

Tao Zhou

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.

53
papers

1,113
citations

18
h-index

32
g-index

59
ext. papers

1,423
ext. citations

4.7
avg, IF

3.98
L-index

#	Paper	IF	Citations
53	A Refined Framework for Precision and Translational Proteomics in Clinical Research. <i>Current Proteomics</i> , 2021 , 18, 436-446	0.7	
52	Key proteins of proteome underlying sperm malformation of rats exposed to low fenvalerate doses are highly related to P53. <i>Environmental Toxicology</i> , 2021 , 36, 1181-1194	4.2	2
51	Diagnostic and Prognostic Value of Long Noncoding RNAs as Potential Novel Biomarkers in Intrahepatic Cholestasis of Pregnancy. <i>BioMed Research International</i> , 2021 , 2021, 8858326	3	1
50	Prognostic value of neutrophil- lymphocyte count ratio (NLCR) among adult ICU patients in comparison to APACHE II score and conventional inflammatory markers: a multi center retrospective cohort study. <i>BMC Emergency Medicine</i> , 2021 , 21, 24	2.4	2
49	Quantitative phosphoproteomics reveals GSK3A substrate network is involved in the cryodamage of sperm motility. <i>Bioscience Reports</i> , 2021 , 41,	4.1	1
48	mRBPome capture identifies the RNA-binding protein TRIM71, an essential regulator of spermatogonial differentiation. <i>Development (Cambridge)</i> , 2020 , 147,	6.6	6
47	A Critical Review of Proteomic Studies in Gestational Diabetes Mellitus. <i>Journal of Diabetes Research</i> , 2020 , 2020, 6450352	3.9	5
46	Proteomics analysis of asthenozoospermia and identification of glucose-6-phosphate isomerase as an important enzyme for sperm motility. <i>Journal of Proteomics</i> , 2019 , 208, 103478	3.9	11
45	Quantitative Proteomic Analysis of Human Seminal Plasma from Normozoospermic and Asthenozoospermic Individuals. <i>BioMed Research International</i> , 2019 , 2019, 2735038	3	5
44	Label-Free Quantitative Proteomic Screening of Candidate Plasma Biomarkers for the Prognosis of Breast Cancer with Different Lymph Node Statuses. <i>Proteomics - Clinical Applications</i> , 2018 , 12, e1700117	3.1	5
43	4-tert-octylphenol injures motility and viability of human sperm by affecting cAMP-PKA/PKC-tyrosine phosphorylation signals. <i>Environmental Toxicology and Pharmacology</i> , 2018 , 62, 234-243	5.8	5
42	Bioinformatics Analysis of Transcriptomic Data Reveals Refined Functional Networks for the Self-Renewal of Mouse Spermatogonial Stem Cells. <i>Stem Cells International</i> , 2018 , 2018, 5842714	5	1
41	A Comparative Proteome Profile of Female Mouse Gonads Suggests a Tight Link between the Electron Transport Chain and Meiosis Initiation. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 31-42	7.6	5
40	Data on comparative proteomic profiling of human sperm affected by 4-tert-octylphenol in vitro. <i>Data in Brief</i> , 2018 , 21, 2242-2245	1.2	1
39	The Glial Cell-Derived Neurotrophic Factor (GDNF)-responsive Phosphoprotein Landscape Identifies Raptor Phosphorylation Required for Spermatogonial Progenitor Cell Proliferation. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 982-997	7.6	17
38	TCTE1 is a conserved component of the dynein regulatory complex and is required for motility and metabolism in mouse spermatozoa. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E5370-E5378	11.5	47
37	circRNADb: A comprehensive database for human circular RNAs with protein-coding annotations. <i>Scientific Reports</i> , 2016 , 6, 34985	4.9	241

36	The need to revisit published data: A concept and framework for complementary proteomics. <i>Proteomics</i> , 2016 , 16, 6-11	4.8	4
35	MaxReport: An Enhanced Proteomic Result Reporting Tool for MaxQuant. <i>PLoS ONE</i> , 2016 , 11, e0152067	3.7	7
34	Comparative transcriptome analysis reveals a regulatory network of microRNA-29b during mouse early embryonic development. <i>Oncotarget</i> , 2016 , 7, 53772-53782	3.3	6
33	Inhibition of the Rac1-WAVE2-Arp2/3 signaling pathway promotes radiosensitivity via downregulation of cofilin-1 in U251 human glioma cells. <i>Molecular Medicine Reports</i> , 2016 , 13, 4414-20	2.9	19
32	Distinct temporal requirements for autophagy and the proteasome in yeast meiosis. <i>Autophagy</i> , 2016 , 12, 671-88	10.2	26
31	The human sperm proteome 2.0: An integrated resource for studying sperm functions at the level of posttranslational modification. <i>Proteomics</i> , 2016 , 16, 2597-2601	4.8	18
30	Proteomic Analysis of Pachytene Spermatocytes of Sterile Hybrid Male Mice. <i>Biology of Reproduction</i> , 2016 , 95, 52	3.9	2
29	Quantitative Proteomics Reveals the Essential Roles of Stromal Interaction Molecule 1 (STIM1) in the Testicular Cord Formation in Mouse Testis. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2682-91	7.6	17
28	Generation of fertile offspring from Kit(w)/Kit(wv) mice through differentiation of gene corrected nuclear transfer embryonic stem cells. <i>Cell Research</i> , 2015 , 25, 851-63	24.7	9
27	Unraveling the proteomic profile of mice testis during the initiation of meiosis. <i>Journal of Proteomics</i> , 2015 , 120, 35-43	3.9	7
26	Quantitative phosphoproteomics analysis reveals a key role of insulin growth factor 1 receptor (IGF1R) tyrosine kinase in human sperm capacitation. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1104-12	7.6	45
25	Beyond single modification: Reanalysis of the acetylproteome of human sperm reveals widespread multiple modifications. <i>Journal of Proteomics</i> , 2015 , 126, 296-302	3.9	11
24	Proteomic analysis of N-glycosylation of human seminal plasma. <i>Proteomics</i> , 2015 , 15, 1255-8	4.8	17
23	Identification of seven genes essential for male fertility through a genome-wide association study of non-obstructive azoospermia and RNA interference-mediated large-scale functional screening in <i>Drosophila</i> . <i>Human Molecular Genetics</i> , 2015 , 24, 1493-503	5.6	30
22	An update of the macaque testis proteome. <i>Data in Brief</i> , 2015 , 5, 95-8	1.2	
21	Establishment of a proteome profile and identification of molecular markers for mouse spermatogonial stem cells. <i>Journal of Cellular and Molecular Medicine</i> , 2015 , 19, 521-34	5.6	19
20	Yeast model identifies ENTPD6 as a potential non-obstructive azoospermia pathogenic gene. <i>Scientific Reports</i> , 2015 , 5, 11762	4.9	4
19	Comparative analysis of macaque and human sperm proteomes: Insights into sperm competition. <i>Proteomics</i> , 2015 , 15, 1564-73	4.8	12

18	Long-term effects of repeated superovulation on ovarian structure and function in rhesus monkeys. <i>Fertility and Sterility</i> , 2014 , 102, 1452-1457.e1	4.8	16
17	Unravelling the proteome of adult rhesus monkey ovaries. <i>Molecular BioSystems</i> , 2014 , 10, 653-62		9
16	Insights into the lysine acetylproteome of human sperm. <i>Journal of Proteomics</i> , 2014 , 109, 199-211	3.9	38
15	Quantitative proteomics analysis of altered protein expression in the placental villous tissue of early pregnancy loss using isobaric tandem mass tags. <i>BioMed Research International</i> , 2014 , 2014, 647143		10
14	Systematic analysis of the phosphoproteome and kinase-substrate networks in the mouse testis. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3626-38	7.6	27
13	In-depth proteomic analysis of whole testis tissue from the adult rhesus macaque. <i>Proteomics</i> , 2014 , 14, 1393-402	4.8	11
12	Establishment of a proteomic profile associated with gonocyte and spermatogonial stem cell maturation and differentiation in neonatal mice. <i>Proteomics</i> , 2014 , 14, 274-85	4.8	20
11	mUbiSiDa: a comprehensive database for protein ubiquitination sites in mammals. <i>PLoS ONE</i> , 2014 , 9, e85744	3.7	38
10	Proteomics analysis of human pericardial fluid. <i>Proteomics</i> , 2013 , 13, 2692-5	4.8	15
9	Genome-wide analysis of human hotspot intersected genes highlights the roles of meiotic recombination in evolution and disease. <i>BMC Genomics</i> , 2013 , 14, 67	4.5	5
8	In-depth proteomic analysis of the human sperm reveals complex protein compositions. <i>Journal of Proteomics</i> , 2013 , 79, 114-22	3.9	135
7	Bioinformatics for spermatogenesis: annotation of male reproduction based on proteomics. <i>Asian Journal of Andrology</i> , 2013 , 15, 594-602	2.8	30
6	Scanning of novel cancer/testis proteins by human testis proteomic analysis. <i>Proteomics</i> , 2013 , 13, 1200-18	4.8	47
5	Mapping of the N-linked glycoproteome of human spermatozoa. <i>Journal of Proteome Research</i> , 2013 , 12, 5750-9	5.6	44
4	Comparative proteomics analysis of placenta from pregnant women with intrahepatic cholestasis of pregnancy. <i>PLoS ONE</i> , 2013 , 8, e83281	3.7	19
3	Predicting miRNA-mediated gene silencing mode based on miRNA-target duplex features. <i>Computers in Biology and Medicine</i> , 2012 , 42, 1-7	7	8
2	PCBP1 is required for maintenance of the transcriptionally silent state in fully grown mouse oocytes. <i>Cell Cycle</i> , 2012 , 11, 2833-42	4.7	18
1	SProtP: a web server to recognize those short-lived proteins based on sequence-derived features in human cells. <i>PLoS ONE</i> , 2011 , 6, e27836	3.7	13

