

# Jian Ren

## List of Publications by Year in Descending Order

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

73  
papers

4,705  
citations

32  
h-index

68  
g-index

84  
ext. papers

6,091  
ext. citations

9.6  
avg, IF

5.29  
L-index

#	Paper	IF	Citations
73	RPS: a comprehensive database of RNAs involved in liquid-liquid phase separation. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	1
72	Unambiguous advanced radiologic extranodal extension determined by MRI predicts worse outcomes in nasopharyngeal carcinoma: Potential improvement for future editions of N category systems. <i>Radiotherapy and Oncology</i> , <b>2021</b> , 157, 114-121	5.3	8
71	MesKit: a tool kit for dissecting cancer evolution of multi-region tumor biopsies through somatic alterations. <i>GigaScience</i> , <b>2021</b> , 10,	7.6	1
70	DeepOMe: A Web Server for the Prediction of 2UO-Me Sites Based on the Hybrid CNN and BLSTM Architecture. <i>Frontiers in Cell and Developmental Biology</i> , <b>2021</b> , 9, 686894	5.7	2
69	RMVar: an updated database of functional variants involved in RNA modifications. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D1405-D1412	20.1	37
68	RAPID: A Rep-Seq Dataset Analysis Platform With an Integrated Antibody Database. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 717496	8.4	2
67	Image-driven classification of functioning and nonfunctioning pituitary adenoma by deep convolutional neural networks. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 3077-3086	6.8	1
66	autoRPA: A web server for constructing cancer staging models by recursive partitioning analysis. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 3361-3367	6.8	2
65	RBMX is required for activation of ATR on repetitive DNAs to maintain genome stability. <i>Cell Death and Differentiation</i> , <b>2020</b> , 27, 3162-3176	12.7	7
64	METTL3 and N6-Methyladenosine Promote Homologous Recombination-Mediated Repair of DSBs by Modulating DNA-RNA Hybrid Accumulation. <i>Molecular Cell</i> , <b>2020</b> , 79, 425-442.e7	17.6	71
63	BBCancer: an expression atlas of blood-based biomarkers in the early diagnosis of cancers. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D789-D796	20.1	22
62	Single AAV-Mediated CRISPR-SaCas9 Inhibits HSV-1 Replication by Editing ICP4 in Trigeminal Ganglion Neurons. <i>Molecular Therapy - Methods and Clinical Development</i> , <b>2020</b> , 18, 33-43	6.4	6
61	CrossICC: iterative consensus clustering of cross-platform gene expression data without adjusting batch effect. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1818-1824	13.4	5
60	PGC1 $\beta$ protects against hepatic steatosis and insulin resistance via enhancing IL10-mediated anti-inflammatory response. <i>FASEB Journal</i> , <b>2020</b> , 34, 10751-10761	0.9	5
59	PTMsnp: A Web Server for the Identification of Driver Mutations That Affect Protein Post-translational Modification. <i>Frontiers in Cell and Developmental Biology</i> , <b>2020</b> , 8, 593661	5.7	1
58	DeepPhagy: a deep learning framework for quantitatively measuring autophagy activity in. <i>Autophagy</i> , <b>2020</b> , 16, 626-640	10.2	8
57	N-Methyladenosine Modulates Nonsense-Mediated mRNA Decay in Human Glioblastoma. <i>Cancer Research</i> , <b>2019</b> , 79, 5785-5798	10.1	98

56	Differential Alternative Splicing Genes in Response to Boron Deficiency in. <i>Genes</i> , <b>2019</b> , 10,	4.2	3
55	Single-base mapping of mA by an antibody-independent method. <i>Science Advances</i> , <b>2019</b> , 5, eaax0250	14.3	128
54	lnCAR: A Comprehensive Resource for lncRNAs from Cancer Arrays. <i>Cancer Research</i> , <b>2019</b> , 79, 2076-2083	20.1	26
53	Proposed modifications and incorporation of plasma Epstein-Barr virus DNA improve the TNM staging system for Epstein-Barr virus-related nasopharyngeal carcinoma. <i>Cancer</i> , <b>2019</b> , 125, 79-89	6.4	85
52	YY1 Positively Regulates Transcription by Targeting Promoters and Super-Enhancers through the BAF Complex in Embryonic Stem Cells. <i>Stem Cell Reports</i> , <b>2018</b> , 10, 1324-1339	8	27
51	m6ASNP: a tool for annotating genetic variants by m6A function. <i>GigaScience</i> , <b>2018</b> , 7,	7.6	22
50	m6AVar: a database of functional variants involved in m6A modification. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D139-D145	20.1	104
49	Pan-Cancer Analysis Reveals the Functional Importance of Protein Lysine Modification in Cancer Development. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 254	4.5	17
48	mA RNA modification controls autophagy through upregulating ULK1 protein abundance. <i>Cell Research</i> , <b>2018</b> , 28, 955-957	24.7	48
47	DeepNitro: Prediction of Protein Nitration and Nitrosylation Sites by Deep Learning. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2018</b> , 16, 294-306	6.5	50
46	Firmiana: towards a one-stop proteomic cloud platform for data processing and analysis. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 409-412	44.5	27
45	VirusMap: A visualization database for the influenza A virus. <i>Journal of Genetics and Genomics</i> , <b>2017</b> , 44, 281-284	4	3
44	A Cisplatin Derivative Tetra-Pt(bpy) as an Oncotherapeutic Agent for Targeting ALT Cancer. <i>Journal of the National Cancer Institute</i> , <b>2017</b> , 109,	9.7	26
43	Expression and regulation of long noncoding RNAs during the osteogenic differentiation of periodontal ligament stem cells in the inflammatory microenvironment. <i>Scientific Reports</i> , <b>2017</b> , 7, 13994	4.9	9
42	A de novo substructure generation algorithm for identifying the privileged chemical fragments of liver X receptor agonists. <i>Scientific Reports</i> , <b>2017</b> , 7, 11121	4.9	5
41	Single-walled carbon nanotube: One specific inhibitor of cancer stem cells in osteosarcoma upon downregulation of the TGF $\beta$ signaling. <i>Biomaterials</i> , <b>2017</b> , 149, 29-40	15.6	19
40	RPFdb: a database for genome wide information of translated mRNA generated from ribosome profiling. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D254-8	20.1	37
39	GPS-Lipid: a robust tool for the prediction of multiple lipid modification sites. <i>Scientific Reports</i> , <b>2016</b> , 6, 28249	4.9	82

38	Mutation profiling in chinese patients with metastatic colorectal cancer and its correlation with clinicopathological features and anti-EGFR treatment response. <i>Oncotarget</i> , <b>2016</b> , 7, 28356-68	3.3	12
37	Conformation Selective Antibody Enables Genome Profiling and Leads to Discovery of Parallel G-Quadruplex in Human Telomeres. <i>Cell Chemical Biology</i> , <b>2016</b> , 23, 1261-1270	8.2	65
36	Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. <i>Journal of Molecular Cell Biology</i> , <b>2015</b> , 7, 187-202	6.3	16
35	MiCroKiTS 4.0: a database of midbody, centrosome, kinetochore, telomere and spindle. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D328-34	20.1	18
34	Dynamic metabonomic and microbiological response of rats to lincomycin exposure: an integrated microbiology and metabonomics analysis. <i>RSC Advances</i> , <b>2015</b> , 5, 65415-65426	3.7	6
33	A systematic simulation of the effect of salicylic acid on sphingolipid metabolism. <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 186	6.2	12
32	Genome-Wide Identification of a Methylation Gene Panel as a Prognostic Biomarker in Nasopharyngeal Carcinoma. <i>Molecular Cancer Therapeutics</i> , <b>2015</b> , 14, 2864-73	6.1	52
31	IBS: an illustrator for the presentation and visualization of biological sequences. <i>Bioinformatics</i> , <b>2015</b> , 31, 3359-61	7.2	473
30	Systematic analysis of the in situ crosstalk of tyrosine modifications reveals no additional natural selection on multiply modified residues. <i>Scientific Reports</i> , <b>2014</b> , 4, 7331	4.9	29
29	Systematic characterization of small RNAome during zebrafish early developmental stages. <i>BMC Genomics</i> , <b>2014</b> , 15, 117	4.5	17
28	CPLM: a database of protein lysine modifications. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D531-6	20.1	121
27	Clinical characteristics, immunohistochemistry, and outcomes of 77 patients with skull base chordomas. <i>World Neurosurgery</i> , <b>2014</b> , 81, 790-7	2.1	32
26	dbPPT: a comprehensive database of protein phosphorylation in plants. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2014</b> , 2014, bau121	5	36
25	An integrated overview of spatiotemporal organization and regulation in mitosis in terms of the proteins in the functional supercomplexes. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 573	5.7	3
24	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W325-30	20.1	274
23	Towards a better understanding of the novel avian-origin H7N9 influenza A virus in China. <i>Scientific Reports</i> , <b>2013</b> , 3, 2318	4.9	13
22	Systematic analysis of the Plk-mediated phosphoregulation in eukaryotes. <i>Briefings in Bioinformatics</i> , <b>2013</b> , 14, 344-60	13.4	24
21	UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D445-51	20.1	74

20	Systematic analysis of protein phosphorylation networks from phosphoproteomic data. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, 1070-83	7.6	123
19	GPS-MBA: computational analysis of MHC class II epitopes in type 1 diabetes. <i>PLoS ONE</i> , <b>2012</b> , 7, e33884	3.7	6
18	GPS-ARM: computational analysis of the APC/C recognition motif by predicting D-boxes and KEN-boxes. <i>PLoS ONE</i> , <b>2012</b> , 7, e34370	3.7	33
17	GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. <i>Molecular BioSystems</i> , <b>2011</b> , 7, 1197-204		74
16	GPS-CCD: a novel computational program for the prediction of calpain cleavage sites. <i>PLoS ONE</i> , <b>2011</b> , 6, e19001	3.7	69
15	GPS-PUP: computational prediction of pupylation sites in prokaryotic proteins. <i>Molecular BioSystems</i> , <b>2011</b> , 7, 2737-40		34
14	CPLA 1.0: an integrated database of protein lysine acetylation. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D1029-34	10.1	50
13	GPS 2.1: enhanced prediction of kinase-specific phosphorylation sites with an algorithm of motif length selection. <i>Protein Engineering, Design and Selection</i> , <b>2011</b> , 24, 255-60	1.9	193
12	Computational analysis of phosphoproteomics: progresses and perspectives. <i>Current Protein and Peptide Science</i> , <b>2011</b> , 12, 591-601	2.8	12
11	GPS-SNO: computational prediction of protein S-nitrosylation sites with a modified GPS algorithm. <i>PLoS ONE</i> , <b>2010</b> , 5, e11290	3.7	176
10	PhosSNP for systematic analysis of genetic polymorphisms that influence protein phosphorylation. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 623-34	7.6	65
9	MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D155-60	20.1	25
8	A summary of computational resources for protein phosphorylation. <i>Current Protein and Peptide Science</i> , <b>2010</b> , 11, 485-96	2.8	46
7	Systematic study of protein sumoylation: Development of a site-specific predictor of SUMOsp 2.0. <i>Proteomics</i> , <b>2009</b> , 9, 3409-3412	4.8	192
6	DOG 1.0: illustrator of protein domain structures. <i>Cell Research</i> , <b>2009</b> , 19, 271-3	24.7	373
5	Comprehensive and reliable phosphorylation site mapping of individual phosphoproteins by combination of multiple stage mass spectrometric analysis with a target-decoy database search. <i>Analytical Chemistry</i> , <b>2009</b> , 81, 5794-805	7.8	22
4	Proteome-wide prediction of PKA phosphorylation sites in eukaryotic kingdom. <i>Genomics</i> , <b>2008</b> , 92, 457-63	4.3	22
3	GPS 2.0, a tool to predict kinase-specific phosphorylation sites in hierarchy. <i>Molecular and Cellular Proteomics</i> , <b>2008</b> , 7, 1598-608	7.6	516

2	CSS-Palm 2.0: an updated software for palmitoylation sites prediction. <i>Protein Engineering, Design and Selection</i> , <b>2008</b> , 21, 639-44	1.9	397
1	SARS-Cov-2-, HIV-1-, Ebola-neutralizing and anti-PD1 clones are predisposed		1