

Tao Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

1,606
citations

361045

20
h-index

315357

38
g-index

59
all docs

59
docs citations

59
times ranked

2713
citing authors

#	ARTICLE	IF	CITATIONS
1	circRNADb: A comprehensive database for human circular RNAs with protein-coding annotations. <i>Scientific Reports</i> , 2016, 6, 34985.	1.6	360
2	In-depth proteomic analysis of the human sperm reveals complex protein compositions. <i>Journal of Proteomics</i> , 2013, 79, 114-122.	1.2	174
3	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.	3.3	74
4	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, 1104-1112.	2.5	70
5	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, 1493-1503.	1.4	65
6	Mapping of the N-Linked Glycoproteome of Human Spermatozoa. <i>Journal of Proteome Research</i> , 2013, 12, 5750-5759.	1.8	56
7	Scanning of novel cancer/testis proteins by human testis proteomic analysis. <i>Proteomics</i> , 2013, 13, 1200-1210.	1.3	54
8	Insights into the lysine acetylproteome of human sperm. <i>Journal of Proteomics</i> , 2014, 109, 199-211.	1.2	52
9	mUbiSiDa: A Comprehensive Database for Protein Ubiquitination Sites in Mammals. <i>PLoS ONE</i> , 2014, 9, e85744.	1.1	51
10	Distinct temporal requirements for autophagy and the proteasome in yeast meiosis. <i>Autophagy</i> , 2016, 12, 671-688.	4.3	42
11	Systematic Analysis of the Phosphoproteome and Kinase-substrate Networks in the Mouse Testis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3626-3638.	2.5	38
12	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.	2.5	33
13	Bioinformatics for spermatogenesis: annotation of male reproduction based on proteomics. <i>Asian Journal of Andrology</i> , 2013, 15, 594-602.	0.8	32
14	Comparative Proteomics Analysis of Placenta from Pregnant Women with Intrahepatic Cholestasis of Pregnancy. <i>PLoS ONE</i> , 2013, 8, e83281.	1.1	30
15	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, 521-534.	1.6	27
16	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.	1.2	27
17	Establishment of a proteomic profile associated with gonocyte and spermatogonial stem cell maturation and differentiation in neonatal mice. <i>Proteomics</i> , 2014, 14, 274-285.	1.3	25
18	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, 4414-4420.	1.1	25

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19	PCBP1 is required for maintenance of the transcriptionally silent state in fully grown mouse oocytes. <i>Cell Cycle</i> , 2012, 11, 2833-2842.	1.3	23
20	Long-term effects of repeated superovulation on ovarian structure and function in rhesus monkeys. <i>Fertility and Sterility</i> , 2014, 102, 1452-1457.e1.	0.5	23
21	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, 2682-2691.	2.5	23
22	Proteomic analysis of N-glycosylation of human seminal plasma. <i>Proteomics</i> , 2015, 15, 1255-1258.	1.3	22
23	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.	1.3	20
24	Proteomics analysis of human pericardial fluid. <i>Proteomics</i> , 2013, 13, 2692-2695.	1.3	18
25	Generation of fertile offspring from Kitw/Kitwv mice through differentiation of gene corrected nuclear transfer embryonic stem cells. <i>Cell Research</i> , 2015, 25, 851-863.	5.7	17
26	Comparative analysis of macaque and human sperm proteomes: Insights into sperm competition. <i>Proteomics</i> , 2015, 15, 1564-1573.	1.3	16
27	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.	1.1	13
28	In-depth proteomic analysis of whole testis tissue from the adult rhesus macaque. <i>Proteomics</i> , 2014, 14, 1393-1402.	1.3	12
29	Unravelling the proteome of adult rhesus monkey ovaries. <i>Molecular BioSystems</i> , 2014, 10, 653.	2.9	12
30	A Critical Review of Proteomic Studies in Gestational Diabetes Mellitus. <i>Journal of Diabetes Research</i> , 2020, 2020, 1-13.	1.0	12
31	MaxReport: An Enhanced Proteomic Result Reporting Tool for MaxQuant. <i>PLoS ONE</i> , 2016, 11, e0152067.	1.1	12
32	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, 1-9.	0.9	11
33	Beyond single modification: Reanalysis of the acetylproteome of human sperm reveals widespread multiple modifications. <i>Journal of Proteomics</i> , 2015, 126, 296-302.	1.2	11
34	Quantitative Proteomic Analysis of Human Seminal Plasma from Normozoospermic and Asthenozoospermic Individuals. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	11
35	mRBPome capture identifies the RNA binding protein TRIM71, an essential regulator of spermatogonial differentiation. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	11
36	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.	0.7	11

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37	Comparative transcriptome analysis reveals a regulatory network of microRNA-29b during mouse early embryonic development. <i>Oncotarget</i> , 2016, 7, 53772-53782.	0.8	11
38	Predicting miRNA-mediated gene silencing mode based on miRNA-target duplex features. <i>Computers in Biology and Medicine</i> , 2012, 42, 1-7.	3.9	10
39	Unraveling the proteomic profile of mice testis during the initiation of meiosis. <i>Journal of Proteomics</i> , 2015, 120, 35-43.	1.2	10
40	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.	2.0	9
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.	2.5	7
42	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.	0.8	6
43	Diagnostic and Prognostic Value of Long Noncoding RNAs as Potential Novel Biomarkers in Intrahepatic Cholestasis of Pregnancy. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	6
44	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.	1.2	5
45	Proteomic Analysis of Pachytene Spermatocytes of Sterile Hybrid Male Mice. <i>Biology of Reproduction</i> , 2016, 95, 52-52.	1.2	5
46	The need to revisit published data: A concept and framework for complementary proteomics. <i>Proteomics</i> , 2016, 16, 6-11.	1.3	5
47	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.	2.1	5
48	Yeast model identifies ENTPD6 as a potential non-obstructive azoospermia pathogenic gene. <i>Scientific Reports</i> , 2015, 5, 11762.	1.6	4
49	Quantitative phosphoproteomics reveals GSK3A substrate network is involved in the cryodamage of sperm motility. <i>Bioscience Reports</i> , 2021, 41, .	1.1	4
50	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, 1-9.	1.2	2
51	Front cover: The human sperm proteome 2.0: An integrated resource for studying sperm functions at the level of post-translational modification. <i>Proteomics</i> , 2016, 16, NA-NA.	1.3	1
52	Data on comparative proteomic profiling of human sperm affected by 4-tert-octylphenol in vitro. <i>Data in Brief</i> , 2018, 21, 2242-2245.	0.5	1
53	Back Cover: 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, 1870021.	0.8	1
54	A Refined Framework for Precision and Translational Proteomics in Clinical Research. <i>Current Proteomics</i> , 2021, 18, 436-446.	0.1	1

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55	microDoR for HUMAN: A web server to predict mode of miRNA-mediated gene silencing. , 2010, , .		0
56	An update of the macaque testis proteome. Data in Brief, 2015, 5, 95-98.	0.5	0