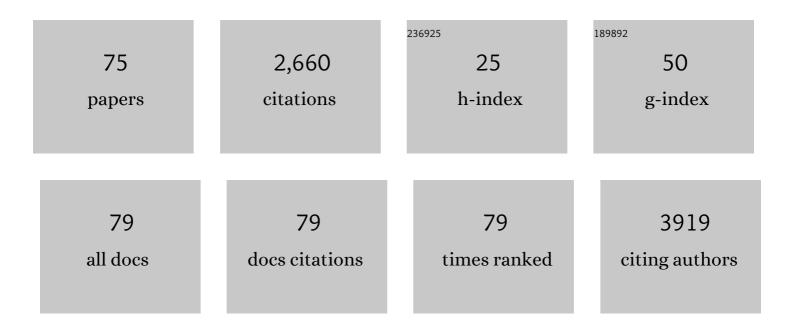
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Naturally Occurring Human Glutathione <i>S</i> â€transferase GSTP1â€1 Isoforms with Isoleucine and Valine in Position 104 Differ in Enzymic Properties. FEBS Journal, 1994, 224, 893-899.	0.2	389
2	AgBase: a functional genomics resource for agriculture. BMC Genomics, 2006, 7, 229.	2.8	286
3	Comprehensive proteomic analysis of bovine spermatozoa of varying fertility rates and identification of biomarkers associated with fertility. BMC Systems Biology, 2008, 2, 19.	3.0	221
4	HPIDB 2.0: a curated database for host–pathogen interactions. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw103.	3.0	202
5	Global Analysis of Lysine Acetylation Suggests the Involvement of Protein Acetylation in Diverse Biological Processes in Rice (Oryza sativa). PLoS ONE, 2014, 9, e89283.	2.5	102
6	Active Site Architecture of Polymorphic Forms of Human GlutathioneS-Transferase P1-1 Accounts for Their Enantioselectivity and Disparate Activity in the Glutathione Conjugation of 7β,8α-Dihydroxy-9α, 10α-oxy-7,8,9,10-tetrahydrobenzo(a)pyrene. Biochemical and Biophysical Research Communications, 1997, 235, 424-428.	2.1	82
7	Pre-steady-state DNA unwinding by bacteriophage T4 Dda helicase reveals a monomeric molecular motor. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14722-14727.	7.1	82
8	Polyamine biosynthesis and transport mechanisms are crucial for fitness and pathogenesis of Streptococcus pneumoniae. Microbiology (United Kingdom), 2011, 157, 504-515.	1.8	80
9	Mechanism of Differential Catalytic Efficiency of Two Polymorphic Forms of Human GlutathioneS-Transferase P1-1 in the Glutathione Conjugation of Carcinogenic Diol Epoxide of Chrysene. Archives of Biochemistry and Biophysics, 1997, 345, 32-38.	3.0	78
10	Identification of novel non-coding small RNAs from Streptococcus pneumoniae TIGR4 using high-resolution genome tiling arrays. BMC Genomics, 2010, 11, 350.	2.8	59
11	Proteomic Analysis of Cross Protection Provided between Cold and Osmotic Stress in <i>Listeria monocytogenes</i> . Journal of Proteome Research, 2014, 13, 1896-1904.	3.7	58
12	Crystal Structure of a Murine GlutathioneS-Transferase in Complex with a Glutathione Conjugate of 4-Hydroxynon-2-enal in One Subunit and Glutathione in the Other:Â Evidence of Signaling across the Dimer Interfaceâ€,‡. Biochemistry, 1999, 38, 11887-11894.	2.5	55
13	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	12.8	49
14	Proteomic analysis using an unfinished bacterial genome: The effects of subminimum inhibitory concentrations of antibiotics onMannheimia haemolytica virulence factor expression. Proteomics, 2005, 5, 4852-4863.	2.2	48
15	ProtQuant: a tool for the label-free quantification of MudPIT proteomics data. BMC Bioinformatics, 2007, 8, S24.	2.6	47
16	Evidence for a Functional Monomeric Form of the Bacteriophage T4 Dda Helicase. Journal of Biological Chemistry, 2001, 276, 19691-19698.	3.4	42
17	Comparative Proteomic Analysis of Listeria monocytogenes Strains F2365 and EGD. Applied and Environmental Microbiology, 2009, 75, 366-373.	3.1	41
18	The Proteogenomic Mapping Tool. BMC Bioinformatics, 2011, 12, 115.	2.6	35

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19	Activity-Based Proteomic Profiling of Deubiquitinating Enzymes in Salmonella-Infected Macrophages Leads to Identification of Putative Function of UCH-L5 in Inflammasome Regulation. PLoS ONE, 2015, 10, e0135531.	2.5	33
20	Whole blood transcriptomic analysis of beef cattle at arrival identifies potential predictive molecules and mechanisms that indicate animals that naturally resist bovine respiratory disease. PLoS ONE, 2020, 15, e0227507.	2.5	33
21	Polyamine transporter in Streptococcus pneumoniae is essential for evading early innate immune responses in pneumococcal pneumonia. Scientific Reports, 2016, 6, 26964.	3.3	30
22	Proteomic analysis of the response of Listeria monocytogenes to bile salts under anaerobic conditions. Journal of Medical Microbiology, 2013, 62, 25-35.	1.8	29
23	Bovine Viral Diarrhea Virus infection affects the expression of proteins related to professional antigen presentation in bovine monocytes. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 14-22.	2.3	28
24	Role of acute ethanol exposure and TLR4 in early events of sepsis in a mouse model. Alcohol, 2011, 45, 795-803.	1.7	28
25	SILAC-Based Quantitative Proteomic Analysis of Human Lung Cell Response to Copper Oxide Nanoparticles. PLoS ONE, 2014, 9, e114390.	2.5	28
26	Deubiquitinating Enzymes as Promising Drug Targets for Infectious Diseases. Current Pharmaceutical Design, 2013, 19, 3234-3247.	1.9	27
27	RNA-Seq Based Transcriptional Map of Bovine Respiratory Disease Pathogen "Histophilus somni 2336― PLoS ONE, 2012, 7, e29435.	2.5	26
28	Quantitative analysis of <i>Streptococcus pneumoniae</i> TIGR4 response to <i>in vitro</i> iron restriction by 2â€D LC ESI MS/MS. Proteomics, 2008, 8, 2104-2114.	2.2	25
29	Proteomic expression profiles of virulent and avirulent strains of Listeria monocytogenes isolated from macrophages. Journal of Proteomics, 2011, 74, 1906-1917.	2.4	25
30	The Effect of Oxygen on Bile Resistance in Listeria monocytogenes. Journal of Proteomics and Bioinformatics, 2016, 04, 107-119.	0.4	25
31	Effects of Subminimum Inhibitory Concentrations of Antibiotics on thePasteurellamultocidaProteome. Journal of Proteome Research, 2006, 5, 572-580.	3.7	24
32	Polyamine Synthesis Effects Capsule Expression by Reduction of Precursors in Streptococcus pneumoniae. Frontiers in Microbiology, 2019, 10, 1996.	3.5	20
33	Experimental annotation of channel catfish virus by probabilistic proteogenomic mapping. Proteomics, 2009, 9, 2634-2647.	2.2	17
34	The Role of Cadaverine Synthesis on Pneumococcal Capsule and Protein Expression. Medical Sciences (Basel, Switzerland), 2018, 6, 8.	2.9	17
35	Dosage scaling of alcohol in binge exposure models in mice: An empirical assessment of the relationship between dose, alcohol exposure, and peak blood concentrations in humans and mice. Alcohol, 2020, 89, 9-17.	1.7	17
36	An automated proteomic data analysis workflow for mass spectrometry. BMC Bioinformatics, 2009, 10, S17.	2.6	16

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37	Ultrasonic Incisions Produce Less Inflammatory Mediator Response during Early Healing than Electrosurgical Incisions. PLoS ONE, 2013, 8, e73032.	2.5	13
38	Streptococcus pneumoniaemetal homeostasis alters cellular metabolism. Metallomics, 2020, 12, 1416-1427.	2.4	13
39	Bovine viral diarrhea viruses differentially alter the expression of the protein kinases and related proteins affecting the development of infection and anti-viral mechanisms in bovine monocytes. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1234-1247.	2.3	12
40	The transcriptional response of Pasteurella multocida to three classes of antibiotics. BMC Genomics, 2009, 10, S4.	2.8	12
41	<p>Modeling the pasture-associated severe equine asthma bronchoalveolar lavage fluid proteome identifies molecular events mediating neutrophilic airway inflammation</p> . Veterinary Medicine: Research and Reports, 2019, Volume 10, 43-63.	0.6	12
42	GOModeler- A tool for hypothesis-testing of functional genomics datasets. BMC Bioinformatics, 2010, 11, S29.	2.6	11
43	Transcriptome profile of a bovine respiratory disease pathogen: Mannheimia haemolytica PHL213. BMC Bioinformatics, 2012, 13, S4.	2.6	11
44	Transcriptomic analysis of early B-cell development in the chicken embryo. Poultry Science, 2019, 98, 5342-5354.	3.4	11
45	Proteomic and transcriptional profiling of rat amygdala following social play. Behavioural Brain Research, 2019, 376, 112210.	2.2	11
46	The expansive effects of polyamines on the metabolism and virulence of Streptococcus pneumoniae. Pneumonia (Nathan Qld), 2021, 13, 4.	6.1	11
47	Comprehensive at-arrival transcriptomic analysis of post-weaned beef cattle uncovers type I interferon and antiviral mechanisms associated with bovine respiratory disease mortality. PLoS ONE, 2021, 16, e0250758.	2.5	11
48	Comparative Proteomic Analysis of Cotton Fiber Development and Protein Extraction Method Comparison in Late Stage Fibers. Proteomes, 2016, 4, 7.	3.5	10
49	Proteome and Membrane Fatty Acid Analyses on Oligotropha carboxidovorans OM5 Grown under Chemolithoautotrophic and Heterotrophic Conditions. PLoS ONE, 2011, 6, e17111.	2.5	10
50	Transcriptomic analysis of peritoneal cells in a mouse model of sepsis: confirmatory and novel results in early and late sepsis. BMC Genomics, 2012, 13, 509.	2.8	9
51	Systems toxicology identifies mechanistic impacts of 2-amino-4,6-dinitrotoluene (2A-DNT) exposure in Northern Bobwhite. BMC Genomics, 2015, 16, 587.	2.8	9
52	Effects of Subminimum Inhibitory Concentrations of Antibiotics on the <i>Pasteurella multocida</i> Proteome: A Systems Approach. Comparative and Functional Genomics, 2008, 2008, 1-12.	2.0	8
53	Analysis of differentially expressed proteins in Yersinia enterocolitica-infected HeLa cells. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 562-569.	2.3	8
54	Binge alcohol consumption 18Âh after induction of sepsis in a mouseÂmodel causes rapid overgrowth of bacteria, a cytokine storm,Âand decreased survival. Alcohol, 2017, 63, 9-17.	1.7	8

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55	Proteogenomic Identification of a Novel Protein-Encoding Gene in Bovine Herpesvirus 1 That Is Expressed during Productive Infection. Viruses, 2018, 10, 499.	3.3	8
56	SP_0916 Is an Arginine Decarboxylase That Catalyzes the Synthesis of Agmatine, Which Is Critical for Capsule Biosynthesis in Streptococcus pneumoniae. Frontiers in Microbiology, 2020, 11, 578533.	3.5	8
57	Application of Functional Genomics for Bovine Respiratory Disease Diagnostics. Bioinformatics and Biology Insights, 2015, 9s2, BBI.S30525.	2.0	7
58	Big data - a 21st century science Maginot Line? No-boundary thinking: shifting from the big data paradigm. BioData Mining, 2015, 8, 7.	4.0	6
59	Gene Model Detection Using Mass Spectrometry. Methods in Molecular Biology, 2010, 604, 137-144.	0.9	5
60	Arginine Decarboxylase Is Essential for Pneumococcal Stress Responses. Pathogens, 2021, 10, 286.	2.8	5
61	Adolescent rat social play: Amygdalar proteomic and transcriptomic data. Data in Brief, 2019, 27, 104589.	1.0	4
62	The Effect of Impaired Polyamine Transport on Pneumococcal Transcriptome. Pathogens, 2021, 10, 1322.	2.8	4
63	TAAPP: Tiling Array Analysis Pipeline for Prokaryotes. Genomics, Proteomics and Bioinformatics, 2011, 9, 56-62.	6.9	3
64	Identification of canine platelet proteins separated by differential detergent fractionation for nonelectrophoretic proteomics analyzed by Gene Ontology and pathways analysis. Veterinary Medicine: Research and Reports, 2014, 5, 1.	0.6	3
65	Use of focused ultrasonication in activity-based profiling of deubiquitinating enzymes in tissue. Analytical Biochemistry, 2016, 515, 9-13.	2.4	3
66	No-boundary thinking: a viable solution to ethical data-driven AI in precision medicine. AI and Ethics, 2022, 2, 635-643.	6.8	3
67	Leveraging Experimental Details for an Improved Understanding of Hostâ€Pathogen Interactome. Current Protocols in Bioinformatics, 2018, 61, 8.26.1-8.26.12.	25.8	2
68	Listeria and -Omics Approaches for Understanding its Biology. , 2015, , 135-158.		1
69	An atlas of the catalytically active liver and spleen kinases in chicken identified by chemoproteomics. Journal of Proteomics, 2020, 225, 103850.	2.4	1
70	Identification of active deubiquitinases in the chicken tissues. Proteomics, 2021, , 2100122.	2.2	1
71	Editorial: Unleashing Innovation on Precision Public Health–Highlights From the MCBIOS and MAQC 2021 Joint Conference. Frontiers in Artificial Intelligence, 2022, 5, 859700.	3.4	0

