Diagnosis of Lung Cancer. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 490-500.	2.5	23
31	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	13.5	430
32	EAGLE: An algorithm that utilizes a small number of genomic features to predict tissue/cell type-specific enhancer-gene interactions. <i>PLoS Computational Biology</i> , 2019, 15, e1007436.	1.5	19
33	Differentially Methylated Super-Enhancers Regulate Target Gene Expression in Human Cancer. <i>Scientific Reports</i> , 2019, 9, 15034.	1.6	9
34	PanoView: An iterative clustering method for single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2019, 15, e1007040.	1.5	16
35	Neutrophils homing into the retina trigger pathology in early age-related macular degeneration. <i>Communications Biology</i> , 2019, 2, 348.	2.0	37
36	Discovery and Validation of a Serologic Autoantibody Panel for Early Diagnosis of Esophageal Squamous Cell Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1454-1460.	1.1	20

#	ARTICLE	IF	CITATIONS
37	Decomposing Cell Identity for Transfer Learning across Cellular Measurements, Platforms, Tissues, and Species. <i>Cell Systems</i> , 2019, 8, 395-411.e8.	2.9	121
38	Epigenomic profiling of retinal progenitors reveals LHX2 is required for developmental regulation of open chromatin. <i>Communications Biology</i> , 2019, 2, 142.	2.0	36
39	AAGMarker 1.0: a resource of serological autoantigen biomarkers for clinical diagnosis and prognosis of various human diseases. <i>Nucleic Acids Research</i> , 2018, 46, D886-D893.	6.5	5
40	ATAC-Seq analysis reveals a widespread decrease of chromatin accessibility in age-related macular degeneration. <i>Nature Communications</i> , 2018, 9, 1364.	5.8	124
41	Global Identification of Small Ubiquitin-related Modifier (SUMO) Substrates Reveals Crosstalk between SUMOylation and Phosphorylation Promotes Cell Migration. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 871-888.	2.5	24
42	MeDReaders: a database for transcription factors that bind to methylated DNA. <i>Nucleic Acids Research</i> , 2018, 46, D146-D151.	6.5	94
43	Multiplexed Biomarker Panels Discriminate Zika and Dengue Virus Infection in Humans. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 349-356.	2.5	19
44	Heterozygous IDH1R132H/WT created by "single base editing" inhibits human astroglial cell growth by downregulating YAP. <i>Oncogene</i> , 2018, 37, 5160-5174.	2.6	27
45	Analysis of KLF4 regulated genes in cancer cells reveals a role of DNA methylation in promoter-enhancer interactions. <i>Epigenetics</i> , 2018, 13, 751-768.	1.3	15
46	Multiplexed CRISPR/Cas9 Targeting of Genes Implicated in Retinal Regeneration and Degeneration. <i>Frontiers in Cell and Developmental Biology</i> , 2018, 6, 88.	1.8	19
47	A Role for Î²A3/A1-Crystallin in Type 2 EMT of RPE Cells Occurring in Dry Age-Related Macular Degeneration. , 2018, 59, AMD104.		62
48	Foxd1 is required for terminal differentiation of anterior hypothalamic neuronal subtypes. <i>Developmental Biology</i> , 2018, 439, 102-111.	0.9	28
49	An Integrated System Approach Identified the Human Proteasome as a Conserved Critical Machinery for ZIKV and DENV Replication. <i>FASEB Journal</i> , 2018, 32, 669.3.	0.2	0
50	The amino acid transporter SLC36A4 regulates the amino acid pool in retinal pigmented epithelial cells and mediates the mechanistic target of rapamycin, complex 1 signaling. <i>Aging Cell</i> , 2017, 16, 349-359.	3.0	32
51	A Human Proteome Array Approach to Identifying Key Host Proteins Targeted by Toxoplasma Kinase ROP18. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 469-484.	2.5	28
52	Global Analysis of SUMO-Binding Proteins Identifies SUMOylation as a Key Regulator of the INO80 Chromatin Remodeling Complex. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 812-823.	2.5	15
53	Activating the <sc>AKT2</sc> "nuclear factor" <sc>Î²</sc> "lipocalin" axis elicits an inflammatory response in age-related macular degeneration. <i>Journal of Pathology</i> , 2017, 241, 583-588.	2.1	55
54	Anatomical differences of the protein profile in the rabbit sclera during growth. <i>Experimental Eye Research</i> , 2017, 154, 53-63.	1.2	6

#	ARTICLE	IF	CITATIONS
55	Identification of Serological Biomarkers for Early Diagnosis of Lung Cancer Using a Protein Array-Based Approach. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2069-2078.	2.5	63
56	Zika-Virus-Encoded NS2A Disrupts Mammalian Cortical Neurogenesis by Degrading Adherens Junction Proteins. <i>Cell Stem Cell</i> , 2017, 21, 349-358.e6.	5.2	163
57	Identification of Novel Biomarkers for Behcet Disease Diagnosis Using Human Proteome Microarray Approach. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 147-156.	2.5	49
58	Methylated cis-regulatory elements mediate KLF4-dependent gene transactivation and cell migration. <i>ELife</i> , 2017, 6, .	2.8	39
59	A proteomic approach to understanding the pathogenesis of idiopathic macular hole formation. <i>Clinical Proteomics</i> , 2017, 14, 37.	1.1	11
60	Assessing the model transferability for prediction of transcription factor binding sites based on chromatin accessibility. <i>BMC Bioinformatics</i> , 2017, 18, 355.	1.2	22
61	ScaPD: a database for human scaffold proteins. <i>BMC Bioinformatics</i> , 2017, 18, 386.	1.2	8
62	Identification and functional analysis of differentially expressed genes in poorly differentiated hepatocellular carcinoma using RNA-seq. <i>Oncotarget</i> , 2017, 8, 35973-35983.	0.8	7
63	Single-Cell Co-expression Analysis Reveals Distinct Functional Modules, Co-regulation Mechanisms and Clinical Outcomes. <i>PLoS Computational Biology</i> , 2016, 12, e1004892.	1.5	36
64	Off Target, but Sequence-Specific, shRNA-Associated Trans-Activation of Promoter Reporters in Transient Transfection Assays. <i>PLoS ONE</i> , 2016, 11, e0167867.	1.1	1
65	Pro-permeability Factors in Diabetic Macular Edema; the Diabetic Macular Edema Treated With Ozurdex Trial. <i>American Journal of Ophthalmology</i> , 2016, 168, 13-23.	1.7	56
66	A nuclease that mediates cell death induced by DNA damage and poly(ADP-ribose) polymerase-1. <i>Science</i> , 2016, 354, .	6.0	266
67	Transcription factors as readers and effectors of DNA methylation. <i>Nature Reviews Genetics</i> , 2016, 17, 551-565.	7.7	482
68	EnhancerAtlas: a resource for enhancer annotation and analysis in 105 human cell/tissue types. <i>Bioinformatics</i> , 2016, 32, 3543-3551.	1.8	148
69	ARQiv-HTS, a versatile whole-organism screening platform enabling in vivo drug discovery at high-throughput rates. <i>Nature Protocols</i> , 2016, 11, 2432-2453.	5.5	50
70	Temporal patterns of gene expression during calyx of held development. <i>Developmental Neurobiology</i> , 2016, 76, 166-189.	1.5	16
71	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. <i>Molecular Cell</i> , 2016, 61, 153-160.	4.5	74
72	Lhx2 Is an Essential Factor for Retinal Gliogenesis and Notch Signaling. <i>Journal of Neuroscience</i> , 2016, 36, 2391-2405.	1.7	79

#	ARTICLE	IF	CITATIONS
73	Serum molecular signature for proliferativeÂdiabeticÂretinopathy in Saudi patients with type 2 diabetes. <i>Molecular Vision</i> , 2016, 22, 636-45.	1.1	6
74	Î²A3/A1-crystallin is a critical mediator of STAT3 signaling in optic nerve astrocytes. <i>Scientific Reports</i> , 2015, 5, 8755.	1.6	11
75	Systematic Prediction of Scaffold Proteins Reveals New Design Principles in Scaffold-Mediated Signal Transduction. <i>PLoS Computational Biology</i> , 2015, 11, e1004508.	1.5	13
76	Differential DNA methylation identified in the blood and retina of AMD patients. <i>Epigenetics</i> , 2015, 10, 698-707.	1.3	62
77	A Screen for Extracellular Signal-Regulated Kinase-Primed Glycogen Synthase Kinase 3 Substrates Identifies the p53 Inhibitor iASPP. <i>Journal of Virology</i> , 2015, 89, 9232-9241.	1.5	10
78	Characterization of tissue-specific differential DNA methylation suggests distinct modes of positive and negative gene expression regulation. <i>BMC Genomics</i> , 2015, 16, 49.	1.2	132
79	Pro-Permeability Factors After Dexamethasone Implant in Retinal Vein Occlusion; the Ozurdex for Retinal Vein Occlusion (ORVO) Study. <i>American Journal of Ophthalmology</i> , 2015, 160, 313-321.e19.	1.7	35
80	Small-moleculeâ€directed, efficient generation of retinal pigment epithelium from human pluripotent stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10950-10955.	3.3	114
81	Oxidative stress induces mitochondrial dysfunction and a protective unfolded protein response in RPE cells. <i>Free Radical Biology and Medicine</i> , 2014, 69, 1-14.	1.3	81
82	PhosphoNetworks: a database for human phosphorylation networks. <i>Bioinformatics</i> , 2014, 30, 141-142.	1.8	106
83	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. <i>Nature Communications</i> , 2014, 5, 4961.	5.8	72
84	Global analysis of phosphorylation networks in humans. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 224-231.	1.1	20
85	Lhx1 Controls Terminal Differentiation and Circadian Function of the Suprachiasmatic Nucleus. <i>Cell Reports</i> , 2014, 7, 609-622.	2.9	88
86	A novel methyl-binding domain protein enrichment method for identifying genome-wide tissue-specific DNA methylation from nanogram DNA samples. <i>Epigenetics and Chromatin</i> , 2013, 6, 17.	1.8	17
87	Hypomethylation of the IL17RC Promoter in Peripheral Blood Leukocytes Is Not A Hallmark of Age-Related Macular Degeneration. <i>Cell Reports</i> , 2013, 5, 1527-1535.	2.9	42
88	Construction of human activityâ€based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013, 9, 655.	3.2	153
89	Integrative analysis of tissue-specific methylation and alternative splicing identifies conserved transcription factor binding motifs. <i>Nucleic Acids Research</i> , 2013, 41, 8503-8514.	6.5	46
90	DNA methylation presents distinct binding sites for human transcription factors. <i>ELife</i> , 2013, 2, e00726.	2.8	292

#	ARTICLE	IF	CITATIONS
91	Phosphorylation of the Chromatin Binding Domain of KSHV LANA. <i>PLoS Pathogens</i> , 2012, 8, e1002972.	2.1	32
92	Rapid Identification of Monospecific Monoclonal Antibodies Using a Human Proteome Microarray. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.016253.	2.5	136
93	A Protein Array Screen for Kaposi's Sarcoma-Associated Herpesvirus LANA Interactors Links LANA to TIP60, PP2A Activity, and Telomere Shortening. <i>Journal of Virology</i> , 2012, 86, 5179-5191.	1.5	56
94	Dynamics of Regulatory Networks in the Developing Mouse Retina. <i>PLoS ONE</i> , 2012, 7, e46521.	1.1	9
95	Conserved Herpesvirus Kinases Target the DNA Damage Response Pathway and TIP60 Histone Acetyltransferase to Promote Virus Replication. <i>Cell Host and Microbe</i> , 2011, 10, 390-400.	5.1	148
96	Dynamic usage of alternative splicing exons during mouse retina development. <i>Nucleic Acids Research</i> , 2011, 39, 7920-7930.	6.5	33
97	Differential substrate selectivity and stability with different forms of protein kinase CK2. <i>FASEB Journal</i> , 2011, 25, lb146.	0.2	0
98	A genomic atlas of mouse hypothalamic development. <i>Nature Neuroscience</i> , 2010, 13, 767-775.	7.1	354
99	MicroRNA Profile of the Developing Mouse Retina. , 2010, 51, 1823.		98
100	Computational analysis of tissue-specific gene networks: application to murine retinal functional studies. <i>Bioinformatics</i> , 2010, 26, 2289-2297.	1.8	26
101	Profiling the Human Protein-DNA Interactome Reveals ERK2 as a Transcriptional Repressor of Interferon Signaling. <i>Cell</i> , 2009, 139, 610-622.	13.5	352
102	Analysis of regulatory network topology reveals functionally distinct classes of microRNAs. <i>Nucleic Acids Research</i> , 2008, 36, 6494-6503.	6.5	81
103	Systems biology approach to integrative comparative genomics. <i>Expert Review of Proteomics</i> , 2007, 4, 107-119.	1.3	25
104	Identification of tissue-specific cis-regulatory modules based on interactions between transcription factors. <i>BMC Bioinformatics</i> , 2007, 8, 437.	1.2	27
105	Transcriptional Regulatory Network Prediction. <i>Biotechnology and Genetic Engineering Reviews</i> , 2006, 22, 45-62.	2.4	0
106	Characterization of Binding Sites of Eukaryotic Transcription Factors. <i>Genomics, Proteomics and Bioinformatics</i> , 2006, 4, 67-79.	3.0	2
107	Computational analysis of tissue-specific combinatorial gene regulation: predicting interaction between transcription factors in human tissues. <i>Nucleic Acids Research</i> , 2006, 34, 4925-4936.	6.5	134
108	Identification of regulatory targets of tissue-specific transcription factors: application to retina-specific gene regulation. <i>Nucleic Acids Research</i> , 2005, 33, 3479-3491.	6.5	59

#	ARTICLE	IF	CITATIONS
109	Genomic analysis of gene expression relationships in transcriptional regulatory networks. Trends in Genetics, 2003, 19, 422-427.	2.9	238
110	Identification of Novel Genes Preferentially Expressed in the Retina Using a Custom Human Retina cDNA Microarray. , 2003, 44, 3732.		53
111	Prediction of regulatory networks: genome-wide identification of transcription factor targets from gene expression data. Bioinformatics, 2003, 19, 1917-1926.	1.8	116
112	Complex transcriptional circuitry at the G1/S transition in Saccharomyces cerevisiae. Genes and Development, 2002, 16, 3017-3033.	2.7	236
113	Integration of genomic datasets to predict protein complexes in yeast. Journal of Structural and Functional Genomics, 2002, 2, 71-81.	1.2	74
114	Beyond synexpression relationships: local clustering of time-shifted and inverted gene expression profiles identifies new, biologically relevant interactions. Journal of Molecular Biology, 2001, 314, 1053-1066.	2.0	171