Jiang Qian

List of Publications by Year
in descending order

114 papers	7,814 citations	61984 43 h-index	62596 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. Autophagy, 2023, 19, 92-111.	9.1	41
2	scEnhancer: a single-cell enhancer resource with annotation across hundreds of tissue/cell types in three species. Nucleic Acids Research, 2022, 50, D371-D379.	14.5	16
3	Aqueous proteins help predict the response of patients with neovascular age-related macular degeneration to anti-VEGF therapy. Journal of Clinical Investigation, 2022, 132, .	8.2	9
4	Cell-specific cis-regulatory elements and mechanisms of non-coding genetic disease in human retina and retinal organoids. Developmental Cell, 2022, 57, 820-836.e6.	7.0	37
5	LRLoop: a method to predict feedback loops in cell–cell communication. Bioinformatics, 2022, 38, 4117-4126.	4.1	9
6	Role of glia in optic nerve. Progress in Retinal and Eye Research, 2021, 81, 100886.	15.5	23
7	Identification of Novel Serological Autoantibodies in Takayasu Arteritis Patients Using HuProt Arrays. Molecular and Cellular Proteomics, 2021, 20, 100036.	3.8	13
8	Proteome Landscape of Epithelial-to-Mesenchymal Transition (EMT) of Retinal Pigment Epithelium Shares Commonalities With Malignancy-Associated EMT. Molecular and Cellular Proteomics, 2021, 20, 100131.	3.8	12
9	Temperature and species-dependent regulation of browning in retrobulbar fat. Scientific Reports, 2021, 11, 3094.	3.3	1
10	An Integrated Systems Biology Approach Identifies the Proteasome as A Critical Host Machinery for ZIKV and DENV Replication. Genomics, Proteomics and Bioinformatics, 2021, 19, 108-122.	6.9	7
11	An all-to-all approach to the identification of sequence-specific readers for epigenetic DNA modifications on cytosine. Nature Communications, 2021, 12, 795.	12.8	22
12	Factors Associated With a Patient's Decision to Select a Cost-effective vs the Most Effective Therapy for Their Own Eye Disease. JAMA Network Open, 2021, 4, e2037880.	5.9	6
13	βA1-crystallin regulates glucose metabolism and mitochondrial function in mouse retinal astrocytes by modulating PTP1B activity. Communications Biology, 2021, 4, 248.	4.4	10
14	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	16.8	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. FASEB Journal, 2021, 35, .	0.5	1
17	Control of neurogenic competence in mammalian hypothalamic tanycytes. Science Advances, 2021, 7, .	10.3	36
18	Large-scale phenotypic drug screen identifies neuroprotectants in zebrafish and mouse models of retinitis pigmentosa. ELife, 2021, 10, .	6.0	15

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19	Î²A3/A1-crystallin regulates apical polarity and EGFR endocytosis in retinal pigmented epithelial cells. Communications Biology, 2021, 4, 850.	4.4	13
20	Primary angle closure glaucoma is characterized by altered extracellular matrix homeostasis in the iris. Proteomics - Clinical Applications, 2021, 15, 2000094.	1.6	3
21	Human retinal organoids release extracellular vesicles that regulate gene expression in target human retinal progenitor cells. Scientific Reports, 2021, 11, 21128.	3.3	18
22	Gene regulatory networks controlling temporal patterning, neurogenesis, and cell-fate specification in mammalian retina. Cell Reports, 2021, 37, 109994.	6.4	52
23	EnhancerAtlas 2.0: an updated resource with enhancer annotation in 586 tissue/cell types across nine species. Nucleic Acids Research, 2020, 48, D58-D64.	14.5	142
24	Gene regulatory networks controlling vertebrate retinal regeneration. Science, 2020, 370, .	12.6	248
25	Glycoproteomics-based signatures for tumor subtyping and clinical outcome prediction of high-grade serous ovarian cancer. Nature Communications, 2020, 11, 6139.	12.8	72
26	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. Cell Reports, 2020, 33, 108276.	6.4	83
27	Knocking Out Non-muscle Myosin II in Retinal Ganglion Cells Promotes Long-Distance Optic Nerve Regeneration. Cell Reports, 2020, 31, 107537.	6.4	33
28	Retinal pigment epithelium transcriptome analysis in chronic smoking reveals a suppressed innate immune response and activation of differentiation pathways. Free Radical Biology and Medicine, 2020, 156, 176-189.	2.9	4
29	Investigating cone photoreceptor development using patient-derived NRL null retinal organoids. Communications Biology, 2020, 3, 82.	4.4	62
30	Integration of IgA and IgG Autoantigens Improves Performance of Biomarker Panels for Early Diagnosis of Lung Cancer. Molecular and Cellular Proteomics, 2020, 19, 490-500.	3.8	23
31	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	28.9	430
32	EAGLE: An algorithm that utilizes a small number of genomic features to predict tissue/cell type-specific enhancer-gene interactions. PLoS Computational Biology, 2019, 15, e1007436.	3.2	19
33	Differentially Methylated Super-Enhancers Regulate Target Gene Expression in Human Cancer. Scientific Reports, 2019, 9, 15034.	3.3	9
34	PanoView: An iterative clustering method for single-cell RNA sequencing data. PLoS Computational Biology, 2019, 15, e1007040.	3.2	16
35	Neutrophils homing into the retina trigger pathology in early age-related macular degeneration. Communications Biology, 2019, 2, 348.	4.4	37
36	Discovery and Validation of a Serologic Autoantibody Panel for Early Diagnosis of Esophageal Squamous Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1454-1460.	2.5	20

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37	Decomposing Cell Identity for Transfer Learning across Cellular Measurements, Platforms, Tissues, and Species. Cell Systems, 2019, 8, 395-411.e8.	6.2	121
38	Epigenomic profiling of retinal progenitors reveals LHX2 is required for developmental regulation of open chromatin. Communications Biology, 2019, 2, 142.	4.4	36
39	AAgMarker 1.0: a resource of serological autoantigen biomarkers for clinical diagnosis and prognosis of various human diseases. Nucleic Acids Research, 2018, 46, D886-D893.	14.5	5
40	ATAC-Seq analysis reveals a widespread decrease of chromatin accessibility in age-related macular degeneration. Nature Communications, 2018, 9, 1364.	12.8	124
41	Global Identification of Small Ubiquitin-related Modifier (SUMO) Substrates Reveals Crosstalk between SUMOylation and Phosphorylation Promotes Cell Migration. Molecular and Cellular Proteomics, 2018, 17, 871-888.	3.8	24
42	MeDReaders: a database for transcription factors that bind to methylated DNA. Nucleic Acids Research, 2018, 46, D146-D151.	14.5	94
43	Multiplexed Biomarker Panels Discriminate Zika and Dengue Virus Infection in Humans. Molecular and Cellular Proteomics, 2018, 17, 349-356.	3.8	19
44	Heterozygous IDH1R132H/WT created by â€œsingle base editingâ€•inhibits human astroglial cell growth by downregulating YAP. Oncogene, 2018, 37, 5160-5174.	5.9	27
45	Analysis of KLF4 regulated genes in cancer cells reveals a role of DNA methylation in promoter-enhancer interactions. Epigenetics, 2018, 13, 751-768.	2.7	15
46	Multiplexed CRISPR/Cas9 Targeting of Genes Implicated in Retinal Regeneration and Degeneration. Frontiers in Cell and Developmental Biology, 2018, 6, 88.	3.7	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. Developmental Biology, 2018, 439, 102-111.	2.0	28
49	An Integrated System Approach Identified the Human Proteasome as a Conserved Critical Machinery for ZIKV and DENV Replication. FASEB Journal, 2018, 32, 669.3.	0.5	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. Aging Cell, 2017, 16, 349-359.	6.7	32
51	A Human Proteome Array Approach to Identifying Key Host Proteins Targeted by Toxoplasma Kinase ROP18. Molecular and Cellular Proteomics, 2017, 16, 469-484.	3.8	28
52	Global Analysis of SUMO-Binding Proteins Identifies SUMOylation as a Key Regulator of the INO80 Chromatin Remodeling Complex. Molecular and Cellular Proteomics, 2017, 16, 812-823.	3.8	15
53	Activating the <scp>AKT2</scp>â€"nuclear factorâ€‹<scp>Î°B</scp>â€"lipocalinâ€‑2 axis elicits an inflammatory response in ageâ€‑related macular degeneration. Journal of Pathology, 2017, 241, 583-588.	4.5	55
54	Anatomical differences of the protein profile in the rabbit sclera during growth. Experimental Eye Research, 2017, 154, 53-63.	2.6	6

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55	Identification of Serological Biomarkers for Early Diagnosis of Lung Cancer Using a Protein Array-Based Approach. Molecular and Cellular Proteomics, 2017, 16, 2069-2078.	3.8	63
56	Zika-Virus-Encoded NS2A Disrupts Mammalian Cortical Neurogenesis by Degrading Adherens Junction Proteins. Cell Stem Cell, 2017, 21, 349-358.e6.	11.1	163
57	Identification of Novel Biomarkers for Behcet Disease Diagnosis Using Human Proteome Microarray Approach. Molecular and Cellular Proteomics, 2017, 16, 147-156.	3.8	49
58	Methylated cis-regulatory elements mediate KLF4-dependent gene transactivation and cell migration. ELife, 2017, 6, .	6.0	39
59	A proteomic approach to understanding the pathogenesis of idiopathic macular hole formation. Clinical Proteomics, 2017, 14, 37.	2.1	11
60	Assessing the model transferability for prediction of transcription factor binding sites based on chromatin accessibility. BMC Bioinformatics, 2017, 18, 355.	2.6	22
61	ScaPD: a database for human scaffold proteins. BMC Bioinformatics, 2017, 18, 386.	2.6	8
62	Identification and functional analysis of differentially expressed genes in poorly differentiated hepatocellular carcinoma using RNA-seq. Oncotarget, 2017, 8, 35973-35983.	1.8	7
63	Single-Cell Co-expression Analysis Reveals Distinct Functional Modules, Co-regulation Mechanisms and Clinical Outcomes. PLoS Computational Biology, 2016, 12, e1004892.	3.2	36
64	Off Target, but Sequence-Specific, shRNA-Associated Trans-Activation of Promoter Reporters in Transient Transfection Assays. PLoS ONE, 2016, 11, e0167867.	2.5	1
65	Pro-permeability Factors in Diabetic Macular Edema; the Diabetic Macular Edema Treated With Ozurdex Trial. American Journal of Ophthalmology, 2016, 168, 13-23.	3.3	56
66	A nuclease that mediates cell death induced by DNA damage and poly(ADP-ribose) polymerase-1. Science, 2016, 354, .	12.6	266
67	Transcription factors as readers and effectors of DNA methylation. Nature Reviews Genetics, 2016, 17, 551-565.	16.3	482
68	EnhancerAtlas: a resource for enhancer annotation and analysis in 105 human cell/tissue types. Bioinformatics, 2016, 32, 3543-3551.	4.1	148
69	ARQiv-HTS, a versatile whole-organism screening platform enabling in vivo drug discovery at high-throughput rates. Nature Protocols, 2016, 11, 2432-2453.	12.0	50
70	Temporal patterns of gene expression during calyx of held development. Developmental Neurobiology, 2016, 76, 166-189.	3.0	16
71	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. Molecular Cell, 2016, 61, 153-160.	9.7	74
72	Lhx2 Is an Essential Factor for Retinal Gliogenesis and Notch Signaling. Journal of Neuroscience, 2016, 36, 2391-2405.	3.6	79

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73	Serum molecular signature for proliferativeÂdiabeticÂretinopathy in Saudi patients with type 2 diabetes. Molecular Vision, 2016, 22, 636-45.	1.1	6
74	Î²A3/A1-crystallin is a critical mediator of STAT3 signaling in optic nerve astrocytes. Scientific Reports, 2015, 5, 8755.	3.3	11
75	Systematic Prediction of Scaffold Proteins Reveals New Design Principles in Scaffold-Mediated Signal Transduction. PLoS Computational Biology, 2015, 11, e1004508.	3.2	13
76	Differential DNA methylation identified in the blood and retina of AMD patients. Epigenetics, 2015, 10, 698-707.	2.7	62
77	A Screen for Extracellular Signal-Regulated Kinase-Primed Glycogen Synthase Kinase 3 Substrates Identifies the p53 Inhibitor iASPP. Journal of Virology, 2015, 89, 9232-9241.	3.4	10
78	Characterization of tissue-specific differential DNA methylation suggests distinct modes of positive and negative gene expression regulation. BMC Genomics, 2015, 16, 49.	2.8	132
79	Pro-Permeability Factors After Dexamethasone Implant in Retinal Vein Occlusion; the Ozurdex for Retinal Vein Occlusion (ORVO) Study. American Journal of Ophthalmology, 2015, 160, 313-321.e19.	3.3	35
80	Small-moleculeâ€"directed, efficient generation of retinal pigment epithelium from human pluripotent stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10950-10955.	7.1	114
81	Oxidative stress induces mitochondrial dysfunction and a protective unfolded protein response in RPE cells. Free Radical Biology and Medicine, 2014, 69, 1-14.	2.9	81
82	PhosphoNetworks: a database for human phosphorylation networks. Bioinformatics, 2014, 30, 141-142.	4.1	106
83	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. Nature Communications, 2014, 5, 4961.	12.8	72
84	Global analysis of phosphorylation networks in humans. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 224-231.	2.3	20
85	Lhx1 Controls Terminal Differentiation and Circadian Function of the Suprachiasmatic Nucleus. Cell Reports, 2014, 7, 609-622.	6.4	88
86	A novel methyl-binding domain protein enrichment method for identifying genome-wide tissue-specific DNA methylation from nanogram DNA samples. Epigenetics and Chromatin, 2013, 6, 17.	3.9	17
87	Hypomethylation of the IL17RC Promoter in Peripheral Blood Leukocytes Is Not A Hallmark of Age-Related Macular Degeneration. Cell Reports, 2013, 5, 1527-1535.	6.4	42
88	Construction of human activityâ€based phosphorylation networks. Molecular Systems Biology, 2013, 9, 655.	7.2	153
89	Integrative analysis of tissue-specific methylation and alternative splicing identifies conserved transcription factor binding motifs. Nucleic Acids Research, 2013, 41, 8503-8514.	14.5	46
90	DNA methylation presents distinct binding sites for human transcription factors. ELife, 2013, 2, e00726.	6.0	292

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91	Phosphorylation of the Chromatin Binding Domain of KSHV LANA. PLoS Pathogens, 2012, 8, e1002972.	4.7	32
92	Rapid Identification of Monospecific Monoclonal Antibodies Using a Human Proteome Microarray. Molecular and Cellular Proteomics, 2012, 11, O111.016253.	3.8	136
93	A Protein Array Screen for Kaposi's Sarcoma-Associated Herpesvirus LANA Interactors Links LANA to TIP60, PP2A Activity, and Telomere Shortening. Journal of Virology, 2012, 86, 5179-5191.	3.4	56
94	Dynamics of Regulatory Networks in the Developing Mouse Retina. PLoS ONE, 2012, 7, e46521.	2.5	9
95	Conserved Herpesvirus Kinases Target the DNA Damage Response Pathway and TIP60 Histone Acetyltransferase to Promote Virus Replication. Cell Host and Microbe, 2011, 10, 390-400.	11.0	148
96	Dynamic usage of alternative splicing exons during mouse retina development. Nucleic Acids Research, 2011, 39, 7920-7930.	14.5	33
97	Differential substrate selectivity and stability with different forms of protein kinase CK2. FASEB Journal, 2011, 25, lb146.	0.5	0
98	A genomic atlas of mouse hypothalamic development. Nature Neuroscience, 2010, 13, 767-775.	14.8	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. Bioinformatics, 2010, 26, 2289-2297.	4.1	26
101	Profiling the Human Protein-DNA Interactome Reveals ERK2 as a Transcriptional Repressor of Interferon Signaling. Cell, 2009, 139, 610-622.	28.9	352
102	Analysis of regulatory network topology reveals functionally distinct classes of microRNAs. Nucleic Acids Research, 2008, 36, 6494-6503.	14.5	81
103	Systems biology approach to integrative comparative genomics. Expert Review of Proteomics, 2007, 4, 107-119.	3.0	25
104	Identification of tissue-specific cis-regulatory modules based on interactions between transcription factors. BMC Bioinformatics, 2007, 8, 437.	2.6	27
105	Transcriptional Regulatory Network Prediction. Biotechnology and Genetic Engineering Reviews, 2006, 22, 45-62.	6.2	0
106	Characterization of Binding Sites of Eukaryotic Transcription Factors. Genomics, Proteomics and Bioinformatics, 2006, 4, 67-79.	6.9	2
107	Computational analysis of tissue-specific combinatorial gene regulation: predicting interaction between transcription factors in human tissues. Nucleic Acids Research, 2006, 34, 4925-4936.	14.5	134
108	Identification of regulatory targets of tissue-specific transcription factors: application to retina-specific gene regulation. Nucleic Acids Research, 2005, 33, 3479-3491.	14.5	59

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109	Genomic analysis of gene expression relationships in transcriptional regulatory networks. Trends in Genetics, 2003, 19, 422-427.	6.7	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.	4.1	116
112	Complex transcriptional circuitry at the G1/S transition in Saccharomyces cerevisiae. Genes and Development, 2002, 16, 3017-3033.	5.9	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.	4.2	171