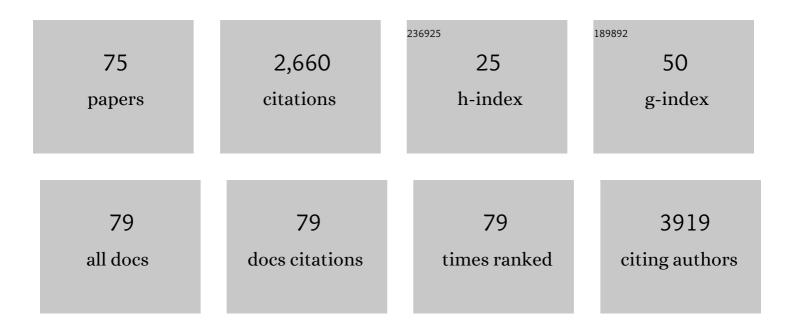
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	No-boundary thinking: a viable solution to ethical data-driven Al in precision medicine. Al and Ethics, 2022, 2, 635-643.	6.8	3
2	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
3	The expansive effects of polyamines on the metabolism and virulence of Streptococcus pneumoniae. Pneumonia (Nathan Qld), 2021, 13, 4.	6.1	11
4	Arginine Decarboxylase Is Essential for Pneumococcal Stress Responses. Pathogens, 2021, 10, 286.	2.8	5
5	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
6	The Effect of Impaired Polyamine Transport on Pneumococcal Transcriptome. Pathogens, 2021, 10, 1322.	2.8	4
7	Identification of active deubiquitinases in the chicken tissues. Proteomics, 2021, , 2100122.	2.2	1
8	Streptococcus pneumoniaemetal homeostasis alters cellular metabolism. Metallomics, 2020, 12, 1416-1427.	2.4	13
9	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	12.8	49
10	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
11	An atlas of the catalytically active liver and spleen kinases in chicken identified by chemoproteomics. Journal of Proteomics, 2020, 225, 103850.	2.4	1
12	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
13	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
14	Title is missing!. , 2020, 15, e0227507.		0
15	Title is missing!. , 2020, 15, e0227507.		0
16	Title is missing!. , 2020, 15, e0227507.		0
17	Title is missing!. , 2020, 15, e0227507.		0
18	Transcriptomic analysis of early B-cell development in the chicken embryo. Poultry Science, 2019, 98, 5342-5354.	3.4	11

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19	Adolescent rat social play: Amygdalar proteomic and transcriptomic data. Data in Brief, 2019, 27, 104589.	1.0	4
20	Proteomic and transcriptional profiling of rat amygdala following social play. Behavioural Brain Research, 2019, 376, 112210.	2.2	11
21	Polyamine Synthesis Effects Capsule Expression by Reduction of Precursors in Streptococcus pneumoniae. Frontiers in Microbiology, 2019, 10, 1996.	3.5	20
22	<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
23	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
24	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
25	The Role of Cadaverine Synthesis on Pneumococcal Capsule and Protein Expression. Medical Sciences (Basel, Switzerland), 2018, 6, 8.	2.9	17
26	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
27	The Effect of Oxygen on Bile Resistance in Listeria monocytogenes. Journal of Proteomics and Bioinformatics, 2016, 04, 107-119.	0.4	25
28	Comparative Proteomic Analysis of Cotton Fiber Development and Protein Extraction Method Comparison in Late Stage Fibers. Proteomes, 2016, 4, 7.	3.5	10
29	Polyamine transporter in Streptococcus pneumoniae is essential for evading early innate immune responses in pneumococcal pneumonia. Scientific Reports, 2016, 6, 26964.	3.3	30
30	Use of focused ultrasonication in activity-based profiling of deubiquitinating enzymes in tissue. Analytical Biochemistry, 2016, 515, 9-13.	2.4	3
31	HPIDB 2.0: a curated database for host–pathogen interactions. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw103.	3.0	202
32	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
33	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
34	Application of Functional Genomics for Bovine Respiratory Disease Diagnostics. Bioinformatics and Biology Insights, 2015, 9s2, BBI.S30525.	2.0	7
35	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
36	Listeria and -Omics Approaches for Understanding its Biology. , 2015, , 135-158.		1

Listeria and -Omics Approaches for Understanding its Biology. , 2015, , 135-158. 36

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37	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
38	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
39	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
40	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
41	SILAC-Based Quantitative Proteomic Analysis of Human Lung Cell Response to Copper Oxide Nanoparticles. PLoS ONE, 2014, 9, e114390.	2.5	28
42	Ultrasonic Incisions Produce Less Inflammatory Mediator Response during Early Healing than Electrosurgical Incisions. PLoS ONE, 2013, 8, e73032.	2.5	13
43	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
44	Deubiquitinating Enzymes as Promising Drug Targets for Infectious Diseases. Current Pharmaceutical Design, 2013, 19, 3234-3247.	1.9	27
45	Transcriptome profile of a bovine respiratory disease pathogen: Mannheimia haemolytica PHL213. BMC Bioinformatics, 2012, 13, S4.	2.6	11
46	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
47	RNA-Seq Based Transcriptional Map of Bovine Respiratory Disease Pathogen "Histophilus somni 2336― PLoS ONE, 2012, 7, e29435.	2.5	26
48	Role of acute ethanol exposure and TLR4 in early events of sepsis in a mouse model. Alcohol, 2011, 45, 795-803.	1.7	28
49	Proteomic expression profiles of virulent and avirulent strains of Listeria monocytogenes isolated from macrophages. Journal of Proteomics, 2011, 74, 1906-1917.	2.4	25
50	TAAPP: Tiling Array Analysis Pipeline for Prokaryotes. Genomics, Proteomics and Bioinformatics, 2011, 9, 56-62.	6.9	3
51	The Proteogenomic Mapping Tool. BMC Bioinformatics, 2011, 12, 115.	2.6	35
52	Polyamine biosynthesis and transport mechanisms are crucial for fitness and pathogenesis of Streptococcus pneumoniae. Microbiology (United Kingdom), 2011, 157, 504-515.	1.8	80
53	Proteome and Membrane Fatty Acid Analyses on Oligotropha carboxidovorans OM5 Grown under Chemolithoautotrophic and Heterotrophic Conditions. PLoS ONE, 2011, 6, e17111.	2.5	10
54	GOModeler- A tool for hypothesis-testing of functional genomics datasets. BMC Bioinformatics, 2010, 11, S29.	2.6	11

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55	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
56	Gene Model Detection Using Mass Spectrometry. Methods in Molecular Biology, 2010, 604, 137-144.	0.9	5
57	An automated proteomic data analysis workflow for mass spectrometry. BMC Bioinformatics, 2009, 10, S17.	2.6	16
58	The transcriptional response of Pasteurella multocida to three classes of antibiotics. BMC Genomics, 2009, 10, S4.	2.8	12
59	Experimental annotation of channel catfish virus by probabilistic proteogenomic mapping. Proteomics, 2009, 9, 2634-2647.	2.2	17
60	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
61	Comparative Proteomic Analysis of Listeria monocytogenes Strains F2365 and EGD. Applied and Environmental Microbiology, 2009, 75, 366-373.	3.1	41
62	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
63	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
64	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
65	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
66	ProtQuant: a tool for the label-free quantification of MudPIT proteomics data. BMC Bioinformatics, 2007, 8, S24.	2.6	47
67	Effects of Subminimum Inhibitory Concentrations of Antibiotics on thePasteurellamultocidaProteome. Journal of Proteome Research, 2006, 5, 572-580.	3.7	24
68	AgBase: a functional genomics resource for agriculture. BMC Genomics, 2006, 7, 229.	2.8	286
69	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
70	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
71	Evidence for a Functional Monomeric Form of the Bacteriophage T4 Dda Helicase. Journal of Biological Chemistry, 2001, 276, 19691-19698.	3.4	42
72	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€,â€j. Biochemistry, 1999, 38, 11887-11894.	2.5	55

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73	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
74	Active Site Architecture of Polymorphic Forms of Human GlutathioneS-Transferase P1-1 Accounts for Their Enantioselectivity and Disparate Activity in the Glutathione Conjugation of 7l ² ,8l [±] -Dihydroxy-9l [±] , 10l [±] -oxy-7,8,9,10-tetrahydrobenzo(a)pyrene. Biochemical and Biophysical Research Communications, 1997, 235, 424-428.	2.1	82
75	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