

Jian Ren

List of Publications by Citations

Source: <https://exaly.com/author-pdf/4388148/jian-ren-publications-by-citations.pdf>

Version: 2024-04-29

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.

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	GPS 2.0, a tool to predict kinase-specific phosphorylation sites in hierarchy. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1598-608	7.6	516
72	IBS: an illustrator for the presentation and visualization of biological sequences. <i>Bioinformatics</i> , 2015 , 31, 3359-61	7.2	473
71	CSS-Palm 2.0: an updated software for palmitoylation sites prediction. <i>Protein Engineering, Design and Selection</i> , 2008 , 21, 639-44	1.9	397
70	DOG 1.0: illustrator of protein domain structures. <i>Cell Research</i> , 2009 , 19, 271-3	24.7	373
69	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. <i>Nucleic Acids Research</i> , 2014 , 42, W325-30	20.1	274
68	GPS 2.1: enhanced prediction of kinase-specific phosphorylation sites with an algorithm of motif length selection. <i>Protein Engineering, Design and Selection</i> , 2011 , 24, 255-60	1.9	193
67	Systematic study of protein sumoylation: Development of a site-specific predictor of SUMOsp 2.0. <i>Proteomics</i> , 2009 , 9, 3409-3412	4.8	192
66	GPS-SNO: computational prediction of protein S-nitrosylation sites with a modified GPS algorithm. <i>PLoS ONE</i> , 2010 , 5, e11290	3.7	176
65	Single-base mapping of mA by an antibody-independent method. <i>Science Advances</i> , 2019 , 5, eaax0250	14.3	128
64	Systematic analysis of protein phosphorylation networks from phosphoproteomic data. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1070-83	7.6	123
63	CPLM: a database of protein lysine modifications. <i>Nucleic Acids Research</i> , 2014 , 42, D531-6	20.1	121
62	m6AVar: a database of functional variants involved in m6A modification. <i>Nucleic Acids Research</i> , 2018 , 46, D139-D145	20.1	104
61	N-Methyladenosine Modulates Nonsense-Mediated mRNA Decay in Human Glioblastoma. <i>Cancer Research</i> , 2019 , 79, 5785-5798	10.1	98
60	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> , 2019 , 125, 79-89	6.4	85
59	GPS-Lipid: a robust tool for the prediction of multiple lipid modification sites. <i>Scientific Reports</i> , 2016 , 6, 28249	4.9	82
58	UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. <i>Nucleic Acids Research</i> , 2013 , 41, D445-51	20.1	74
57	GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. <i>Molecular BioSystems</i> , 2011 , 7, 1197-204		74

56	METTL3 and N6-Methyladenosine Promote Homologous Recombination-Mediated Repair of DSBs by Modulating DNA-RNA Hybrid Accumulation. <i>Molecular Cell</i> , 2020 , 79, 425-442.e7	17.6	71
55	GPS-CCD: a novel computational program for the prediction of calpain cleavage sites. <i>PLoS ONE</i> , 2011 , 6, e19001	3.7	69
54	PhosSNP for systematic analysis of genetic polymorphisms that influence protein phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 623-34	7.6	65
53	Conformation Selective Antibody Enables Genome Profiling and Leads to Discovery of Parallel G-Quadruplex in Human Telomeres. <i>Cell Chemical Biology</i> , 2016 , 23, 1261-1270	8.2	65
52	Genome-Wide Identification of a Methylation Gene Panel as a Prognostic Biomarker in Nasopharyngeal Carcinoma. <i>Molecular Cancer Therapeutics</i> , 2015 , 14, 2864-73	6.1	52
51	CPLA 1.0: an integrated database of protein lysine acetylation. <i>Nucleic Acids Research</i> , 2011 , 39, D1029-34	10.1	50
50	DeepNitro: Prediction of Protein Nitration and Nitrosylation Sites by Deep Learning. <i>Genomics, Proteomics and Bioinformatics</i> , 2018 , 16, 294-306	6.5	50
49	mA RNA modification controls autophagy through upregulating ULK1 protein abundance. <i>Cell Research</i> , 2018 , 28, 955-957	24.7	48
48	A summary of computational resources for protein phosphorylation. <i>Current Protein and Peptide Science</i> , 2010 , 11, 485-96	2.8	46
47	RPFdb: a database for genome wide information of translated mRNA generated from ribosome profiling. <i>Nucleic Acids Research</i> , 2016 , 44, D254-8	20.1	37
46	RMVar: an updated database of functional variants involved in RNA modifications. <i>Nucleic Acids Research</i> , 2021 , 49, D1405-D1412	20.1	37
45	dbPPT: a comprehensive database of protein phosphorylation in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014, bau121	5	36
44	GPS-PUP: computational prediction of pupylation sites in prokaryotic proteins. <i>Molecular BioSystems</i> , 2011 , 7, 2737-40		34
43	GPS-ARM: computational analysis of the APC/C recognition motif by predicting D-boxes and KEN-boxes. <i>PLoS ONE</i> , 2012 , 7, e34370	3.7	33
42	Clinical characteristics, immunohistochemistry, and outcomes of 77 patients with skull base chordomas. <i>World Neurosurgery</i> , 2014 , 81, 790-7	2.1	32
41	Systematic analysis of the in situ crosstalk of tyrosine modifications reveals no additional natural selection on multiply modified residues. <i>Scientific Reports</i> , 2014 , 4, 7331	4.9	29
40	Firmiana: towards a one-stop proteomic cloud platform for data processing and analysis. <i>Nature Biotechnology</i> , 2017 , 35, 409-412	44.5	27
39	YY1 Positively Regulates Transcription by Targeting Promoters and Super-Enhancers through the BAF Complex in Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2018 , 10, 1324-1339	8	27

38	A Cisplatin Derivative Tetra-Pt(bpy) as an Oncotherapeutic Agent for Targeting ALT Cancer. <i>Journal of the National Cancer Institute</i> , 2017 , 109,	9.7	26
37	lnCAR: A Comprehensive Resource for lncRNAs from Cancer Arrays. <i>Cancer Research</i> , 2019 , 79, 2076-2083.	20.1	26
36	MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. <i>Nucleic Acids Research</i> , 2010 , 38, D155-60	20.1	25
35	Systematic analysis of the Plk-mediated phosphoregulation in eukaryotes. <i>Briefings in Bioinformatics</i> , 2013 , 14, 344-60	13.4	24
34	m6ASNP: a tool for annotating genetic variants by m6A function. <i>GigaScience</i> , 2018 , 7,	7.6	22
33	BBcancer: an expression atlas of blood-based biomarkers in the early diagnosis of cancers. <i>Nucleic Acids Research</i> , 2020 , 48, D789-D796	20.1	22
32	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> , 2009 , 81, 5794-805	7.8	22
31	Proteome-wide prediction of PKA phosphorylation sites in eukaryotic kingdom. <i>Genomics</i> , 2008 , 92, 457-63	4.3	22
30	Single-walled carbon nanotube: One specific inhibitor of cancer stem cells in osteosarcoma upon downregulation of the TGF β signaling. <i>Biomaterials</i> , 2017 , 149, 29-40	15.6	19
29	MiCroKITS 4.0: a database of midbody, centrosome, kinetochore, telomere and spindle. <i>Nucleic Acids Research</i> , 2015 , 43, D328-34	20.1	18
28	Pan-Cancer Analysis Reveals the Functional Importance of Protein Lysine Modification in Cancer Development. <i>Frontiers in Genetics</i> , 2018 , 9, 254	4.5	17
27	Systematic characterization of small RNAome during zebrafish early developmental stages. <i>BMC Genomics</i> , 2014 , 15, 117	4.5	17
26	Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. <i>Journal of Molecular Cell Biology</i> , 2015 , 7, 187-202	6.3	16
25	Towards a better understanding of the novel avian-origin H7N9 influenza A virus in China. <i>Scientific Reports</i> , 2013 , 3, 2318	4.9	13
24	A systematic simulation of the effect of salicylic acid on sphingolipid metabolism. <i>Frontiers in Plant Science</i> , 2015 , 6, 186	6.2	12
23	Mutation profiling in chinese patients with metastatic colorectal cancer and its correlation with clinicopathological features and anti-EGFR treatment response. <i>Oncotarget</i> , 2016 , 7, 28356-68	3.3	12
22	Computational analysis of phosphoproteomics: progresses and perspectives. <i>Current Protein and Peptide Science</i> , 2011 , 12, 591-601	2.8	12
21	Expression and regulation of long noncoding RNAs during the osteogenic differentiation of periodontal ligament stem cells in the inflammatory microenvironment. <i>Scientific Reports</i> , 2017 , 7, 13994.	4.9	9

20	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> , 2021 , 157, 114-121	5.3	8
19	DeepPhagy: a deep learning framework for quantitatively measuring autophagy activity in. <i>Autophagy</i> , 2020 , 16, 626-640	10.2	8
18	RBMX is required for activation of ATR on repetitive DNAs to maintain genome stability. <i>Cell Death and Differentiation</i> , 2020 , 27, 3162-3176	12.7	7
17	Dynamic metabonomic and microbiological response of rats to lincomycin exposure: an integrated microbiology and metabonomics analysis. <i>RSC Advances</i> , 2015 , 5, 65415-65426	3.7	6
16	GPS-MBA: computational analysis of MHC class II epitopes in type 1 diabetes. <i>PLoS ONE</i> , 2012 , 7, e33884	3.7	6
15	Single AAV-Mediated CRISPR-SaCas9 Inhibits HSV-1 Replication by Editing ICP4 in Trigeminal Ganglion Neurons. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020 , 18, 33-43	6.4	6
14	A de novo substructure generation algorithm for identifying the privileged chemical fragments of liver X receptor agonists. <i>Scientific Reports</i> , 2017 , 7, 11121	4.9	5
13	CrossICC: iterative consensus clustering of cross-platform gene expression data without adjusting batch effect. <i>Briefings in Bioinformatics</i> , 2020 , 21, 1818-1824	13.4	5
12	PGC1 β protects against hepatic steatosis and insulin resistance via enhancing IL10-mediated anti-inflammatory response. <i>FASEB Journal</i> , 2020 , 34, 10751-10761	0.9	5
11	VirusMap: A visualization database for the influenza A virus. <i>Journal of Genetics and Genomics</i> , 2017 , 44, 281-284	4	3
10	Differential Alternative Splicing Genes in Response to Boron Deficiency in. <i>Genes</i> , 2019 , 10,	4.2	3
9	An integrated overview of spatiotemporal organization and regulation in mitosis in terms of the proteins in the functional supercomplexes. <i>Frontiers in Microbiology</i> , 2014 , 5, 573	5.7	3
8	autoRPA: A web server for constructing cancer staging models by recursive partitioning analysis. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 3361-3367	6.8	2
7	DeepOMe: A Web Server for the Prediction of 2HO-Me Sites Based on the Hybrid CNN and BLSTM Architecture. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 686894	5.7	2
6	RAPID: A Rep-Seq Dataset Analysis Platform With an Integrated Antibody Database. <i>Frontiers in Immunology</i> , 2021 , 12, 717496	8.4	2
5	RPS: a comprehensive database of RNAs involved in liquid-liquid phase separation. <i>Nucleic Acids Research</i> , 2021 ,	20.1	1
4	SARS-Cov-2-, HIV-1-, Ebola-neutralizing and anti-PD1 clones are predisposed		1
3	PTMsnp: A Web Server for the Identification of Driver Mutations That Affect Protein Post-translational Modification. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 593661	5.7	1

- 2 MesKit: a tool kit for dissecting cancer evolution of multi-region tumor biopsies through somatic alterations. *GigaScience*, **2021**, 10, 7.6 1
- 1 Image-driven classification of functioning and nonfunctioning pituitary adenoma by deep convolutional neural networks. *Computational and Structural Biotechnology Journal*, **2021**, 19, 3077-3086^{6.8} 1