

# 2016 update of the PRIDE database and its related tools

Nucleic Acids Research

44, D447-D456

DOI: [10.1093/nar/gkv1145](https://doi.org/10.1093/nar/gkv1145)

Citation Report

#	ARTICLE	IF	CITATIONS
11	Immunoproteomic identification of MbovP579, a promising diagnostic biomarker for serological detection of <i>Mycoplasma bovis</i> infection. <i>Oncotarget</i> , 2016, 7, 39376-39395.	0.8	32
12	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016, 7, 238.	1.5	66
13	The composition and organization of <i>Drosophila</i> heterochromatin are heterogeneous and dynamic. <i>ELife</i> , 2016, 5, .	2.8	53
14	Systems Medicine as an Emerging Tool for Cardiovascular Genetics. <i>Frontiers in Cardiovascular Medicine</i> , 2016, 3, 27.	1.1	8
15	Transcriptome and Proteome Studies Reveal Candidate Attachment Genes during the Development of the Barnacle <i>Amphibalanus Amphitrite</i> . <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	12
16	Tyrosine 601 of <i>Bacillus subtilis</i> DnaK Undergoes Phosphorylation and Is Crucial for Chaperone Activity and Heat Shock Survival. <i>Frontiers in Microbiology</i> , 2016, 7, 533.	1.5	13
17	Identification of Quantitative Proteomic Differences between <i>Mycobacterium tuberculosis</i> Lineages with Altered Virulence. <i>Frontiers in Microbiology</i> , 2016, 7, 813.	1.5	34
18	Proteomic Analysis of the Hydrogen and Carbon Monoxide Metabolism of <i>Methanothermobacter marburgensis</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1049.	1.5	27
19	Characterization of Outer Membrane Proteome of <i>Akkermansia muciniphila</i> Reveals Sets of Novel Proteins Exposed to the Human Intestine. <i>Frontiers in Microbiology</i> , 2016, 7, 1157.	1.5	106
20	Monitoring Perinatal Gut Microbiota in Mouse Models by Mass Spectrometry Approaches: Parental Genetic Background and Breastfeeding Effects. <i>Frontiers in Microbiology</i> , 2016, 7, 1523.	1.5	15
21	Membrane Complexes of <i>Syntrophomonas wolfei</i> Involved in Syntrophic Butyrate Degradation and Hydrogen Formation. <i>Frontiers in Microbiology</i> , 2016, 7, 1795.	1.5	34
22	Proteome Profile and Quantitative Proteomic Analysis of Buffalo ( <i>Bubalus bubalis</i> ) Follicular Fluid during Follicle Development. <i>International Journal of Molecular Sciences</i> , 2016, 17, 618.	1.8	33
23	Drought-Induced Leaf Proteome Changes in Switchgrass Seedlings. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1251.	1.8	18
24	Proteome and Peptidome of <i>Vipera berus berus</i> Venom. <i>Molecules</i> , 2016, 21, 1398.	1.7	27
25	A proteomics approach reveals molecular manipulators of distinct cellular processes in the salivary glands of <i>Glossina m. morsitans</i> in response to <i>Trypanosoma b. brucei</i> infections. <i>Parasites and Vectors</i> , 2016, 9, 424.	1.0	11
26	Quantitative and Selective Analysis of Feline Growth Related Proteins Using Parallel Reaction Monitoring High Resolution Mass Spectrometry. <i>PLoS ONE</i> , 2016, 11, e0167138.	1.1	7
27	Quantitative Proteomic Analysis of Wheat Seeds during Artificial Ageing and Priming Using the Isobaric Tandem Mass Tag Labeling. <i>PLoS ONE</i> , 2016, 11, e0162851.	1.1	40
28	Site-Specific Cleavage of Ribosomal RNA in <i>Escherichia coli</i> -Based Cell-Free Protein Synthesis Systems. <i>PLoS ONE</i> , 2016, 11, e0168764.	1.1	20

#	ARTICLE	IF	CITATIONS
29	Static Clathrin Assemblies at the Peripheral Vacuoleâ€”Plasma Membrane Interface of the Parasitic Protozoan <i>Giardia lamblia</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005756.	2.1	44
30	Deep Phosphoproteomic Measurements Pinpointing Drug Induced Protective Mechanisms in Neuronal Cells. <i>Frontiers in Physiology</i> , 2016, 7, 635.	1.3	6
31	Transcriptome- Assisted Label-Free Quantitative Proteomics Analysis Reveals Novel Insights into <i>Piper nigrum</i> â€” <i>Phytophthora capsici</i> Phytopathosystem. <i>Frontiers in Plant Science</i> , 2016, 7, 785.	1.7	29
32	Quantitative Proteomic and Transcriptomic Study on Autotetraploid <i>Paulownia</i> and Its Diploid Parent Reveal Key Metabolic Processes Associated with <i>Paulownia</i> Autotetraploidization. <i>Frontiers in Plant Science</i> , 2016, 7, 892.	1.7	13
33	Circadian Profiling of the <i>Arabidopsis</i> Proteome Using 2D-DIGE. <i>Frontiers in Plant Science</i> , 2016, 7, 1007.	1.7	32
34	Comprehensive Analysis of the Membrane Phosphoproteome Regulated by Oligogalacturonides in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1107.	1.7	43
35	A Role for Barley Calcium-Dependent Protein Kinase CPK2a in the Response to Drought. <i>Frontiers in Plant Science</i> , 2016, 7, 1550.	1.7	40
36	Global Lysine Acetylome Analysis of Desiccated Somatic Embryos of <i>Picea asperata</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1927.	1.7	14
37	HVint: A Strategy for Identifying Novel Protein-Protein Interactions in Herpes Simplex Virus Type 1. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2939-2953.	2.5	17
38	Analysis of lowâ€”density lipoproteinâ€”associated proteins using the method of digitized native protein mapping. <i>Electrophoresis</i> , 2016, 37, 2063-2074.	1.3	7
39	Mass spectrometry insights into a tandem ubiquitin-binding domain hybrid engineered for the selective recognition of unanchored polyubiquitin. <i>Proteomics</i> , 2016, 16, 1961-1969.	1.3	11
40	Myostatin deficiency but not anti-myostatin blockade induces marked proteomic changes in mouse skeletal muscle. <i>Proteomics</i> , 2016, 16, 2019-2027.	1.3	9
41	Protein precipitation of diluted samples in SDSâ€”containing buffer with acetone leads to higher protein recovery and reproducibility in comparison with TCA/acetone approach. <i>Proteomics</i> , 2016, 16, 1847-1851.	1.3	42
42	Preferential Phosphorylation on Old Histones during Early Mitosis in Human Cells. <i>Journal of Biological Chemistry</i> , 2016, 291, 15342-15357.	1.6	30
43	A Human Lectin Microarray for Sperm Surface Glycosylation Analysis. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2839-2851.	2.5	22
44	Identification of glycoproteins associated with HIV latently infected cells using quantitative glycoproteomics. <i>Proteomics</i> , 2016, 16, 1872-1880.	1.3	10
45	Antibody-independent identification of bovine milk-derived peptides in breast-milk. <i>Food and Function</i> , 2016, 7, 3402-3409.	2.1	12
46	Automated SDS Depletion for Mass Spectrometry of Intact Membrane Proteins through Transmembrane Electrophoresis. <i>Journal of Proteome Research</i> , 2016, 15, 2634-2642.	1.8	23

#	ARTICLE	IF	CITATIONS
47	Evidence That G-quadruplex DNA Accumulates in the Cytoplasm and Participates in Stress Granule Assembly in Response to Oxidative Stress. <i>Journal of Biological Chemistry</i> , 2016, 291, 18041-18057.	1.6	71
48	Increased Levels of Extracellular Microvesicle Markers and Decreased Levels of Endocytic/Exocytic Proteins in the Alzheimer's Disease Brain. <i>Journal of Alzheimer's Disease</i> , 2016, 54, 1671-1686.	1.2	22
49	Open-gate mutants of the mammalian proteasome show enhanced ubiquitin-conjugate degradation. <i>Nature Communications</i> , 2016, 7, 10963.	5.8	82
50	Proteomic and metabolomic analyses reveal metabolic responses to 3-hydroxypropionic acid synthesized internally in cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Biotechnology for Biofuels</i> , 2016, 9, 209.	6.2	30
51	Global changes of the RNA-bound proteome during the maternal-to-zygotic transition in <i>Drosophila</i> . <i>Nature Communications</i> , 2016, 7, 12128.	5.8	134
52	Quantitative Profiling of Single Formalin Fixed Tumour Sections: proteomics for translational research. <i>Scientific Reports</i> , 2016, 6, 34949.	1.6	100
53	Quantitative deep mapping of the cultured podocyte proteome uncovers shifts in proteostatic mechanisms during differentiation. <i>American Journal of Physiology - Cell Physiology</i> , 2016, 311, C404-C417.	2.1	31
54	Quantitative analyses of the hepatic proteome of methylmercury-exposed Atlantic cod ( <i>Gadus morhua</i> ) suggest oxidative stress-mediated effects on cellular energy metabolism. <i>BMC Genomics</i> , 2016, 17, 554.	1.2	27
55	Quantitative profiling of spreading-coupled protein tyrosine phosphorylation in migratory cells. <i>Scientific Reports</i> , 2016, 6, 31811.	1.6	6
56	Distinctive proteomic profiles among different regions of human carotid plaques in men and women. <i>Scientific Reports</i> , 2016, 6, 26231.	1.6	36
57	Cellulose and hemicellulose decomposition by forest soil bacteria proceeds by the action of structurally variable enzymatic systems. <i>Scientific Reports</i> , 2016, 6, 25279.	1.6	328
58	The impact of sequence database choice on metaproteomic results in gut microbiota studies. <i>Microbiome</i> , 2016, 4, 51.	4.9	124
59	The Safety Limits Of An Extended Fast: Lessons from a Non-Model Organism. <i>Scientific Reports</i> , 2016, 6, 39008.	1.6	10
60	TDP43 loss of function inhibits endosomal trafficking and alters trophic signaling in neurons. <i>EMBO Journal</i> , 2016, 35, 2350-2370.	3.5	76
61	The membrane scaffold SLP2 anchors a proteolytic hub in mitochondria containing PARL and the AAA protease YME1L. <i>EMBO Reports</i> , 2016, 17, 1844-1856.	2.0	142
62	Extracellular IL-33 cytokine, but not endogenous nuclear IL-33, regulates protein expression in endothelial cells. <i>Scientific Reports</i> , 2016, 6, 34255.	1.6	74
63	Changes over lactation in breast milk serum proteins involved in the maturation of immune and digestive system of the infant. <i>Data in Brief</i> , 2016, 7, 362-365.	0.5	19
64	Quantitative proteomic analysis of two different rice varieties reveals that drought tolerance is correlated with reduced abundance of photosynthetic machinery and increased abundance of ClpD1 protease. <i>Journal of Proteomics</i> , 2016, 143, 73-82.	1.2	50

#	ARTICLE	IF	CITATIONS
65	Proteome Modification in Tomato Plants upon Long-Term Aluminum Treatment. <i>Journal of Proteome Research</i> , 2016, 15, 1670-1684.	1.8	37
66	Compensating the Fitness Costs of Synonymous Mutations. <i>Molecular Biology and Evolution</i> , 2016, 33, 1461-1477.	3.5	45
67	Nuclear Functions of Nucleolin through Global Proteomics and Interactomic Approaches. <i>Journal of Proteome Research</i> , 2016, 15, 1659-1669.	1.8	48
68	The adaptive metabolic response involves specific protein glutathionylation during the filamentation process in the pathogen <i>Candida albicans</i> . <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1309-1323.	1.8	5
69	Prolyl hydroxylation regulates protein degradation, synthesis, and splicing in human induced pluripotent stem cell-derived cardiomyocytes. <i>Cardiovascular Research</i> , 2016, 110, 346-358.	1.8	27
70	Detergent-Assisted Glycoprotein Capture: A Versatile Tool for In-Depth N-Glycoproteome Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 2080-2086.	1.8	13
71	NAD <sup>+</sup> repletion improves mitochondrial and stem cell function and enhances life span in mice. <i>Science</i> , 2016, 352, 1436-1443.	6.0	907
72	Freezing effects on the acute myeloid leukemia cell proteome and phosphoproteome revealed using optimal quantitative workflows. <i>Journal of Proteomics</i> , 2016, 145, 214-225.	1.2	35
73	<i>Pseudomonas fluorescens</i> PICF7 displays an endophytic lifestyle in cultivated cereals and enhances yield in barley. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw092.	1.3	25
74	The Metacaspase (Mca1p) Restricts O-glycosylation During Farnesol-induced Apoptosis in <i>Candida albicans</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2308-2323.	2.5	6
75	PRICKLE1 Contributes to Cancer Cell Dissemination through Its Interaction with mTORC2. <i>Developmental Cell</i> , 2016, 37, 311-325.	3.1	63
76	Proteome Changes during Transition from Human Embryonic to Vascular Progenitor Cells. <i>Journal of Proteome Research</i> , 2016, 15, 1995-2007.	1.8	10
77	A novel nuclear genetic code alteration in yeasts and the evolution of codon reassignment in eukaryotes. <i>Genome Research</i> , 2016, 26, 945-955.	2.4	61
78	Venus flytrap carnivorous lifestyle builds on herbivore defense strategies. <i>Genome Research</i> , 2016, 26, 812-825.	2.4	88
79	Novel IEF Peptide Fractionation Method Reveals a Detailed Profile of N-Terminal Acetylation in Chemotherapy-Responsive and -Resistant Ovarian Cancer Cells. <i>Journal of Proteome Research</i> , 2016, 15, 4073-4081.	1.8	7
80	<i>Fasciola hepatica</i> Surface Tegument: Glycoproteins at the Interface of Parasite and Host. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3139-3153.	2.5	55
81	Minimal cytosolic iron-sulfur cluster assembly machinery of <i>Giardia intestinalis</i> is partially associated with mitosomes. <i>Molecular Microbiology</i> , 2016, 102, 701-714.	1.2	19
82	Detection of Missing Proteins Using the PRIDE Database as a Source of Mass Spectrometry Evidence. <i>Journal of Proteome Research</i> , 2016, 15, 4101-4115.	1.8	15

#	ARTICLE	IF	CITATIONS
83	Human Leukocyte Antigen (HLA) Peptides Derived from Tumor Antigens Induced by Inhibition of DNA Methylation for Development of Drug-facilitated Immunotherapy. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3058-3070.	2.5	62
84	Uterine flushing proteome of the tammar wallaby after reactivation from diapause. <i>Reproduction</i> , 2016, 152, 491-505.	1.1	11
85	Data from quantitative label free proteomics analysis of rat spleen. <i>Data in Brief</i> , 2016, 8, 494-500.	0.5	4
86	Comprehensive Proteome Profiling of Platelet Identified a Protein Profile Predictive of Responses to An Antiplatelet Agent Sarpogrelate. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3461-3472.	2.5	21
87	The Proteasome Acts as a Hub for Plant Immunity and Is Targeted by <i>Pseudomonas</i> Type III Effectors. <i>Plant Physiology</i> , 2016, 172, 1941-1958.	2.3	94
88	PAXX Is an Accessory c-NHEJ Factor that Associates with Ku70 and Has Overlapping Functions with XLF. <i>Cell Reports</i> , 2016, 17, 541-555.	2.9	77
89	A Portrait of the Human Organelle Proteome In Space and Time during Cytomegalovirus Infection. <i>Cell Systems</i> , 2016, 3, 361-373.e6.	2.9	170
90	Insulin stimulated MCF7 breast cancer cells: Proteome dataset. <i>Data in Brief</i> , 2016, 9, 579-584.	0.5	6
91	Global mapping of rat plasma proteins with a native proteomic approach using nondenaturing micro 2DE and quantitative LC-MS/MS. <i>Electrophoresis</i> , 2016, 37, 3126-3136.	1.3	0
92	Proteomic dataset of <i>Paracentrotus lividus</i> gonads of different sexes and at different maturation stages. <i>Data in Brief</i> , 2016, 8, 824-827.	0.5	2
93	A comprehensive and scalable database search system for metaproteomics. <i>BMC Genomics</i> , 2016, 17, 642.	1.2	45
94	Impact of Moderate Temperature Changes on <i>Neisseria meningitidis</i> Adhesion Phenotypes and Proteome. <i>Infection and Immunity</i> , 2016, 84, 3484-3495.	1.0	10
95	A standardized production pipeline for high profile targets from <i>Mycobacterium tuberculosis</i> . <i>Proteomics - Clinical Applications</i> , 2016, 10, 1049-1057.	0.8	5
96	Characterization of Gonadotrope Secretoproteome Identifies Neurosecretory Protein VGF-derived Peptide Suppression of Follicle-stimulating Hormone Gene Expression. <i>Journal of Biological Chemistry</i> , 2016, 291, 21322-21334.	1.6	9
97	ZMYND8 Co-localizes with NuRD on Target Genes and Regulates Poly(ADP-Ribose)-Dependent Recruitment of GATAD2A/NuRD to Sites of DNA Damage. <i>Cell Reports</i> , 2016, 17, 783-798.	2.9	100
98	Proteome Remodeling in Response to Sulfur Limitation in <i>Candidatus Pelagibacter ubique</i> . <i>MSystems</i> , 2016, 1, .	1.7	18
99	Comparative Ploidy Proteomics of <i>Candida albicans</i> Biofilms Unraveled the Role of the AHP1 Gene in the Biofilm Persistence Against Amphotericin B. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3488-3500.	2.5	37
100	Comprehensive Proteomic Analysis of Human Milk-derived Extracellular Vesicles Unveils a Novel Functional Proteome Distinct from Other Milk Components. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3412-3423.	2.5	129

#	ARTICLE	IF	CITATIONS
101	Characterization of human pineal gland proteome. <i>Molecular BioSystems</i> , 2016, 12, 3622-3632.	2.9	9
102	Modulating the selectivity of affinity absorbents to multi-phosphopeptides by a competitive substitution strategy. <i>Journal of Chromatography A</i> , 2016, 1461, 35-41.	1.8	15
103	A systems biology-led insight into the role of the proteome in neurodegenerative diseases. <i>Expert Review of Proteomics</i> , 2016, 13, 845-855.	1.3	22
104	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016, 15, 3961-3970.	1.8	158
105	Global iTRAQ-based proteomic profiling of <i>Toxoplasma gondii</i> oocysts during sporulation. <i>Journal of Proteomics</i> , 2016, 148, 12-19.	1.2	34
106	Nucleation of DNA repair factors by FOXA1 links DNA demethylation to transcriptional pioneering. <i>Nature Genetics</i> , 2016, 48, 1003-1013.	9.4	58
107	Glycoproteomic Analysis of Malignant Ovarian Cancer Ascites Fluid Identifies Unusual Glycopeptides. <i>Journal of Proteome Research</i> , 2016, 15, 3358-3376.	1.8	28
108	Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications. <i>Journal of Proteome Research</i> , 2016, 15, 3951-3960.	1.8	72
109	Endoplasmic Reticulum Chaperones Are Potential Active Factors in Thyroid Tumorigenesis. <i>Journal of Proteome Research</i> , 2016, 15, 3377-3387.	1.8	14
110	Normal human mitral valve proteome: A preliminary investigation by gelâ€based and gelâ€free proteomic approaches. <i>Electrophoresis</i> , 2016, 37, 2633-2643.	1.3	3
111	The protein inventory of <i>Clostridium difficile</i> grown in complex and minimal medium. <i>Proteomics - Clinical Applications</i> , 2016, 10, 1068-1072.	0.8	36
112	Approach for Identifying Human Leukocyte Antigen (HLA)-DR Bound Peptides from Scarce Clinical Samples. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3017-3029.	2.5	46
113	A detailed proteomic profiling of plasma membrane from zebrafish brain. <i>Proteomics - Clinical Applications</i> , 2016, 10, 1264-1268.	0.8	11
114	Immunological detection of denatured proteins as a method for rapid identification of food residues on archaeological pottery. <i>Journal of Archaeological Science</i> , 2016, 73, 25-35.	1.2	14
115	Activation of an Endoribonuclease by Non-intein Protein Splicing. <i>Journal of Biological Chemistry</i> , 2016, 291, 15911-15922.	1.6	0
116	Protein Interaction Network of Human Protein Kinase D2 Revealed by Chemical Cross-Linking/Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 3686-3699.	1.8	14
117	Dynamic Rearrangement in Snake Venom Gland Proteome: Insights into <i>Bothrops jararaca</i> Intraspecific Venom Variation. <i>Journal of Proteome Research</i> , 2016, 15, 3752-3762.	1.8	30
118	Identification of Oligosaccharides in Feces of Breast-fed Infants and Their Correlation with the Gut Microbial Community. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2987-3002.	2.5	77

#	ARTICLE	IF	CITATIONS
119	Label-free quantitative proteomic analysis of tolerance to drought in <i>Pisum sativum</i> . <i>Proteomics</i> , 2016, 16, 2776-2787.	1.3	12
120	The arginylation branch of the N-end rule pathway positively regulates cellular autophagic flux and clearance of proteotoxic proteins. <i>Autophagy</i> , 2016, 12, 2197-2212.	4.3	22
121	Toward Automated N-Glycopeptide Identification in Glycoproteomics. <i>Journal of Proteome Research</i> , 2016, 15, 3904-3915.	1.8	105
122	Ability of the marine bacterium <i>Pseudomonas fluorescens</i> BA3SM1 to counteract the toxicity of CdSe nanoparticles. <i>Journal of Proteomics</i> , 2016, 148, 213-227.	1.2	14
123	Proteomic analysis reveals dynamic regulation of fruit development and sugar and acid accumulation in apple. <i>Journal of Experimental Botany</i> , 2016, 67, 5145-5157.	2.4	84
124	The innate immune protein calprotectin promotes <i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> interaction. <i>Nature Communications</i> , 2016, 7, 11951.	5.8	114
125	Sequence basis of Barnacle Cement Nanostructure is Defined by Proteins with Silk Homology. <i>Scientific Reports</i> , 2016, 6, 36219.	1.6	79
126	A proteomic adaptation of small intestinal mucosa in response to dietary protein limitation. <i>Scientific Reports</i> , 2016, 6, 36888.	1.6	12
127	Enhanced limonene production in cyanobacteria reveals photosynthesis limitations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14225-14230.	3.3	152
128	Distinct biological events generated by ECM proteolysis by two homologous collagenases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10884-10889.	3.3	34
129	Proteomics of Human Dendritic Cell Subsets Reveals Subset-Specific Surface Markers and Differential Inflammasome Function. <i>Cell Reports</i> , 2016, 16, 2953-2966.	2.9	72
130	Quantitative Mass Spectrometry To Study Inflammatory Cartilage Degradation and Resulting Interactions with the Complement System. <i>Journal of Immunology</i> , 2016, 197, 3415-3424.	0.4	13
131	Dynamic Protein Interactions of the Polycomb Repressive Complex 2 during Differentiation of Pluripotent Cells. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3450-3460.	2.5	60
132	Up-to-Date Workflow for Plant (Phospho)proteomics Identifies Differential Drought-Responsive Phosphorylation Events in Maize Leaves. <i>Journal of Proteome Research</i> , 2016, 15, 4304-4317.	1.8	50
133	Biochemical Foundations of Health and Energy Conservation in Hibernating Free-ranging Subadult Brown Bear <i>Ursus arctos</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 22509-22523.	1.6	37
134	Characterization of the <i>Arabidopsis thaliana</i> 2-Cys peroxiredoxin interactome. <i>Plant Science</i> , 2016, 252, 30-41.	1.7	43
135	Integrated Omic Analysis of a Guinea Pig Model of Heart Failure and Sudden Cardiac Death. <i>Journal of Proteome Research</i> , 2016, 15, 3009-3028.	1.8	37
136	Comparative Proteomics and Functional Analysis Reveal a Role of <i>Plasmodium falciparum</i> Osmiophilic Bodies in Malaria Parasite Transmission. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3243-3255.	2.5	40



#	ARTICLE	IF	CITATIONS
137	Bacillus cereus Group-Type Strain-Specific Diagnostic Peptides. Journal of Proteome Research, 2016, 15, 3098-3107.	1.8	40
138	Quantitative proteomics identifies myoferlin as a novel regulator of A Disintegrin and Metalloproteinase 12 in HeLa cells. Journal of Proteomics, 2016, 148, 94-104.	1.2	16
139	On the Statistical Significance of Compressed Ratios in Isobaric Labeling: A Cross-Platform Comparison. Journal of Proteome Research, 2016, 15, 3029-3038.	1.8	13
140	Secretomic analysis of extracellular vesicles originating from polyomavirus-negative and polyomavirus-positive Merkel cell carcinoma cell lines. Proteomics, 2016, 16, 2587-2591.	1.3	20
141	Importance of Translocon Subunit Tic56 for rRNA Processing and Chloroplast Ribosome Assembly. Plant Physiology, 2016, 172, 2429-2444.	2.3	27
142	Thermophilic archaea activate butane via alkyl-coenzyme M formation. Nature, 2016, 539, 396-401.	13.7	279
143	Translocon component Sec62 acts in endoplasmic reticulum turnover during stress recovery. Nature Cell Biology, 2016, 18, 1173-1184.	4.6	350
144	Immunoseroproteomic Profiling in African American Men with Prostate Cancer: Evidence for an Autoantibody Response to Glycolysis and Plasminogen-Associated Proteins. Molecular and Cellular Proteomics, 2016, 15, 3564-3580.	2.5	21
145	Robust Label-free, Quantitative Profiling of Circulating Plasma Microparticle (MP) Associated Proteins. Molecular and Cellular Proteomics, 2016, 15, 3640-3652.	2.5	33
146	Profiling of adhesive-related genes in the freshwater cnidarian <i>Hydra magnipapillata</i> by transcriptomics and proteomics. Biofouling, 2016, 32, 1115-1129.	0.8	36
147	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. Nature Communications, 2016, 7, 13250.	5.8	74
148	Proteomic characterization of neuromelanin granules isolated from human substantia nigra by laser-microdissection. Scientific Reports, 2016, 6, 37139.	1.6	35
149	Protein kinase A-dependent phosphorylation stimulates the transcriptional activity of hypoxia-inducible factor 1. Science Signaling, 2016, 9, ra56.	1.6	76
150	Unconventional endosome-like compartment and retromer complex in Toxoplasma gondii govern parasite integrity and host infection. Nature Communications, 2016, 7, 11191.	5.8	59
151	In vivo protein interaction network analysis reveals porin-localized antibiotic inactivation in Acinetobacter baumannii strain AB5075. Nature Communications, 2016, 7, 13414.	5.8	81
152	Neuronal GPCR OCTR-1 regulates innate immunity by controlling protein synthesis in Caenorhabditis elegans. Scientific Reports, 2016, 6, 36832.	1.6	22
153	Lsd1 Ablation Triggers Metabolic Reprogramming of Brown Adipose Tissue. Cell Reports, 2016, 17, 1008-1021.	2.9	63
154	Flexible Data Analysis Pipeline for High-Confidence Proteogenomics. Journal of Proteome Research, 2016, 15, 4686-4695.	1.8	11

#	ARTICLE	IF	CITATIONS
155	Ska3 Ensures Timely Mitotic Progression by Interacting Directly With Microtubules and Ska1 Microtubule Binding Domain. <i>Scientific Reports</i> , 2016, 6, 34042.	1.6	36
156	Quantitative Chemical Proteomic Profiling of Ubiquitin Specific Proteases in Intact Cancer Cells. <i>ACS Chemical Biology</i> , 2016, 11, 3268-3272.	1.6	62
157	circRNADb: A comprehensive database for human circular RNAs with protein-coding annotations. <i>Scientific Reports</i> , 2016, 6, 34985.	1.6	360
158	Integrative omics connects N-glycoproteome-wide alterations with pathways and regulatory events in induced pluripotent stem cells. <i>Scientific Reports</i> , 2016, 6, 36109.	1.6	2
159	Cross-linking reveals laminin coiled-coil architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13384-13389.	3.3	27
160	KAT2A/KAT2B-targeted acetylome reveals a role for PLK4 acetylation in preventing centrosome amplification. <i>Nature Communications</i> , 2016, 7, 13227.	5.8	84
161	MASP-3 is the exclusive pro-factor D activator in resting blood: the lectin and the alternative complement pathways are fundamentally linked. <i>Scientific Reports</i> , 2016, 6, 31877.	1.6	108
162	SCAI promotes DNA double-strand break repair in distinct chromosomal contexts. <i>Nature Cell Biology</i> , 2016, 18, 1357-1366.	4.6	32
163	Toll-like receptor 2 activation depends on lipopeptide shedding by bacterial surfactants. <i>Nature Communications</i> , 2016, 7, 12304.	5.8	86
164	HIV host interactome revealed directly from infected cells. <i>Nature Microbiology</i> , 2016, 1, 16068.	5.9	49
165	A protein extraction method for low protein concentration solutions compatible with the proteomic analysis of rubber particles. <i>Electrophoresis</i> , 2016, 37, 2930-2939.	1.3	15
166	Nascent Proteome Remodeling following Homeostatic Scaling at Hippocampal Synapses. <i>Neuron</i> , 2016, 92, 358-371.	3.8	125
167	Integrative proteomic profiling of ovarian cancer cell lines reveals precursor cell associated proteins and functional status. <i>Nature Communications</i> , 2016, 7, 12645.	5.8	171
168	Quantitative Proteomics of the SMAD (Suppressor of Mothers against Decapentaplegic) Transcription Factor Family Identifies Importin 5 as a Bone Morphogenic Protein Receptor SMAD-specific Importin. <i>Journal of Biological Chemistry</i> , 2016, 291, 24121-24132.	1.6	15
169	Efficient Exploitation of Separation Space in Two-Dimensional Liquid Chromatography System for Comprehensive and Efficient Proteomic Analyses. <i>Analytical Chemistry</i> , 2016, 88, 11734-11741.	3.2	16
170	Detection of Proteome Changes in Human Colon Cancer Induced by Cell Surface Binding of Growth-Inhibitory Human Galectin-4 Using Quantitative SILAC-Based Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 4412-4422.	1.8	20
171	Analysis of the Biotechnological Potential of a <i>Lentinus crinitus</i> isolate in the Light of Its Secretome. <i>Journal of Proteome Research</i> , 2016, 15, 4557-4568.	1.8	16
172	A proteinaceous organic matrix regulates carbonate mineral production in the marine teleost intestine. <i>Scientific Reports</i> , 2016, 6, 34494.	1.6	11

#	ARTICLE	IF	CITATIONS
173	Novel insight into the composition of human single-stranded DNA-binding protein 1 (hSSB1)-containing protein complexes. <i>BMC Molecular Biology</i> , 2016, 17, 24.	3.0	9
174	A proteome analysis of freezing tolerance in red clover ( <i>Trifolium pratense</i> L.). <i>BMC Plant Biology</i> , 2016, 16, 65.	1.6	31
175	Proteomic changes occurring along gonad maturation in the edible sea urchin <i>Paracentrotus lividus</i> . <i>Journal of Proteomics</i> , 2016, 144, 63-72.	1.2	19
176	Quantitative Proteomics Reveals $\beta$ 2 Integrin-mediated Cytoskeletal Rearrangement in Vascular Endothelial Growth Factor (VEGF)-induced Retinal Vascular Hyperpermeability. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1681-1691.	2.5	14
177	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016, 13, 651-656.	9.0	147
178	Top-down venomomics of the East African green mamba, <i>Dendroaspis angusticeps</i> , and the black mamba, <i>Dendroaspis polylepis</i> , highlight the complexity of their toxin arsenals. <i>Journal of Proteomics</i> , 2016, 146, 148-164.	1.2	60
179	Determination of the interactome of non-structural protein 2 from highly pathogenic porcine reproductive and respiratory syndrome virus with host cellular proteins using high throughput proteomics and identification of HSP70 as a cellular factor for virus replication. <i>Journal of Proteomics</i> , 2016, 146, 58-69.	1.2	20
180	Minichromosome Maintenance Complex Is a Critical Node in the miR-183 Signaling Network of MYCN-Amplified Neuroblastoma Cells. <i>Journal of Proteome Research</i> , 2016, 15, 2178-2186.	1.8	6
181	The CENP-T/W complex is a binding partner of the histone chaperone FACT. <i>Genes and Development</i> , 2016, 30, 1313-1326.	2.7	45
182	Hydroxytyrosol and its complex forms (secoiridoids) modulate aorta and heart proteome in healthy rats: Potential cardioprotective effects. <i>Molecular Nutrition and Food Research</i> , 2016, 60, 2114-2129.	1.5	25
183	MetaPro-IQ: a universal metaproteomic approach to studying human and mouse gut microbiota. <i>Microbiome</i> , 2016, 4, 31.	4.9	154
184	Comparative proteomic analysis of <i>Phalaenopsis</i> leaves in the vegetative and flowering phase. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	4
185	Unsupervised Quality Assessment of Mass Spectrometry Proteomics Experiments by Multivariate Quality Control Metrics. <i>Journal of Proteome Research</i> , 2016, 15, 1300-1307.	1.8	15
186	The 2016 database issue of <i>Nucleic Acids Research</i> and an updated molecular biology database collection. <i>Nucleic Acids Research</i> , 2016, 44, D1-D6.	6.5	119
187	Proteomic data reveals a physiological basis for costs and benefits associated with thermal acclimation. <i>Journal of Experimental Biology</i> , 2016, 219, 969-76.	0.8	35
188	Identification of cypermethrin induced protein changes in green algae by iTRAQ quantitative proteomics. <i>Journal of Proteomics</i> , 2016, 139, 67-76.	1.2	32
189	Phosphorylation of plastoglobular proteins in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 3975-3984.	2.4	17
190	Molecular architecture of the Dam1 complex-microtubule interaction. <i>Open Biology</i> , 2016, 6, 150237.	1.5	26

#	ARTICLE	IF	CITATIONS
191	Global Liver Proteome Analysis Using iTRAQ Reveals AMPKâ€“mTORâ€“Autophagy Signaling Is Altered by Intrauterine Growth Restriction in Newborn Piglets. <i>Journal of Proteome Research</i> , 2016, 15, 1262-1273.	1.8	27
192	The European Bioinformatics Institute in 2016: Data growth and integration. <i>Nucleic Acids Research</i> , 2016, 44, D20-D26.	6.5	108
193	Proteomics offers insight to the mechanism behind <i>Pisum sativum</i> L. response to pea seed-borne mosaic virus (PSbMV). <i>Journal of Proteomics</i> , 2017, 153, 78-88.	1.2	30
194	UniProt: the universal protein knowledgebase. <i>Nucleic Acids Research</i> , 2017, 45, D158-D169.	6.5	4,240
195	Discrete cytosolic macromolecular <scp>BRAF</scp> complexes exhibit distinct activities and composition. <i>EMBO Journal</i> , 2017, 36, 646-663.	3.5	52
196	Mechanosensing by the nucleus: From pathways to scaling relationships. <i>Journal of Cell Biology</i> , 2017, 216, 305-315.	2.3	301
197	Venom-gland transcriptomics and venom proteomics of the black-back scorpion ( <i>Hadrurus spadix</i> ) reveal detectability challenges and an unexplored realm of animal toxin diversity. <i>Toxicon</i> , 2017, 128, 23-37.	0.8	51
198	Personalized Proteome Profiles of Healthy and Tumor Human Colon Organoids Reveal Both Individual Diversity and Basic Features of Colorectal Cancer. <i>Cell Reports</i> , 2017, 18, 263-274.	2.9	126
199	Vascular Endothelial Growth Factor (VEGF) Promotes Assembly of the p130Cas Interactome to Drive Endothelial Chemotactic Signaling and Angiogenesis. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 168-180.	2.5	25
200	The 24th annual<i>Nucleic Acids Research</i> database issue: a look back and upcoming changes. <i>Nucleic Acids Research</i> , 2017, 45, D1-D11.	6.5	144
201	Correlation of cell surface proteins of distinct <i>Beauveria bassiana</i> cell types and adaption to varied environment and interaction with the host insect. <i>Fungal Genetics and Biology</i> , 2017, 99, 13-25.	0.9	22
202	jPOSTrepo: an international standard data repository for proteomes. <i>Nucleic Acids Research</i> , 2017, 45, D1107-D1111.	6.5	451
203	Sex differences in tendon structure and function. <i>Journal of Orthopaedic Research</i> , 2017, 35, 2117-2126.	1.2	54
204	Plasma proteome and metabolome characterization of an experimental human thyrotoxicosis model. <i>BMC Medicine</i> , 2017, 15, 6.	2.3	30
205	Discovery of gastric cancer specific biomarkers by the application of serum proteomics. <i>Proteomics</i> , 2017, 17, 1600332.	1.3	27
206	A Golden Age for Working with Public Proteomics Data. <i>Trends in Biochemical Sciences</i> , 2017, 42, 333-341.	3.7	92
207	SILAC-Based Quantitative Proteomic Analysis Unveils Arsenite-Induced Perturbation of Multiple Pathways in Human Skin Fibroblast Cells. <i>Chemical Research in Toxicology</i> , 2017, 30, 1006-1014.	1.7	13
208	Variations of metabolites and proteome in <i>Lonicera japonica</i> Thunb. buds and flowers under UV radiation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 404-413.	1.1	12

#	ARTICLE	IF	CITATIONS
209	Combined Proteome and Eicosanoid Profiling Approach for Revealing Implications of Human Fibroblasts in Chronic Inflammation. <i>Analytical Chemistry</i> , 2017, 89, 1945-1954.	3.2	33
210	Norovirus-Mediated Modification of the Translational Landscape via Virus and Host-Induced Cleavage of Translation Initiation Factors. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S215-S229.	2.5	40
211	Impact of Cystinosin Glycosylation on Protein Stability by Differential Dynamic Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). <i>Molecular and Cellular Proteomics</i> , 2017, 16, 457-468.	2.5	15
212	Label-free deep shotgun proteomics reveals protein dynamics during tomato fruit tissues development. <i>Plant Journal</i> , 2017, 90, 396-417.	2.8	76
213	Improved surfaceome coverage with a label-free nonaffinity-purified workflow. <i>Proteomics</i> , 2017, 17, 1600344.	1.3	9
214	Identifying components required for OMP biogenesis as novel targets for anti-infective drugs. <i>Virulence</i> , 2017, 8, 1170-1188.	1.8	26
215	Differential signaling networks of Bcr-Abl p210 and p190 kinases in leukemia cells defined by functional proteomics. <i>Leukemia</i> , 2017, 31, 1502-1512.	3.3	84
216	Mixed colonies of <i>Aspergillus niger</i> and <i>Aspergillus oryzae</i> cooperatively degrading wheat bran. <i>Fungal Genetics and Biology</i> , 2017, 102, 31-37.	0.9	23
217	Assessment of Label-Free Quantification in Discovery Proteomics and Impact of Technological Factors and Natural Variability of Protein Abundance. <i>Journal of Proteome Research</i> , 2017, 16, 1410-1424.	1.8	91
218	Methylated-antibody affinity purification to improve proteomic identification of plant RNA polymerase Pol V complex and the interacting proteins. <i>Scientific Reports</i> , 2017, 7, 42943.	1.6	7
219	Characterisation of urinary WFDC12 in small nocturnal basal primates, mouse lemurs ( <i>Microcebus</i> ). <i>PLoS One</i> , 2017, 12, e0171111.	1.6	11
220	Melt With This Kiss: Paralyzing and Liquefying Venom of The Assassin Bug <i>Pristhesancus plagipennis</i> (Hemiptera: Reduviidae). <i>Molecular and Cellular Proteomics</i> , 2017, 16, 552-566.	2.5	53
221	Mapping Atheroprotective Functions and Related Proteins/Lipoproteins in Size Fractionated Human Plasma. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 680-693.	2.5	28
222	Comparative iTRAQ proteomic profiling of susceptible and resistant apple cultivars infected by <i>Alternaria alternata</i> apple pathotype. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	9
223	Quirks of Error Estimation in Cross-Linking/Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 3829-3833.	3.2	136
224	Temperature-Induced Remodeling of the Photosynthetic Machinery Tunes Photosynthesis in the Thermophilic Alga <i>Cyanidioschyzon merolae</i> . <i>Plant Physiology</i> , 2017, 174, 35-46.	2.3	21
225	Comprehensive proteomic characterization of stem cell-derived extracellular matrices. <i>Biomaterials</i> , 2017, 128, 147-159.	5.7	132
226	iTRAQ-based quantitative proteomic analysis reveals potential virulence factors of <i>Erysipelothrix rhusiopathiae</i> . <i>Journal of Proteomics</i> , 2017, 160, 28-37.	1.2	11

#	ARTICLE	IF	CITATIONS
227	Defining the Akt1 interactome data and delineating alterations in its composition as a function of cell cycle progression. <i>Data in Brief</i> , 2017, 11, 252-257.	0.5	0
228	Toward an Optimized Workflow for Middle-Down Proteomics. <i>Analytical Chemistry</i> , 2017, 89, 3318-3325.	3.2	91
229	Fatty acid synthase inhibits the O-GlcNAcase during oxidative stress. <i>Journal of Biological Chemistry</i> , 2017, 292, 6493-6511.	1.6	52
230	Prophage WO genes recapitulate and enhance <i>Wolbachia</i> -induced cytoplasmic incompatibility. <i>Nature</i> , 2017, 543, 243-247.	13.7	366
231	Proteome and Secretome Analysis Reveals Differential Post-transcriptional Regulation of Toll-like Receptor Responses. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S172-S186.	2.5	29
232	Comparative Phosphoproteomics Reveals an Important Role of MKK2 in Banana ( <i>Musa spp.</i> ) Cold Signal Network. <i>Scientific Reports</i> , 2017, 7, 40852.	1.6	40
233	Cellular proteomic analysis of porcine circovirus type 2 and classical swine fever virus coinfection in porcine kidney cells using isobaric tags for relative and absolute quantitation-coupled LC-MS/MS. <i>Electrophoresis</i> , 2017, 38, 1276-1291.	1.3	16
234	A Comprehensive Analytical Strategy To Identify Malondialdehyde-Modified Proteins and Peptides. <i>Analytical Chemistry</i> , 2017, 89, 3847-3852.	3.2	7
235	Proteomic analysis of cell cycle arrest and differentiation induction caused by ATPR, a derivative of all-trans retinoic acid, in human gastric cancer SGC7901 cells. <i>Proteomics - Clinical Applications</i> , 2017, 11, 1600099.	0.8	20
236	A cytoplasmic role of Wnt/ $\beta$ -catenin transcriptional cofactors Bcl9, Bcl9l, and Pygopus in tooth enamel formation. <i>Science Signaling</i> , 2017, 10, .	1.6	50
237	Diversity and functions of the sheep faecal microbiota: a multi-omic characterization. <i>Microbial Biotechnology</i> , 2017, 10, 541-554.	2.0	51
238	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. <i>Cell Reports</i> , 2017, 18, 1527-1542.	2.9	79
239	Phylointeractomics reconstructs functional evolution of protein binding. <i>Nature Communications</i> , 2017, 8, 14334.	5.8	26
240	An Interaction Landscape of Ubiquitin Signaling. <i>Molecular Cell</i> , 2017, 65, 941-955.e8.	4.5	109
241	Evolution of complexity in the zebrafish synapse proteome. <i>Nature Communications</i> , 2017, 8, 14613.	5.8	112
242	A ZIP6-ZIP10 heteromer controls NCAM1 phosphorylation and integration into focal adhesion complexes during epithelial-to-mesenchymal transition. <i>Scientific Reports</i> , 2017, 7, 40313.	1.6	22
243	Large-Scale Filter-Aided Sample Preparation Method for the Analysis of the Ubiquitinome. <i>Analytical Chemistry</i> , 2017, 89, 3840-3846.	3.2	13
244	Key metabolic traits of <i>Pisum sativum</i> maintain cell vitality during <i>Didymella pinodes</i> infection: cultivar resistance and the microsymbionts' influence. <i>Journal of Proteomics</i> , 2017, 169, 189-201.	1.2	31

#	ARTICLE	IF	CITATIONS
245	A temporal proteome dynamics study reveals the molecular basis of induced phenotypic resistance in <i>Mycobacterium smegmatis</i> at sub-lethal rifampicin concentrations. <i>Scientific Reports</i> , 2017, 7, 43858.	1.6	22
246	Cultivation of <i>Podospira anserina</i> on soybean hulls results in an efficient enzyme cocktail for plant biomass hydrolysis. <i>New Biotechnology</i> , 2017, 37, 162-171.	2.4	22
247	Farnesoid X Receptor Activation Promotes Hepatic Amino Acid Catabolism and Ammonium Clearance in Mice. <i>Gastroenterology</i> , 2017, 152, 1462-1476.e10.	0.6	51
248	Effects of ErbB2 Overexpression on the Proteome and ErbB Ligand-specific Phosphosignaling in Mammary Luminal Epithelial Cells. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 608-621.	2.5	6
249	Proteomic Screen for Cellular Targets of the Vaccinia Virus F10 Protein Kinase Reveals that Phosphorylation of mDia Regulates Stress Fiber Formation. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S124-S143.	2.5	8
250	On-column trypsinization allows for re-use of matrix in modified multiplexed inhibitor beads assay. <i>Analytical Biochemistry</i> , 2017, 523, 10-16.	1.1	9
251	The Human Leukocyte Antigen (HLA)-B27 Peptidome in Vivo, in Spondyloarthritis-susceptible HLA-B27 Transgenic Rats and the Effect of Erap1 Deletion. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 642-662.	2.5	50
252	Understanding Epstein-Barr Virus Life Cycle with Proteomics: A Temporal Analysis of Ubiquitination During Virus Reactivation. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 27-37.	1.0	9
253	Comparative Proteomics of Purified Pathogen Vacuoles Correlates Intracellular Replication of <i>Legionella pneumophila</i> with the Small GTPase Ras-related protein 1 (Rap1). <i>Molecular and Cellular Proteomics</i> , 2017, 16, 622-641.	2.5	54
254	Architecture of the yeast Elongator complex. <i>EMBO Reports</i> , 2017, 18, 264-279.	2.0	75
255	Relative protein quantification and accessible biology in lung tumor proteomes from four LC-MS/MS discovery platforms. <i>Proteomics</i> , 2017, 17, 1600300.	1.3	15
256	Combining affinity enrichment, cross-linking with photo amino acids, and mass spectrometry for probing protein kinase D2 interactions. <i>Proteomics</i> , 2017, 17, e1600459.	1.3	21
257	Cytosine modifications modulate the chromatin architecture of transcriptional enhancers. <i>Genome Research</i> , 2017, 27, 947-958.	2.4	34
258	Vertex-Specific Proteins pUL17 and pUL25 Mechanically Reinforce Herpes Simplex Virus Capsids. <i>Journal of Virology</i> , 2017, 91, .	1.5	32
259	YAP-mediated mechanotransduction determines the podocyte's response to damage. <i>Science Signaling</i> , 2017, 10, .	1.6	61
260	Determining the bacterial cell biology of Planctomycetes. <i>Nature Communications</i> , 2017, 8, 14853.	5.8	175
261	Galectin-1 inhibition attenuates profibrotic signaling in hypoxia-induced pulmonary fibrosis. <i>Cell Death Discovery</i> , 2017, 3, 17010.	2.0	48
262	N-terminal Proteomics Assisted Profiling of the Unexplored Translation Initiation Landscape in <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1064-1080.	2.5	54

#	ARTICLE	IF	CITATIONS
263	Proteome analysis of human embryonic stem cells organelles. <i>Journal of Proteomics</i> , 2017, 162, 108-118.	1.2	12
265	Targeted mass spectrometry: An emerging powerful approach to unblock the bottleneck in phosphoproteomics. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1055-1056, 29-38.	1.2	22
266	SmProt: a database of small proteins encoded by annotated coding and non-coding RNA loci. <i>Briefings in Bioinformatics</i> , 2018, 19, bbx005.	3.2	85
267	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
268	Global analysis of glycoproteins identifies markers of endotoxin tolerant monocytes and GPR84 as a modulator of TNF $\alpha$ expression. <i>Scientific Reports</i> , 2017, 7, 838.	1.6	39
269	Investigating Acquisition Performance on the Orbitrap Fusion When Using Tandem MS/MS/MS Scanning with Isobaric Tags. <i>Journal of Proteome Research</i> , 2017, 16, 1839-1846.	1.8	20
270	Evaluating the Characteristics of Reporter Ion Signal Acquired in the Orbitrap Analyzer for Isobaric Mass Tag Proteome Quantification Experiments. <i>Journal of Proteome Research</i> , 2017, 16, 1831-1838.	1.8	8
271	Activation of the Amino Acid Response Pathway Blunts the Effects of Cardiac Stress. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	26
272	Gel-free/label-free proteomic, photosynthetic, and biochemical analysis of cowpea ( <i>Vigna unguiculata</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T 76-91.	1.2	17
273	Translating Divergent Environmental Stresses into a Common Proteome Response through Hik33 in a Model Cyanobacterium. <i>Molecular and Cellular Proteomics</i> , 2017, , mcp.M117.068080.	2.5	0
274	<scp>ZBTB</scp>48 is both a vertebrate telomereâ€binding protein and a transcriptional activator. <i>EMBO Reports</i> , 2017, 18, 929-946.	2.0	50
275	Multipronged quantitative proteomics reveals serum proteome alterations in breast cancer intrinsic subtypes. <i>Journal of Proteomics</i> , 2017, 163, 1-13.	1.2	18
276	A proteomic characterization shows differences in the milk fat globule membrane of buffalo and bovine milk. <i>Food Bioscience</i> , 2017, 19, 7-16.	2.0	23
277	Hydrophobic Interaction Chromatography for Bottom-Up Proteomics Analysis of Single Proteins and Protein Complexes. <i>Journal of Proteome Research</i> , 2017, 16, 2318-2323.	1.8	4
278	Database-independent Protein Sequencing (DiPS) Enables Full-length de Novo Protein and Antibody Sequence Determination. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1151-1161.	2.5	19
279	Charting organellar importomes by quantitative mass spectrometry. <i>Nature Communications</i> , 2017, 8, 15272.	5.8	80
280	Expression proteomics study to determine metallodrug targets and optimal drug combinations. <i>Scientific Reports</i> , 2017, 7, 1590.	1.6	19
281	A microRNAâ€129â€5p/Rbfox crosstalk coordinates homeostatic downscaling of excitatory synapses. <i>EMBO Journal</i> , 2017, 36, 1770-1787.	3.5	85



#	ARTICLE	IF	CITATIONS
282	Unbiased Protein Association Study on the Public Human Proteome Reveals Biological Connections between Co-Occurring Protein Pairs. <i>Journal of Proteome Research</i> , 2017, 16, 2204-2212.	1.8	3
283	Dominant protection from HLA-linked autoimmunity by antigen-specific regulatory T cells. <i>Nature</i> , 2017, 545, 243-247.	13.7	181
284	Validation, Identification, and Biological Consequences of the Site-specific O-GlcNAcylation Dynamics of Carbohydrate-responsive Element-binding Protein (ChREBP). <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1233-1243.	2.5	23
285	Proteome profile of spinneret from the silkworm, <i>Bombyx mori</i> . <i>Proteomics</i> , 2017, 17, 1600301.	1.3	6
286	Expression of ALS/FTD-linked mutant CCNF in zebrafish leads to increased cell death in the spinal cord and an aberrant motor phenotype. <i>Human Molecular Genetics</i> , 2017, 26, 2616-2626.	1.4	44
287	Dynamics of the Interaction between Cotton Bollworm <i>Helicoverpa armigera</i> and Nucleopolyhedrovirus as Revealed by Integrated Transcriptomic and Proteomic Analyses. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1009-1028.	2.5	40
288	A novel ex vivo immunoproteomic approach characterising <i>Fasciola hepatica</i> tegumental antigens identified using immune antibody from resistant sheep. <i>International Journal for Parasitology</i> , 2017, 47, 555-567.	1.3	20
289	Quantitative cardiac phosphoproteomics profiling during ischemia-reperfusion in an immature swine model. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2017, 313, H125-H137.	1.5	9
290	Human Spermatozoa Quantitative Proteomic Signature Classifies Normo- and Asthenozoospermia. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 57-72.	2.5	69
291	Insufficient antibody validation challenges oestrogen receptor beta research. <i>Nature Communications</i> , 2017, 8, 15840.	5.8	170
292	Exhaled breath condensate biomarkers for the early diagnosis of lung cancer using proteomics. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2017, 313, L664-L676.	1.3	64
293	Combined Mass Spectrometry Imaging and Top-down Microproteomics Reveals Evidence of a Hidden Proteome in Ovarian Cancer. <i>EBioMedicine</i> , 2017, 21, 55-64.	2.7	45
294	Proteomic characterization of EL4 lymphoma-derived tumors upon chemotherapy treatment reveals potential roles for lysosomes and caspase-6 during tumor cell death in vivo. <i>Proteomics</i> , 2017, 17, 1700060.	1.3	16
295	A Temporal Proteomic Map of Epstein-Barr Virus Lytic Replication in B Cells. <i>Cell Reports</i> , 2017, 19, 1479-1493.	2.9	83
296	Quantitative analyses of the global proteome and phosphoproteome reveal the different impacts of propofol and dexmedetomidine on HT22 cells. <i>Scientific Reports</i> , 2017, 7, 46455.	1.6	5
297	Mammalian O-mannosylation of cadherins and plexins is independent of protein O-mannosyltransferases 1 and 2. <i>Journal of Biological Chemistry</i> , 2017, 292, 11586-11598.	1.6	39
298	Sorting nexin 27 interactome in T lymphocytes identifies zona occludens dynamic redistribution at the immune synapse. <i>Traffic</i> , 2017, 18, 491-504.	1.3	18
299	Comparative membrane proteomics analyses of breast cancer cell lines to understand the molecular mechanism of breast cancer brain metastasis. <i>Electrophoresis</i> , 2017, 38, 2124-2134.	1.3	21

#	ARTICLE	IF	CITATIONS
300	Microbial functionality as affected by experimental warming of a temperate mountain forest soil—A metaproteomics survey. <i>Applied Soil Ecology</i> , 2017, 117-118, 196-202.	2.1	48
301	Oral squamous cell carcinoma patients can be differentiated from healthy individuals with label-free serum proteomics. <i>British Journal of Cancer</i> , 2017, 117, 376-384.	2.9	16
302	Deciphering the protein—protein interaction network regulating hepatocellular carcinoma metastasis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1114-1122.	1.1	15
303	Protein expression in tension wood formation monitored at high tissue resolution in <i>Populus</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 3405-3417.	2.4	37
304	Large scale phosphoprotein profiling to explore <i>Drosophila</i> cold acclimation regulatory mechanisms. <i>Scientific Reports</i> , 2017, 7, 1713.	1.6	28
305	A comprehensive proteogenomic study of the human <i>Brucella</i> vaccine strain 104—M. <i>BMC Genomics</i> , 2017, 18, 402.	1.2	12
306	Proteomic composition and immunomodulatory properties of urinary bladder matrix scaffolds in homeostasis and injury. <i>Seminars in Immunology</i> , 2017, 29, 14-23.	2.7	73
307	Proteome-wide Adaptations of Mouse Skeletal Muscles during a Full Month in Space. <i>Journal of Proteome Research</i> , 2017, 16, 2623-2638.	1.8	33
308	Ndfip1 restricts mTORC1 signalling and glycolysis in regulatory T cells to prevent autoinflammatory disease. <i>Nature Communications</i> , 2017, 8, 15677.	5.8	34
309	Proteome-wide Identification of Glycosylation-dependent Interactors of Galectin-1 and Galectin-3 on Mesenchymal Retinal Pigment Epithelial (RPE) Cells. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1528-1546.	2.5	35
310	Quantification of egg proteome changes during fertilization in sterlet <i>Acipenser ruthenus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 490, 189-193.	1.0	19
311	Insights into the early stage of <i>Pinus nigra</i> Arn. somatic embryogenesis using discovery proteomics. <i>Journal of Proteomics</i> , 2017, 169, 99-111.	1.2	40
312	Comparative Evaluation of Small Molecular Additives and Their Effects on Peptide/Protein Identification. <i>Analytical Chemistry</i> , 2017, 89, 5784-5792.	3.2	3
313	Matrix Mechanosensing: From Scaling Concepts in —Omics Data to Mechanisms in the Nucleus, Regeneration, and Cancer. <i>Annual Review of Biophysics</i> , 2017, 46, 295-315.	4.5	89
314	Quantitative Phospho-proteomic Analysis of TNF—/NF—B Signaling Reveals a Role for RIPK1 Phosphorylation in Suppressing Necrotic Cell Death. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1200-1216.	2.5	18
315	Global mapping of CARM1 substrates defines enzyme specificity and substrate recognition. <i>Nature Communications</i> , 2017, 8, 15571.	5.8	100
316	Systematic Evaluation of Protein Reduction and Alkylation Reveals Massive Unspecific Side Effects by Iodine-containing Reagents. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1173-1187.	2.5	122
317	In-Culture Cross-Linking of Bacterial Cells Reveals Large-Scale Dynamic Protein—Protein Interactions at the Peptide Level. <i>Journal of Proteome Research</i> , 2017, 16, 2457-2471.	1.8	44

#	ARTICLE	IF	CITATIONS
318	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017, 2, 17087.	5.9	183
319	Temporal Transcriptomic and Proteomic Landscapes of Deteriorating Pancreatic Islets in Type 2 Diabetic Rats. <i>Diabetes</i> , 2017, 66, 2188-2200.	0.3	54
320	WIPI3 and WIPI4 $\hat{I}^2$ -propellers are scaffolds for LKB1-AMPK-TSC signalling circuits in the control of autophagy. <i>Nature Communications</i> , 2017, 8, 15637.	5.8	156
321	A Class of Environmental and Endogenous Toxins Induces BRCA2 Haploinsufficiency and Genome Instability. <i>Cell</i> , 2017, 169, 1105-1118.e15.	13.5	149
322	OpenMS $\hat{a}^{\epsilon}$ A platform for reproducible analysis of mass spectrometry data. <i>Journal of Biotechnology</i> , 2017, 261, 142-148.	1.9	85
323	Comparative proteomic profiling of the serum differentiates pancreatic cancer from chronic pancreatitis. <i>Cancer Medicine</i> , 2017, 6, 1738-1751.	1.3	39
324	Quantitative Proteomics Shows Extensive Remodeling Induced by Nitrogen Limitation in <i>Prochlorococcus marinus</i> SS120. <i>MSystems</i> , 2017, 2, .	1.7	25
325	BioInfra.Prot: A comprehensive proteomics workflow including data standardization, protein inference, expression analysis and data publication. <i>Journal of Biotechnology</i> , 2017, 261, 116-125.	1.9	21
326	Proteome dynamics during postnatal mouse corpus callosum development. <i>Scientific Reports</i> , 2017, 7, 45359.	1.6	5
327	Inference and quantification of peptidoforms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017, 35, 781-788.	9.4	122
328	Dataset to delineate changes in association between Akt1 and its interacting partners as a function of active state of Akt1 protein. <i>Data in Brief</i> , 2017, 13, 187-191.	0.5	1
329	CMG2/ANTXR2 regulates extracellular collagen VI which accumulates in hyaline fibromatosis syndrome. <i>Nature Communications</i> , 2017, 8, 15861.	5.8	56
330	Loss of Cln3 impacts protein secretion in the social amoeba <i>Dictyostelium</i> . <i>Cellular Signalling</i> , 2017, 35, 61-72.	1.7	29
331	Morphoproteomic Characterization of Lung Squamous Cell Carcinoma Fragmentation, a Histological Marker of Increased Tumor Invasiveness. <i>Cancer Research</i> , 2017, 77, 2585-2593.	0.4	15
332	SIRT4 Is a Lysine Deacylase that Controls Leucine Metabolism and Insulin Secretion. <i>Cell Metabolism</i> , 2017, 25, 838-855.e15.	7.2	259
333	Changes in cellular signaling proteins in extracts from A549, H460, and U2OS cells treated with cisplatin or docetaxel. <i>Data in Brief</i> , 2017, 12, 18-21.	0.5	0
334	A Proteomic Approach to Identify Alterations in the Small Ubiquitin-like Modifier (SUMO) Network during Controlled Mechanical Ventilation in Rat Diaphragm Muscle. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1081-1097.	2.5	12
335	Hypoxia Reduces the Pathogenicity of <i>Pseudomonas aeruginosa</i> by Decreasing the Expression of Multiple Virulence Factors. <i>Journal of Infectious Diseases</i> , 2017, 215, 1459-1467.	1.9	22

#	ARTICLE	IF	CITATIONS
336	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. <i>Cell</i> , 2017, 169, 350-360.e12.	13.5	322
337	Trade-off between Transcriptome Plasticity and Genome Evolution in Cephalopods. <i>Cell</i> , 2017, 169, 191-202.e11.	13.5	268
338	Intraatrial Transplantation of Human Neural Stem Cells Restores the Impaired Subventricular Zone in Parkinsonian Mice. <i>Stem Cells</i> , 2017, 35, 1519-1531.	1.4	27
339	PTEN <sup>2</sup> is an alternatively translated isoform of PTEN that regulates rDNA transcription. <i>Nature Communications</i> , 2017, 8, 14771.	5.8	91
340	Real-time iTRAQ-based proteome profiling revealed the central metabolism involved in nitrogen starvation induced lipid accumulation in microalgae. <i>Scientific Reports</i> , 2017, 7, 45732.	1.6	59
341	Dynamic RNA-protein interactions underlie the zebrafish maternal-to-zygotic transition. <i>Genome Research</i> , 2017, 27, 1184-1194.	2.4	58
342	TGFBR2-dependent alterations of exosomal cargo and functions in DNA mismatch repair-deficient HCT116 colorectal cancer cells. <i>Cell Communication and Signaling</i> , 2017, 15, 14.	2.7	26
343	Protein interaction networks at the host-microbe interface in <i>Diaphorina citri</i> , the insect vector of the citrus greening pathogen. <i>Royal Society Open Science</i> , 2017, 4, 160545.	1.1	65
344	CLK-dependent exon recognition and conjoined gene formation revealed with a novel small molecule inhibitor. <i>Nature Communications</i> , 2017, 8, 7.	5.8	108
345	Long Noncoding RNA MANTIS Facilitates Endothelial Angiogenic Function. <i>Circulation</i> , 2017, 136, 65-79.	1.6	196
346	Identification of Novel STAT6-Regulated Proteins in Mouse B Cells by Comparative Transcriptome and Proteome Analysis. <i>Journal of Immunology</i> , 2017, 198, 3737-3745.	0.4	14
347	SPOP Mutation Drives Prostate Tumorigenesis In Vivo through Coordinate Regulation of PI3K/mTOR and AR Signaling. <i>Cancer Cell</i> , 2017, 31, 436-451.	7.7	152
348	Harnessing the power of proteomics for identification of oncogenic, druggable signalling pathways in cancer. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 431-447.	2.5	15
349	Glycoproteins in Claudin-Low Breast Cancer Cell Lines Have a Unique Expression Profile. <i>Journal of Proteome Research</i> , 2017, 16, 1391-1400.	1.8	7
350	Human Immunoglobulin Heavy Gamma Chain Polymorphisms: Molecular Confirmation Of Proteomic Assessment. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 824-839.	2.5	9
351	Deciphering the Acute Cellular Phosphoproteome Response to Irradiation with X-rays, Protons and Carbon Ions. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 855-872.	2.5	27
352	PP2A Cdc55 Phosphatase Imposes Ordered Cell-Cycle Phosphorylation by Opposing Threonine Phosphorylation. <i>Molecular Cell</i> , 2017, 65, 393-402.e3.	4.5	91
353	Internally tagged ubiquitin: a tool to identify linear polyubiquitin-modified proteins by mass spectrometry. <i>Nature Methods</i> , 2017, 14, 504-512.	9.0	59

#	ARTICLE	IF	CITATIONS
354	Extended Multiplexing of Tandem Mass Tags (TMT) Labeling Reveals Age and High Fat Diet Specific Proteome Changes in Mouse Epididymal Adipose Tissue. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 873-890.	2.5	240
355	Protein Phosphatase 2Cs and <i>Microtubule-Associated Stress Protein 1</i> Control Microtubule Stability, Plant Growth, and Drought Response. <i>Plant Cell</i> , 2017, 29, 169-191.	3.1	96
356	Overexpression of a stress-responsive U-box protein gene VaPUB affects the accumulation of resistance related proteins in <i>Vitis vinifera</i> "Thompson Seedless"™. <i>Plant Physiology and Biochemistry</i> , 2017, 112, 53-63.	2.8	30
357	Quantitative Metaproteomics and Activity-Based Probe Enrichment Reveals Significant Alterations in Protein Expression from a Mouse Model of Inflammatory Bowel Disease. <i>Journal of Proteome Research</i> , 2017, 16, 1014-1026.	1.8	65
358	Biotransformation and reduction of estrogenicity of bisphenol A by the biphenyl-degrading <i>Cupriavidus basilensis</i> . <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 3743-3758.	1.7	16
359	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. <i>Molecular Cell</i> , 2017, 65, 347-360.	4.5	123
360	Proteomic signatures reveal a dualistic and clinically relevant classification of anal canal carcinoma. <i>Journal of Pathology</i> , 2017, 241, 522-533.	2.1	32
361	Comparative proteomic analysis of hemolymph from uninfected and <i>Candidatus Liberibacter asiaticus</i> -infected <i>Diaphorina citri</i> . <i>Amino Acids</i> , 2017, 49, 389-406.	1.2	13
362	The "PepSAVI-MS" Pipeline for Natural Product Bioactive Peptide Discovery. <i>Analytical Chemistry</i> , 2017, 89, 1194-1201.	3.2	34
363	Proteomic Data Storage and Sharing. <i>Methods in Molecular Biology</i> , 2017, 1549, 5-15.	0.4	2
364	A Strong Neutrophil Elastase Proteolytic Fingerprint Marks the Carcinoma Tumor Proteome. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 213-227.	2.5	17
365	A Molecular Basis for the Presentation of Phosphorylated Peptides by HLA-B Antigens. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 181-193.	2.5	52
366	Large-scale reduction of the <i>Bacillus subtilis</i> genome: consequences for the transcriptional network, resource allocation, and metabolism. <i>Genome Research</i> , 2017, 27, 289-299.	2.4	137
367	Posttranscriptional Regulation in Adenovirus Infected Cells. <i>Journal of Proteome Research</i> , 2017, 16, 872-888.	1.8	20
368	A Luciferase-fragment Complementation Assay to Detect Lipid Droplet-associated Protein-Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 329-345.	2.5	24
369	Structure-aware enhancement of imaging mass spectrometry data for semantic segmentation. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2017, 171, 259-265.	1.8	2
370	Single-Shot Top-Down Proteomics with Capillary Zone Electrophoresis-Electrospray Ionization-Tandem Mass Spectrometry for Identification of Nearly 600 <i>Escherichia coli</i> Proteoforms. <i>Analytical Chemistry</i> , 2017, 89, 12059-12067.	3.2	75
371	A short linear motif in scaffold Nup145C connects Y-complex with pre-assembled outer ring Nup82 complex. <i>Nature Communications</i> , 2017, 8, 1107.	5.8	32

#	ARTICLE	IF	CITATIONS
372	Optimization of Experimental Parameters in Data-Independent Mass Spectrometry Significantly Increases Depth and Reproducibility of Results. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2296-2309.	2.5	349
373	Bivalent complexes of PRC1 with orthologs of BRD4 and MOZ/MORF target developmental genes in <i>Drosophila</i> . <i>Genes and Development</i> , 2017, 31, 1988-2002.	2.7	25
374	Selective Proteomic Analysis of Antibiotic-Tolerant Cellular Subpopulations in <i>Pseudomonas aeruginosa</i> Biofilms. <i>MBio</i> , 2017, 8, .	1.8	40
375	Increased serotransferrin and ceruloplasmin turnover in diet-controlled patients with type 2 diabetes. <i>Free Radical Biology and Medicine</i> , 2017, 113, 461-469.	1.3	41
376	Enhanced Missing Proteins Detection in NCI60 Cell Lines Using an Integrative Search Engine Approach. <i>Journal of Proteome Research</i> , 2017, 16, 4374-4390.	1.8	13
377	Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2017, 16, 4035-4044.	1.8	10
378	Carbene Footprinting Reveals Binding Interfaces of a Multimeric Membrane-Spanning Protein. <i>Angewandte Chemie</i> , 2017, 129, 15069-15073.	1.6	11
379	Multi-Protease Strategy Identifies Three PE2 Missing Proteins in Human Testis Tissue. <i>Journal of Proteome Research</i> , 2017, 16, 4352-4363.	1.8	21
380	Remodeling of the <i>Streptococcus mutans</i> proteome in response to LrgAB and external stresses. <i>Scientific Reports</i> , 2017, 7, 14063.	1.6	23
381	Calcineurin-mediated Dephosphorylation of Acetyl-coA Carboxylase is Required for Pheromone Biosynthesis Activating Neuropeptide (PBAN)-induced Sex Pheromone Biosynthesis in <i>Helicoverpa armigera</i> . <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2138-2152.	2.5	35
382	Selective aggregation of the splicing factor Hsh155 suppresses splicing upon genotoxic stress. <i>Journal of Cell Biology</i> , 2017, 216, 4027-4040.	2.3	10
383	Gel-based and gel-free proteome data associated with controlled deterioration treatment of Glycine max seeds. <i>Data in Brief</i> , 2017, 15, 449-453.	0.5	3
384	Multiplexed Thiol Reactivity Profiling for Target Discovery of Electrophilic Natural Products. <i>Cell Chemical Biology</i> , 2017, 24, 1416-1427.e5.	2.5	43
385	Systematic Identification of <i>Mycobacterium tuberculosis</i> Effectors Reveals that BfrB Suppresses Innate Immunity. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2243-2253.	2.5	18
386	Carbene Footprinting Reveals Binding Interfaces of a Multimeric Membrane-Spanning Protein. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 14873-14877.	7.2	33
387	Converging Small Ubiquitin-like Modifier (SUMO) and Ubiquitin Signaling: Improved Methodology Identifies Co-modified Target Proteins. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2281-2295.	2.5	22
388	Salivary Cystatins: Exploring New Post-Translational Modifications and Polymorphisms by Top-Down High-Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 4196-4207.	1.8	22
389	<i>RBPJ</i> / <i>CBF</i> 1 interacts with L3 <i>MBTL</i> 3/ <i>MBT</i> 1 to promote repression of Notch signaling via histone demethylase <i>KDM</i> 1A/ <i>LSD</i> 1. <i>EMBO Journal</i> , 2017, 36, 3232-3249.	3.5	54

#	ARTICLE	IF	CITATIONS
390	Ricin-like proteins from the castor plant do not influence liquid chromatography-mass spectrometry detection of ricin in forensically relevant samples. <i>Toxicon</i> , 2017, 140, 18-31.	0.8	18
391	Proteolytic signatures define unique thrombin-derived peptides present in human wound fluid in vivo. <i>Scientific Reports</i> , 2017, 7, 13136.	1.6	18
392	Comparative Proteomic Analysis of Three <i>Xanthomonas</i> spp. Cultured in Minimal and Rich Media. <i>Proteomics</i> , 2017, 17, 1700142.	1.3	21
393	Identification of cross talk between SUMOylation and ubiquitylation using a sequential peptide immunopurification approach. <i>Nature Protocols</i> , 2017, 12, 2354-2355.	5.5	26
394	Comprehensive profiling of lysine ubiquitome reveals diverse functions of lysine ubiquitination in common wheat. <i>Scientific Reports</i> , 2017, 7, 13601.	1.6	31
395	Quantitative proteomics reveals that long non-coding RNA MALAT1 interacts with DBC1 to regulate p53 acetylation. <i>Nucleic Acids Research</i> , 2017, 45, 9947-9959.	6.5	144
396	Revisiting the <i>Ancylostoma Caninum</i> Secretome Provides New Information on Hookworm-Host Interactions. <i>Proteomics</i> , 2017, 17, 1700186.	1.3	25
397	Ubiquitome Analysis Reveals PCNA-Associated Factor 15 (PAF15) as a Specific Ubiquitination Target of UHRF1 in Embryonic Stem Cells. <i>Journal of Molecular Biology</i> , 2017, 429, 3814-3824.	2.0	43
398	PKM2 methylation by CARM1 activates aerobic glycolysis to promote tumorigenesis. <i>Nature Cell Biology</i> , 2017, 19, 1358-1370.	4.6	212
399	MAZ induces MYB expression during the exit from quiescence via the E2F site in the MYB promoter. <i>Nucleic Acids Research</i> , 2017, 45, 9960-9975.	6.5	13
400	Pervasive coexpression of spatially proximal genes is buffered at the protein level. <i>Molecular Systems Biology</i> , 2017, 13, 937.	3.2	90
401	Ketone Body Acetoacetate Buffers Methylglyoxal via a Non-enzymatic Conversion during Diabetic and Dietary Ketosis. <i>Cell Chemical Biology</i> , 2017, 24, 935-943.e7.	2.5	32
402	Transcriptome analysis of the response of Burmese python to digestion. <i>GigaScience</i> , 2017, 6, 1-18.	3.3	17
403	Transposon Sequencing Uncovers an Essential Regulatory Function of Phosphoribulokinase for Methylo-trophy. <i>Current Biology</i> , 2017, 27, 2579-2588.e6.	1.8	34
404	A Simple Light Isotope Metabolic Labeling (SLIM-labeling) Strategy: A Powerful Tool to Address the Dynamics of Proteome Variations In Vivo. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2017-2031.	2.5	8
405	Extracellular Matrix Proteins Mediate HIV-1 gp120 Interactions with $\hat{\pm}^4^7$ . <i>Journal of Virology</i> , 2017, 91, .	1.5	8
406	The Experiment Data Depot: A Web-Based Software Tool for Biological Experimental Data Storage, Sharing, and Visualization. <i>ACS Synthetic Biology</i> , 2017, 6, 2248-2259.	1.9	45
407	Exercise-responsive phosphoproteins in the heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2017, 111, 61-68.	0.9	13

#	ARTICLE	IF	CITATIONS
408	A heterochromatin-dependent transcription machinery drives piRNA expression. <i>Nature</i> , 2017, 549, 54-59.	13.7	213
409	Proteome Dynamics in Biobanked Horse Peripheral Blood Derived Lymphocytes (PBL) with Induced Autoimmune Uveitis. <i>Proteomics</i> , 2017, 17, 1700013.	1.3	21
410	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	1.8	87
411	Persulfidation proteome reveals the regulation of protein function by hydrogen sulfide in diverse biological processes in Arabidopsis. <i>Journal of Experimental Botany</i> , 2017, 68, 4915-4927.	2.4	233
412	New Genes and Functional Innovation in Mammals. <i>Genome Biology and Evolution</i> , 2017, 9, 1886-1900.	1.1	50
413	Proteomic landscape of the primary somatosensory cortex upon sensory deprivation. <i>GigaScience</i> , 2017, 6, 1-10.	3.3	10
414	Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. <i>Journal of Proteome Research</i> , 2017, 16, 4281-4287.	1.8	55
415	Metabolic crosstalk regulates <i>Porphyromonas gingivalis</i> colonization and virulence during oral polymicrobial infection. <i>Nature Microbiology</i> , 2017, 2, 1493-1499.	5.9	100
416	A Linear Diubiquitin-Based Probe for Efficient and Selective Detection of the Deubiquitinating Enzyme OTULIN. <i>Cell Chemical Biology</i> , 2017, 24, 1299-1313.e7.	2.5	41
417	iTRAQ and virus-induced gene silencing revealed three proteins involved in cold response in bread wheat. <i>Scientific Reports</i> , 2017, 7, 7524.	1.6	29
418	Verringerung der Virulenz von multiresistentem <i>Staphylococcus aureus</i> mithilfe eines chemischen Disruptors des ClpX-Chaperon-Komplexes. <i>Angewandte Chemie</i> , 2017, 129, 15952-15957.	1.6	2
419	N <sup>1</sup> - and O-Acetylation in <i>Mycobacterium tuberculosis</i> Lineage 7 and Lineage 4 Strains: Proteins Involved in Bioenergetics, Virulence, and Antimicrobial Resistance Are Acetylated. <i>Journal of Proteome Research</i> , 2017, 16, 4045-4059.	1.8	37
420	Mapping Protein Targets of Bioactive Small Molecules Using Lipid-Based Chemical Proteomics. <i>ACS Chemical Biology</i> , 2017, 12, 2671-2681.	1.6	25
421	The autophagy initiator ULK1 sensitizes AMPK to allosteric drugs. <i>Nature Communications</i> , 2017, 8, 571.	5.8	65
422	Myst2/Kat7 histone acetyltransferase interaction proteomics reveals tumour-suppressor Niam as a novel binding partner in embryonic stem cells. <i>Scientific Reports</i> , 2017, 7, 8157.	1.6	12
423	Landscape of submitochondrial protein distribution. <i>Nature Communications</i> , 2017, 8, 290.	5.8	123
424	Quantitative proteomics of Sf21 cells during Baculovirus infection reveals progressive host proteome changes and its regulation by viral miRNA. <i>Scientific Reports</i> , 2017, 7, 10902.	1.6	14
425	Novel Organelles with Elements of Bacterial and Eukaryotic Secretion Systems Weaponize Parasites of <i>Drosophila</i> . <i>Current Biology</i> , 2017, 27, 2869-2877.e6.	1.8	37



#	ARTICLE	IF	CITATIONS
426	Delayed effects of transcriptional responses in <i>Mycobacterium tuberculosis</i> exposed to nitric oxide suggest other mechanisms involved in survival. <i>Scientific Reports</i> , 2017, 7, 8208.	1.6	39
427	Global Analysis of Membrane-associated Protein Oligomerization Using Protein Correlation Profiling. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1972-1989.	2.5	32
428	Estrogenic regulation of skeletal muscle proteome: a study of premenopausal women and postmenopausal <sc>MZ</sc> cotwins discordant for hormonal therapy. <i>Aging Cell</i> , 2017, 16, 1276-1287.	3.0	50
429	Differential Enzymatic <sup>16</sup>O/<sup>18</sup>O Labeling for the Detection of Cross-Linked Nucleic Acidâ€“Protein Heteroconjugates. <i>Analytical Chemistry</i> , 2017, 89, 11208-11213.	3.2	1
430	Proteome Analysis of Hypoxic Glioblastoma Cells Reveals Sequential Metabolic Adaptation of One-Carbon Metabolic Pathways. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1906-1921.	2.5	29
431	Glareosin: a novel sexually dimorphic urinary lipocalin in the bank vole, <i>Myodes glareolus</i>. <i>Open Biology</i> , 2017, 7, 170135.	1.5	7
432	Using the PRIDE Database and ProteomeXchange for Submitting and Accessing Public Proteomics Datasets. <i>Current Protocols in Bioinformatics</i> , 2017, 59, 13.31.1-13.31.12.	25.8	48
433	A Chemical Disruptor of the ClpX Chaperone Complex Attenuates the Virulence of Multidrugâ€“Resistant <i>Staphylococcus aureus</i>. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 15746-15750.	7.2	34
434	Quantitative proteomic characterization of lung-MSC and bone marrow-MSC using DIA-mass spectrometry. <i>Scientific Reports</i> , 2017, 7, 9316.	1.6	33
435	Lysine acetylation stoichiometry and proteomics analyses reveal pathways regulated by sirtuin 1 in human cells. <i>Journal of Biological Chemistry</i> , 2017, 292, 18129-18144.	1.6	36
436	Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy. <i>Autophagy</i> , 2017, 13, 1969-1980.	4.3	48
437	The splicing co-factor Barricade/Tat-SF1, is required for cell cycle and lineage progression in <i>Drosophila</i> neural stem cells. <i>Development (Cambridge)</i> , 2017, 144, 3932-3945.	1.2	14
438	Correlation profiling of brain sub-cellular proteomes reveals co-assembly of synaptic proteins and subcellular distribution. <i>Scientific Reports</i> , 2017, 7, 12107.	1.6	55
439	The bacterial arginine glycosyltransferase effector NleB preferentially modifies Fas-associated death domain protein (FADD). <i>Journal of Biological Chemistry</i> , 2017, 292, 17337-17350.	1.6	53
440	14-3-3 regulation of Ncd reveals a new mechanism for targeting proteins to the spindle in oocytes. <i>Journal of Cell Biology</i> , 2017, 216, 3029-3039.	2.3	29
441	IgSF21 promotes differentiation of inhibitory synapses via binding to neurexin2Î±. <i>Nature Communications</i> , 2017, 8, 408.	5.8	50
442	Comparative proteomic profiling of the choline transporterâ€“like 1 (<sc>CHER</sc>1) mutant provides insights into plasmodesmata composition of fully developed <i>Arabidopsis thaliana</i> leaves. <i>Plant Journal</i> , 2017, 92, 696-709.	2.8	45
443	Topological N-glycosylation and site-specific N-glycan sulfation of influenza proteins in the highly expressed H1N1 candidate vaccines. <i>Scientific Reports</i> , 2017, 7, 10232.	1.6	27

#	ARTICLE	IF	CITATIONS
444	Proteogenomic Insights into the Intestinal Parasite <i>Blastocystis</i> sp. Subtype 4 Isolate WR1. <i>Proteomics</i> , 2017, 17, 1700211.	1.3	5
445	A comparative analysis of human plasma and serum proteins by combining native PAGE, whole gel slicing and quantitative LC-MS/MS: Utilizing native MS-electropherograms in proteomic analysis for discovering structure and interaction-correlated differences. <i>Electrophoresis</i> , 2017, 38, 3111-3123.	1.3	7
446	Comprehensive Proteomic Analysis of PGC7-Interacting Proteins. <i>Journal of Proteome Research</i> , 2017, 16, 3113-3123.	1.8	5
447	Proteomic Analysis of Neuroblastoma-Derived Exosomes: New Insights into a Metastatic Signature. <i>Proteomics</i> , 2017, 17, 1600430.	1.3	32
448	Protein abundance of AKT and ERK pathway components governs cell type-specific regulation of proliferation. <i>Molecular Systems Biology</i> , 2017, 13, 904.	3.2	72
449	N-Degradomic Analysis Reveals a Proteolytic Network Processing the Podocyte Cytoskeleton. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 2867-2878.	3.0	41
450	Proteomic analysis of the secretome of human bone marrow-derived mesenchymal stem cells primed by pro-inflammatory cytokines. <i>Journal of Proteomics</i> , 2017, 166, 115-126.	1.2	80
451	A Cell Wall Proteome and Targeted Cell Wall Analyses Provide Novel Information on Hemicellulose Metabolism in Flax. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1634-1651.	2.5	23
452	Feedback Microtubule Control and Microtubule-Actin Cross-talk in Arabidopsis Revealed by Integrative Proteomic and Cell Biology Analysis of KATANIN 1 Mutants. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1591-1609.	2.5	52
453	Gastrointestinal digestion of hazelnut allergens on molecular level: Elucidation of degradation kinetics and resistant immunoactive peptides using mass spectrometry. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1700130.	1.5	21
454	Comparison of fractionation proteomics for local SWATH library building. <i>Proteomics</i> , 2017, 17, 1700052.	1.3	18
455	Proteomic analysis and bioluminescent reporter gene assays to investigate effects of simulated microgravity on Caco-2 cells. <i>Proteomics</i> , 2017, 17, 1700081.	1.3	11
456	Revisiting venom of the sea anemone <i>Stichodactyla haddoni</i> : Omics techniques reveal the complete toxin arsenal of a well-studied sea anemone genus. <i>Journal of Proteomics</i> , 2017, 166, 83-92.	1.2	64
457	Glycolytic Enzymes Coalesce in G Bodies under Hypoxic Stress. <i>Cell Reports</i> , 2017, 20, 895-908.	2.9	139
458	Synaptic GAP and GEF Complexes Cluster Proteins Essential for GTP Signaling. <i>Scientific Reports</i> , 2017, 7, 5272.	1.6	33
459	Genes essential for phototrophic growth by a purple alphaproteobacterium. <i>Environmental Microbiology</i> , 2017, 19, 3567-3578.	1.8	23
460	The ciliary membrane-associated proteome reveals actin-binding proteins as key components of cilia. <i>EMBO Reports</i> , 2017, 18, 1521-1535.	2.0	119
461	The effect of <i>Fusarium culmorum</i> infection and deoxynivalenol (DON) application on proteome response in barley cultivars Chevron and Pedant. <i>Journal of Proteomics</i> , 2017, 169, 112-124.	1.2	17

#	ARTICLE	IF	CITATIONS
462	Mass spectrometry data from label-free quantitative proteomic analysis of harmless and pathogenic strains of infectious microalgae, <i>Prototheca</i> spp. <i>Data in Brief</i> , 2017, 12, 320-326.	0.5	5
463	hSSB1 phosphorylation is dynamically regulated by DNA-PK and PPP-family protein phosphatases. <i>DNA Repair</i> , 2017, 54, 30-39.	1.3	15
464	Identification of Differentially Expressed Splice Variants by the Proteogenomic Pipeline Splicify. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1850-1863.	2.5	33
465	Statistical Models for the Analysis of Isobaric Tags Multiplexed Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2017, 16, 3124-3136.	1.8	30
466	MEIS homeodomain proteins facilitate PARP1/ARTD1-mediated eviction of histone H1. <i>Journal of Cell Biology</i> , 2017, 216, 2715-2729.	2.3	25
467	Comparative Proteomic Analysis of the Effect of the Four-Herb Chinese Medicine ANBP on Promoting Mouse Skin Wound Healing. <i>International Journal of Lower Extremity Wounds</i> , 2017, 16, 154-162.	0.6	9
468	Structural insights into transcription initiation by yeast RNA polymerase I. <i>EMBO Journal</i> , 2017, 36, 2698-2709.	3.5	58
469	Quantitative Temporal in Vivo Proteomics Deciphers the Transition of Virus-Driven Myeloid Cells into M2 Macrophages. <i>Journal of Proteome Research</i> , 2017, 16, 3391-3406.	1.8	15
470	HLA-E Presents Glycopeptides from the Mycobacterium tuberculosis Protein MPT32 to Human CD8+ T cells. <i>Scientific Reports</i> , 2017, 7, 4622.	1.6	32
471	Quantitative Proteomics of Cerebrospinal Fluid in Paediatric Pneumococcal Meningitis. <i>Scientific Reports</i> , 2017, 7, 7042.	1.6	14
472	KNIME for reproducible cross-domain analysis of life science data. <i>Journal of Biotechnology</i> , 2017, 261, 149-156.	1.9	138
473	Cryo-EM Structure of the TOM Core Complex from <i>Neurospora crassa</i> . <i>Cell</i> , 2017, 170, 693-700.e7.	13.5	138
474	Bioinformatics Resources for Interpreting Proteomics Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2017, 1647, 267-295.	0.4	1
475	UBE2O remodels the proteome during terminal erythroid differentiation. <i>Science</i> , 2017, 357, .	6.0	121
476	Functional and structural characterization of synthetic cardosin B-derived rennet. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6951-6968.	1.7	15
477	Label-free quantitative proteomic analysis of <i>Lactobacillus fermentum</i> NCDC 400 during bile salt exposure. <i>Journal of Proteomics</i> , 2017, 167, 36-45.	1.2	32
478	Sensitive, Robust, and Cost-Effective Approach for Tyrosine Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 9307-9314.	3.2	27
479	Quantitative proteomic analysis of host responses triggered by <i>Mycobacterium tuberculosis</i> infection in human macrophage cells. <i>Acta Biochimica Et Biophysica Sinica</i> , 2017, 49, 835-844.	0.9	23

#	ARTICLE	IF	CITATIONS
480	Alternative splicing shapes transcriptome but not proteome diversity in <i>Physcomitrella patens</i> . <i>Scientific Reports</i> , 2017, 7, 2698.	1.6	17
481	Proteomic Analysis of Human Angiogenin Interactions Reveals Cytoplasmic PCNA as a Putative Binding Partner. <i>Journal of Proteome Research</i> , 2017, 16, 3606-3622.	1.8	8
482	Systems Pharmacology Dissection of Cholesterol Regulation Reveals Determinants of Large Pharmacodynamic Variability between Cell Lines. <i>Cell Systems</i> , 2017, 5, 604-619.e7.	2.9	17
483	Proteomic analyses identify ARH3 as a serine mono-ADP-ribosylhydrolase. <i>Nature Communications</i> , 2017, 8, 2055.	5.8	98
484	Proteome-wide Analysis of Lysine 2-hydroxyisobutyrylation in Developing Rice ( <i>Oryza sativa</i> ) Seeds. <i>Scientific Reports</i> , 2017, 7, 17486.	1.6	56
485	A meta-proteomics approach to study the interspecies interactions affecting microbial biofilm development in a model community. <i>Scientific Reports</i> , 2017, 7, 16483.	1.6	51
486	Selected reaction monitoring approach for validating peptide biomarkers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13519-13524.	3.3	28
487	IL-33 and ST2 mediate FAK-dependent antitumor immune evasion through transcriptional networks. <i>Science Signaling</i> , 2017, 10, .	1.6	64
488	Proteomics and antivenomics of <i>Echis carinatus carinatus</i> venom: Correlation with pharmacological properties and pathophysiology of envenomation. <i>Scientific Reports</i> , 2017, 7, 17119.	1.6	76
489	MAPKs Influence Pollen Tube Growth by Controlling the Formation of Phosphatidylinositol 4,5-Bisphosphate in an Apical Plasma Membrane Domain. <i>Plant Cell</i> , 2017, 29, 3030-3050.	3.1	34
490	Proteomics of phosphorylation and protein dynamics during fertilization and meiotic exit in the <i>Xenopus</i> egg. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10838-E10847.	3.3	43
491	Assessing species biomass contributions in microbial communities via metaproteomics. <i>Nature Communications</i> , 2017, 8, 1558.	5.8	211
492	The Ndc80 complex targets Bod1 to human mitotic kinetochores. <i>Open Biology</i> , 2017, 7, 170099.	1.5	8
493	The food-borne pathogen <i>Campylobacter jejuni</i> responds to the bile salt deoxycholate with countermeasures to reactive oxygen species. <i>Scientific Reports</i> , 2017, 7, 15455.	1.6	27
494	A microRNA screen reveals that elevated hepatic ectodysplasin A expression contributes to obesity-induced insulin resistance in skeletal muscle. <i>Nature Medicine</i> , 2017, 23, 1466-1473.	15.2	51
495	A multiregional proteomic survey of the postnatal human brain. <i>Nature Neuroscience</i> , 2017, 20, 1787-1795.	7.1	138
496	Pharmacoproteomic characterisation of human colon and rectal cancer. <i>Molecular Systems Biology</i> , 2017, 13, 951.	3.2	44
497	The immunopeptidomic landscape of ovarian carcinomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9942-E9951.	3.3	152

#	ARTICLE	IF	CITATIONS
498	Dietary changes in nutritional studies shape the structural and functional composition of the pig's fecal microbiome from days to weeks. <i>Microbiome</i> , 2017, 5, 144.	4.9	66
499	Prediction of Protein Complexes in <i>Trypanosoma brucei</i> by Protein Correlation Profiling Mass Spectrometry and Machine Learning. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2254-2267.	2.5	24
500	A PLC- $\beta$ 1 Feedback Pathway Regulates Lck Substrate Phosphorylation at the T-Cell Receptor and SLP-76 Complex. <i>Journal of Proteome Research</i> , 2017, 16, 2729-2742.	1.8	7
501	Variation in auxin sensing guides AUX/IAA transcriptional repressor ubiquitylation and destruction. <i>Nature Communications</i> , 2017, 8, 15706.	5.8	56
502	Spatiotemporal Proteomic Profiling of Human Cerebral Development. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1548-1562.	2.5	45
503	An exported protein-interacting complex involved in the trafficking of virulence determinants in <i>Plasmodium</i> -infected erythrocytes. <i>Nature Communications</i> , 2017, 8, 16044.	5.8	65
504	Proteome remodelling by the stress sigma factor RpoS/ $\sigma$ S in <i>Salmonella</i> : identification of small proteins and evidence for post-transcriptional regulation. <i>Scientific Reports</i> , 2017, 7, 2127.	1.6	37
505	Reduced Protein Expression in a Virus Attenuated by Codon Deoptimization. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2957-2968.	0.8	21
506	In-depth proteomic analysis of <i>Glycine max</i> seeds during controlled deterioration treatment reveals a shift in seed metabolism. <i>Journal of Proteomics</i> , 2017, 169, 125-135.	1.2	61
507	Characterization of the Extracellular Matrix of Normal and Diseased Tissues Using Proteomics. <i>Journal of Proteome Research</i> , 2017, 16, 3083-3091.	1.8	183
508	Targeted Feature Detection for Data-Dependent Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2017, 16, 2964-2974.	1.8	43
509	Comparative genetic, proteomic and phosphoproteomic analysis of <i>C. elegans</i> embryos with a focus on ham-1/STOX and pig-1/MELK in dopaminergic neuron development. <i>Scientific Reports</i> , 2017, 7, 4314.	1.6	11
510	Sec61 blockade by mycolactone inhibits antigen cross-presentation independently of endosome-to-cytosol export. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5910-E5919.	3.3	77
511	Metaproteomics reveals functional differences in intestinal microbiota development of preterm infants. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1610-1620.	2.5	35
512	Activation of Human Peripheral Blood Eosinophils by Cytokines in a Comparative Time-Course Proteomic/Phosphoproteomic Study. <i>Journal of Proteome Research</i> , 2017, 16, 2663-2679.	1.8	15
513	Proteomic Analysis of Differences in Fiber Development between Wild and Cultivated <i>Gossypium hirsutum</i> L.. <i>Journal of Proteome Research</i> , 2017, 16, 2811-2824.	1.8	11
514	Proteomic analysis reveals large amounts of decomposition enzymes and major metabolic pathways involved in algicidal process of <i>Trametes versicolor</i> F21a. <i>Scientific Reports</i> , 2017, 7, 3907.	1.6	25
515	Proteomic profiling of archaeological human bone. <i>Royal Society Open Science</i> , 2017, 4, 161004.	1.1	76

#	ARTICLE	IF	CITATIONS
516	Definition of a High-Confidence Mitochondrial Proteome at Quantitative Scale. <i>Cell Reports</i> , 2017, 19, 2836-2852.	2.9	346
517	β-catenin downregulates Dicer to promote ovarian cancer metastasis. <i>Oncogene</i> , 2017, 36, 5927-5938.	2.6	39
518	Immune signatures of pathogenesis in the peritoneal compartment during early infection of sheep with <i>Fasciola hepatica</i> . <i>Scientific Reports</i> , 2017, 7, 2782.	1.6	33
519	Autologous chondrocyte implantation-derived synovial fluids display distinct responder and non-responder proteomic profiles. <i>Arthritis Research and Therapy</i> , 2017, 19, 150.	1.6	19
520	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
521	Translating Divergent Environmental Stresses into a Common Proteome Response through the Histidine Kinase 33 (Hik33) in a Model Cyanobacterium. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1258-1274.	2.5	26
522	DISMS2: A flexible algorithm for direct proteome-wide distance calculation of LC-MS/MS runs. <i>BMC Bioinformatics</i> , 2017, 18, 148.	1.2	15
523	Comparative proteomic analysis of <i>Neisseria meningitidis</i> wildtype and dprA null mutant strains links DNA processing to pilus biogenesis. <i>BMC Microbiology</i> , 2017, 17, 96.	1.3	8
524	Orchestrating differential data access for translational research: a pilot implementation. <i>BMC Medical Informatics and Decision Making</i> , 2017, 17, 30.	1.5	5
525	Proteomic analysis of protein purified derivative of <i>Mycobacterium bovis</i> . <i>Journal of Translational Medicine</i> , 2017, 15, 68.	1.8	11
526	Immune recognition of salivary proteins from the cattle tick <i>Rhipicephalus microplus</i> differs according to the genotype of the bovine host. <i>Parasites and Vectors</i> , 2017, 10, 144.	1.0	22
527	MS_HistoneDB, a manually curated resource for proteomic analysis of human and mouse histones. <i>Epigenetics and Chromatin</i> , 2017, 10, 2.	1.8	40
528	Current Proteomic Approaches Applied to Brain Function. <i>Neuroinformatics</i> , 2017, , .	0.2	4
529	A Generic HPLC Method for Absolute Quantification of Oxidation in Monoclonal Antibodies and Fc-Fusion Proteins Using UV and MS Detection. <i>Analytical Chemistry</i> , 2017, 89, 8391-8398.	3.2	24
530	Qualitative and Quantitative Analysis of Proteome and Peptidome of Human Follicular Fluid Using Multiple Samples from Single Donor with LC-MS and SWATH Methodology. <i>Journal of Proteome Research</i> , 2017, 16, 3053-3067.	1.8	26
531	Structural and regulatory diversity shape HLA-C protein expression levels. <i>Nature Communications</i> , 2017, 8, 15924.	5.8	98
532	METTL21B Is a Novel Human Lysine Methyltransferase of Translation Elongation Factor 1A: Discovery by CRISPR/Cas9 Knockout. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2229-2242.	2.5	38
533	Metabolic and physiological interdependencies in the <i>Bathymodiolus azoricus</i> symbiosis. <i>ISME Journal</i> , 2017, 11, 463-477.	4.4	116

#	ARTICLE	IF	CITATIONS
534	Protein content and functional characteristics of serum-purified exosomes from patients with colorectal cancer revealed by quantitative proteomics. <i>International Journal of Cancer</i> , 2017, 140, 900-913.	2.3	101
535	Specific mixing facilitates the comparative quantification of phosphorylation sites with significant dysregulations. <i>Analytica Chimica Acta</i> , 2017, 950, 129-137.	2.6	4
536	The human-induced pluripotent stem cell initiative's data resources for cellular genetics. <i>Nucleic Acids Research</i> , 2017, 45, D691-D697.	6.5	81
537	Tapered-Tip Capillary Electrophoresis Nano-Electrospray Ionization Mass Spectrometry for Ultrasensitive Proteomics: the Mouse Cortex. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 597-607.	1.2	53
538	Enzyme Kinetics for Complex System Enables Accurate Determination of Specificity Constants of Numerous Substrates in a Mixture by Proteomics Platform. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 135-145.	2.5	11
539	The Caveolin-3 G56S sequence variant of unknown significance: Muscle biopsy findings and functional cell biological analysis. <i>Proteomics - Clinical Applications</i> , 2017, 11, 1600007.	0.8	6
540	AKT-dependent phosphorylation of the SAM domain induces oligomerization and activation of the scaffold protein CNK1. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 89-100.	1.9	6
541	<i>Mycobacterium tuberculosis</i> Infection Manipulates the Glycosylation Machinery and the N-Glycoproteome of Human Macrophages and Their Microparticles. <i>Journal of Proteome Research</i> , 2017, 16, 247-263.	1.8	36
542	Different Donors Mesenchymal Stromal Cells Secretomes Reveal Heterogeneous Profile of Relevance for Therapeutic Use. <i>Stem Cells and Development</i> , 2017, 26, 206-214.	1.1	54
543	<i>Pseudomonas aeruginosa</i> develops Ciprofloxacin resistance from low to high level with distinctive proteome changes. <i>Journal of Proteomics</i> , 2017, 152, 75-87.	1.2	32
544	MZH29 is a novel potent inhibitor that overcomes drug resistance FLT3 mutations in acute myeloid leukemia. <i>Leukemia</i> , 2017, 31, 913-921.	3.3	20
545	Synthesis and deposition of basement membrane proteins by primary brain capillary endothelial cells in a murine model of the blood-brain barrier. <i>Journal of Neurochemistry</i> , 2017, 140, 741-754.	2.1	67
546	The proteome of baker's yeast mitochondria. <i>Mitochondrion</i> , 2017, 33, 15-21.	1.6	22
547	Computational quality control tools for mass spectrometry proteomics. <i>Proteomics</i> , 2017, 17, 1600159.	1.3	34
548	Antimicrobial peptide exposure selects for <i>Staphylococcus aureus</i> resistance to human defence peptides. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 115-127.	1.3	74
549	Proteomic and genomic characterization of a yeast model for Ogden syndrome. <i>Yeast</i> , 2017, 34, 19-37.	0.8	15
550	Isotope-targeted glycoproteomics (IsoTaG) analysis of sialylated N- and O-glycopeptides on an Orbitrap Fusion Tribrid using azido and alkynyl sugars. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 579-588.	1.9	26
551	Conservation of miRNA-mediated silencing mechanisms across 600 million years of animal evolution. <i>Nucleic Acids Research</i> , 2017, 45, 938-950.	6.5	26

#	ARTICLE	IF	CITATIONS
552	Proteomic and Bioinformatic Characterization of Extracellular Vesicles Released from Human Macrophages upon Influenza A Virus Infection. <i>Journal of Proteome Research</i> , 2017, 16, 217-227.	1.8	55
553	In-Depth Cerebrospinal Fluid Quantitative Proteome and Deglycoproteome Analysis: Presenting a Comprehensive Picture of Pathways and Processes Affected by Multiple Sclerosis. <i>Journal of Proteome Research</i> , 2017, 16, 179-194.	1.8	29
554	Embryonic lethal abnormal vision proteins and adenine and uridine-rich element mRNAs after global cerebral ischemia and reperfusion in the rat. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2017, 37, 1494-1507.	2.4	7
555	Opposite Electron-Transfer Dissociation and Higher-Energy Collisional Dissociation Fragmentation Characteristics of Proteolytic K/R(X) <sub>n</sub> and (X) <sub>n</sub> /K/R Peptides Provide Benefits for Peptide Sequencing in Proteomics and Phosphoproteomics. <i>Journal of Proteome Research</i> , 2017, 16, 852-861.	1.8	21
556	INA complex liaises the F1Fo-ATP synthase membrane motor modules. <i>Nature Communications</i> , 2017, 8, 1237.	5.8	24
557	Unbiased Quantitative Proteomics Reveals a Crucial Role of the Allergen Context for the Activation of Human Dendritic Cells. <i>Scientific Reports</i> , 2017, 7, 16638.	1.6	12
558	Bypass of Activation Loop Phosphorylation by Aspartate 836 in Activation of the Endoribonuclease Activity of Ire1. <i>Molecular and Cellular Biology</i> , 2017, 37, .	1.1	12
559	Sex determination of human remains from peptides in tooth enamel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13649-13654.	3.3	118
560	RNA degradation by the plant RNA exosome involves both phosphorolytic and hydrolytic activities. <i>Nature Communications</i> , 2017, 8, 2162.	5.8	44
561	Draft genome of the honey bee ectoparasitic mite, <i>Tropilaelaps mercedesae</i> , is shaped by the parasitic life history. <i>GigaScience</i> , 2017, 6, 1-17.	3.3	39
562	A compendium of multi-omic sequence information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170160.	2.4	35
563	Monitoring of the spatial and temporal dynamics of BER/SSBR pathway proteins, including MYH, UNG2, MPG, NTH1 and NEIL1-3, during DNA replication. <i>Nucleic Acids Research</i> , 2017, 45, 8291-8301.	6.5	25
564	MSP22.8 is a protease inhibitor-like protein involved in shell mineralization in the edible mussel <i>Mytilus galloprovincialis</i> . <i>FEBS Open Bio</i> , 2017, 7, 1539-1556.	1.0	9
565	RNA sequencing and proteomics approaches reveal novel deficits in the cortex of Mecp2-deficient mice, a model for Rett syndrome. <i>Molecular Autism</i> , 2017, 8, 56.	2.6	75
566	Characterizing the O-glycosylation landscape of human plasma, platelets, and endothelial cells. <i>Blood Advances</i> , 2017, 1, 429-442.	2.5	121
567	In-depth PtdIns(3,4,5)P3 signalosome analysis identifies DAPP1 as a negative regulator of GPVI-driven platelet function. <i>Blood Advances</i> , 2017, 1, 918-932.	2.5	34
568	Proteasome Activity Profiling Uncovers Alteration of Catalytic Î²2 and Î²5 Subunits of the Stress-Induced Proteasome during Salinity Stress in Tomato Roots. <i>Frontiers in Plant Science</i> , 2017, 8, 107.	1.7	17
569	Proteome Profiling of Wheat Shoots from Different Cultivars. <i>Frontiers in Plant Science</i> , 2017, 8, 332.	1.7	16



#	ARTICLE	IF	CITATIONS
570	Proteogenomic Analysis Greatly Expands the Identification of Proteins Related to Reproduction in the Apogamous Fern <i>Dryopteris affinis</i> ssp. <i>affinis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 336.	1.7	31
571	Proteomic Analysis of Lipid Droplets from <i>Arabidopsis</i> Aging Leaves Brings New Insight into Their Biogenesis and Functions. <i>Frontiers in Plant Science</i> , 2017, 8, 894.	1.7	78
572	Comparative Proteomic Analysis of Flag Leaves Reveals New Insight into Wheat Heat Adaptation. <i>Frontiers in Plant Science</i> , 2017, 8, 1086.	1.7	41
573	Dynamic Acclimation to High Light in <i>Arabidopsis thaliana</i> Involves Widespread Reengineering of the Leaf Proteome. <i>Frontiers in Plant Science</i> , 2017, 8, 1239.	1.7	39
574	Rhizobium Impacts on Seed Productivity, Quality, and Protection of <i>Pisum sativum</i> upon Disease Stress Caused by <i>Didymella pinodes</i> : Phenotypic, Proteomic, and Metabolomic Traits. <i>Frontiers in Plant Science</i> , 2017, 8, 1961.	1.7	55
575	Identification and Validation of a Salivary Protein Panel to Detect Heart Failure Early. <i>Theranostics</i> , 2017, 7, 4350-4358.	4.6	18
576	Integrated analysis of zone-specific protein and metabolite profiles within nitrogen-fixing <i>Medicago truncatula</i> - <i>Sinorhizobium medicae</i> nodules. <i>PLoS ONE</i> , 2017, 12, e0180894.	1.1	14
577	The Small Heat Shock Protein $\alpha$ -Crystallin B Shows Neuroprotective Properties in a Glaucoma Animal Model. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2418.	1.8	22
578	Exogenous Auxin Elicits Changes in the <i>Arabidopsis thaliana</i> Root Proteome in a Time-Dependent Manner. <i>Proteomes</i> , 2017, 5, 16.	1.7	10
579	A Microsomal Proteomics View of H <sub>2</sub> O <sub>2</sub> - and ABA-Dependent Responses. <i>Proteomes</i> , 2017, 5, 22.	1.7	10
580	A Proteomic Approach to Investigate the Drought Response in the Orphan Crop <i>Eragrostis tef</i> . <i>Proteomes</i> , 2017, 5, 32.	1.7	18
581	Multi-Omic Biogeography of the Gastrointestinal Microbiota of a Pre-Weaned Lamb. <i>Proteomes</i> , 2017, 5, 36.	1.7	10
582	Combined Proteomics/Genomics Approach Reveals Proteomic Changes of Mature Virions as a Novel Poxvirus Adaptation Mechanism. <i>Viruses</i> , 2017, 9, 337.	1.5	6
583	Contrasting patterns of evolutionary constraint and novelty revealed by comparative sperm proteomic analysis in <i>Lepidoptera</i> . <i>BMC Genomics</i> , 2017, 18, 931.	1.2	18
584	Ambra1 spatially regulates Src activity and Src/FAK-mediated cancer cell invasion via trafficking networks. <i>ELife</i> , 2017, 6, .	2.8	32
585	Direct Identification of Functional Amyloid Proteins by Label-Free Quantitative Mass Spectrometry. <i>Biomolecules</i> , 2017, 7, 58.	1.8	13
586	Identification of Proteins Interacting with Cytoplasmic High-Mobility Group Box 1 during the Hepatocellular Response to Ischemia Reperfusion Injury. <i>International Journal of Molecular Sciences</i> , 2017, 18, 167.	1.8	11
587	Proteomic Analysis of Mitochondria-Enriched Fraction Isolated from the Frontal Cortex and Hippocampus of Apolipoprotein E Knockout Mice Treated with Alda-1, an Activator of Mitochondrial Aldehyde Dehydrogenase (ALDH2). <i>International Journal of Molecular Sciences</i> , 2017, 18, 435.	1.8	6

#	ARTICLE	IF	CITATIONS
588	Mechanism Investigation of Rifampicin-Induced Liver Injury Using Comparative Toxicoproteomics in Mice. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1417.	1.8	56
589	Colistin Resistance in <i>Acinetobacter baumannii</i> MDR-ZJ06 Revealed by a Multiomics Approach. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 45.	1.8	50
590	The Eukaryote-Like Serine/Threonine Kinase STK Regulates the Growth and Metabolism of Zoonotic <i>Streptococcus suis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 66.	1.8	52
591	Global Proteomics Revealed <i>Klebsiella pneumoniae</i> Induced Autophagy and Oxidative Stress in <i>Caenorhabditis elegans</i> by Inhibiting PI3K/AKT/mTOR Pathway during Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 393.	1.8	29
592	The Multiple Localized Glyceraldehyde-3-Phosphate Dehydrogenase Contributes to the Attenuation of the <i>Francisella tularensis</i> dsbA Deletion Mutant. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 503.	1.8	19
593	Identification of Post-translational Modifications on Odorant-Binding Protein Isoforms from Pig Olfactory Secretome by High-Resolution Mass Spectrometry: O- <sup>12</sup> -N-acetylglucosamylation and Phosphorylation. <i>Frontiers in Ecology and Evolution</i> , 2017, 5, .	1.1	11
594	Phosphoproteomics Reveals Regulatory T Cell-Mediated DEF6 Dephosphorylation That Affects Cytokine Expression in Human Conventional T Cells. <i>Frontiers in Immunology</i> , 2017, 8, 1163.	2.2	13
595	Metaproteogenomics Reveals Taxonomic and Functional Changes between Cecal and Fecal Microbiota in Mouse. <i>Frontiers in Microbiology</i> , 2017, 8, 391.	1.5	66
596	Complementary Metaproteomic Approaches to Assess the Bacterioplankton Response toward a Phytoplankton Spring Bloom in the Southern North Sea. <i>Frontiers in Microbiology</i> , 2017, 8, 442.	1.5	13
597	Host Plant Compatibility Shapes the Proteogenome of <i>Frankia coriariae</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 720.	1.5	23
598	Predicting Species-Resolved Macronutrient Acquisition during Succession in a Model Phototrophic Biofilm Using an Integrated <sup>2</sup> Omics Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 1020.	1.5	287
599	Combination of Metabolomic and Proteomic Analysis Revealed Different Features among <i>Lactobacillus delbrueckii</i> Subspecies <i>bulgaricus</i> and <i>lactis</i> Strains While In Vivo Testing in the Model Organism <i>Caenorhabditis elegans</i> Highlighted Probiotic Properties. <i>Frontiers in Microbiology</i> , 2017, 8, 1206.	1.5	30
600	Outer Membrane Proteome of <i>Veillonella parvula</i> : A Diderm Firmicute of the Human Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 1215.	1.5	55
601	Proteomic Response of <i>Pseudomonas aeruginosa</i> PAO1 Adhering to Solid Surfaces. <i>Frontiers in Microbiology</i> , 2017, 8, 1465.	1.5	27
602	A Structural and Functional Elucidation of the Rumen Microbiome Influenced by Various Diets and Microenvironments. <i>Frontiers in Microbiology</i> , 2017, 8, 1605.	1.5	207
603	Lipid Metabolic Versatility in <i>Malassezia</i> spp. Yeasts Studied through Metabolic Modeling. <i>Frontiers in Microbiology</i> , 2017, 8, 1772.	1.5	31
604	Analyzing the Complex Regulatory Landscape of Hfq <sup>2</sup> an Integrative, Multi-Omics Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 1784.	1.5	17
605	Vanillin Promotes the Germination of <i>Antrodia camphorata</i> Arthroconidia through PKA and MAPK Signaling Pathways. <i>Frontiers in Microbiology</i> , 2017, 8, 2048.	1.5	3

#	ARTICLE	IF	CITATIONS
606	Phosphoproteome Profiling Reveals Circadian Clock Regulation of Posttranslational Modifications in the Murine Hippocampus. <i>Frontiers in Neurology</i> , 2017, 8, 110.	1.1	35
607	Proteomic Analysis of Post-synaptic Density Fractions from Shank3 Mutant Mice Reveals Brain Region Specific Changes Relevant to Autism Spectrum Disorder. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 26.	1.4	66
608	Synaptic Interactome Mining Reveals p140Cap as a New Hub for PSD Proteins Involved in Psychiatric and Neurological Disorders. <i>Frontiers in Molecular Neuroscience</i> , 2017, 10, 212.	1.4	30
609	Isolation and Characterization of Serum Extracellular Vesicles (EVs) from Atlantic Salmon Infected with <i>Piscirickettsia salmonis</i> . <i>Proteomes</i> , 2017, 5, 34.	1.7	27
610	Cardiac Metabolic Deregulation Induced by the Tyrosine Kinase Receptor Inhibitor Sunitinib is rescued by Endothelin Receptor Antagonism. <i>Theranostics</i> , 2017, 7, 2757-2774.	4.6	27
611	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017, 45, D1100-D1106.	6.5	860
612	The use of urinary proteomics in the assessment of suitability of mouse models for ageing. <i>PLoS ONE</i> , 2017, 12, e0166875.	1.1	17
613	Comprehensive Identification of mRNA-Binding Proteins of <i>Leishmania donovani</i> by Interactome Capture. <i>PLoS ONE</i> , 2017, 12, e0170068.	1.1	26
614	Quantitative liver proteomics identifies FGF19 targets that couple metabolism and proliferation. <i>PLoS ONE</i> , 2017, 12, e0171185.	1.1	29
615	Protein abundances can distinguish between naturally-occurring and laboratory strains of <i>Yersinia pestis</i> , the causative agent of plague. <i>PLoS ONE</i> , 2017, 12, e0183478.	1.1	6
616	Scrambled eggs: Proteomic portraits and novel biomarkers of egg quality in zebrafish ( <i>Danio rerio</i> ). <i>PLoS ONE</i> , 2017, 12, e0188084.	1.1	34
617	The nuclear proteome of <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2017, 12, e0181884.	1.1	51
618	Transcription-translation coupling: direct interactions of RNA polymerase with ribosomes and ribosomal subunits. <i>Nucleic Acids Research</i> , 2017, 45, 11043-11055.	6.5	64
619	Mutations in mitochondrial DNA causing tubulointerstitial kidney disease. <i>PLoS Genetics</i> , 2017, 13, e1006620.	1.5	52
620	Meioc maintains an extended meiotic prophase I in mice. <i>PLoS Genetics</i> , 2017, 13, e1006704.	1.5	103
621	Vulvar squamous cell carcinoma aggressiveness is associated with differential expression of collagen and STAT1. <i>Clinical Proteomics</i> , 2017, 14, 40.	1.1	2
622	Ribosome signatures aid bacterial translation initiation site identification. <i>BMC Biology</i> , 2017, 15, 76.	1.7	26
623	RNA-binding activity of TRIM25 is mediated by its PRY/SPRY domain and is required for ubiquitination. <i>BMC Biology</i> , 2017, 15, 105.	1.7	125

#	ARTICLE	IF	CITATIONS
624	Using omics approaches to understand pulmonary diseases. <i>Respiratory Research</i> , 2017, 18, 149.	1.4	90
625	Brain ureido degenerative protein modifications are associated with neuroinflammation and proteinopathy in Alzheimer's disease with cerebrovascular disease. <i>Journal of Neuroinflammation</i> , 2017, 14, 175.	3.1	35
626	The nuclear receptor ER $\beta$ engages AGO2 in regulation of gene transcription, RNA splicing and RISC loading. <i>Genome Biology</i> , 2017, 18, 189.	3.8	63
627	Global proteomic profiling of <i>Yersinia ruckeri</i> strains. <i>Veterinary Research</i> , 2017, 48, 55.	1.1	16
628	HIF prolyl hydroxylase PHD3 regulates translational machinery and glucose metabolism in clear cell renal cell carcinoma. <i>Cancer &amp; Metabolism</i> , 2017, 5, 5.	2.4	24
629	Potential and active functions in the gut microbiota of a healthy human cohort. <i>Microbiome</i> , 2017, 5, 79.	4.9	123
630	A Quantitative Acetyloomic Analysis of Early Seed Development in Rice ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2017, 18, 1376.	1.8	20
631	Modulation of proteostasis counteracts oxidative stress and affects DNA base excision repair capacity in ATM-deficient cells. <i>Nucleic Acids Research</i> , 2017, 45, 10042-10055.	6.5	13
632	Proteomic analysis of lung metastases in a murine breast cancer model reveals divergent influence of CTSB and CTSL overexpression. <i>Journal of Cancer</i> , 2017, 8, 4065-4074.	1.2	10
633	Comprehensive Metaproteomic Analyses of Urine in the Presence and Absence of Neutrophil-Associated Inflammation in the Urinary Tract. <i>Theranostics</i> , 2017, 7, 238-252.	4.6	34
634	Proteomic profiling of early degenerative retina of RCS rats. <i>International Journal of Ophthalmology</i> , 2017, 10, 878-889.	0.5	6
635	Metaproteomics of Colonic Microbiota Unveils Discrete Protein Functions among Colitic Mice and Control Groups. <i>Proteomics</i> , 2018, 18, 1700391.	1.3	10
636	Integrated omics analysis reveals new drug-induced mitochondrial perturbations in human hepatocytes. <i>Toxicology Letters</i> , 2018, 289, 1-13.	0.4	16
637	Quantitative mapping of RNA-mediated nuclear estrogen receptor $\beta$ interactome in human breast cancer cells. <i>Scientific Data</i> , 2018, 5, 180031.	2.4	22
638	Proteomics of <i>Aspergillus fumigatus</i> Conidia-containing Phagolysosomes Identifies Processes Governing Immune Evasion. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1084-1096.	2.5	36
639	Three unrelated protease inhibitors enhance accumulation of pharmaceutical recombinant proteins in <i>Nicotiana benthamiana</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1797-1810.	4.1	61
640	Proteomic Identification of Interferon-Induced Proteins with Tetratricopeptide Repeats as Markers of M1 Macrophage Polarization. <i>Journal of Proteome Research</i> , 2018, 17, 1485-1499.	1.8	35
641	The use of SWATH to analyse the dynamic changes of bacterial proteome of carbapenemase-producing <i>Escherichia coli</i> under antibiotic pressure. <i>Scientific Reports</i> , 2018, 8, 3871.	1.6	18

#	ARTICLE	IF	CITATIONS
642	Proteome Analysis of a <i>M. avium</i> Mutant Exposes a Novel Role of the Bifunctional Protein LysX in the Regulation of Metabolic Activity. <i>Journal of Infectious Diseases</i> , 2018, 218, 291-299.	1.9	7
643	The MYO6 interactome reveals adaptor complexes coordinating early endosome and cytoskeletal dynamics. <i>EMBO Reports</i> , 2018, 19, .	2.0	49
644	Strong cation exchange-reversed phase liquid chromatography-capillary zone electrophoresis-tandem mass spectrometry platform with high peak capacity for deep bottom-up proteomics. <i>Analytica Chimica Acta</i> , 2018, 1012, 1-9.	2.6	43
645	Phenazines Regulate Nap-Dependent Denitrification in <i>Pseudomonas aeruginosa</i> Biofilms. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	29
646	Green Algae and Networks for Adverse Outcome Pathways. , 2018, , 133-148.		1
647	Disentangling thermal stress responses in a reef-calcifier and its photosymbionts by shotgun proteomics. <i>Scientific Reports</i> , 2018, 8, 3524.	1.6	24
648	A Systems Biology Approach to Advancing Adverse Outcome Pathways for Risk Assessment. , 2018, , .		8
649	On the Reproducibility of Label-Free Quantitative Cross-Linking/Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 405-412.	1.2	39
650	Zc3h10 is a novel mitochondrial regulator. <i>EMBO Reports</i> , 2018, 19, .	2.0	23
651	Interactome Analysis Reveals Regulator of G Protein Signaling 14 (RGS14) is a Novel Calcium/Calmodulin (Ca <sup>2+</sup> /CaM) and CaM Kinase II (CaMKII) Binding Partner. <i>Journal of Proteome Research</i> , 2018, 17, 1700-1711.	1.8	21
652	Quantitative proteomics reveals decreased expression of major urinary proteins in the liver of apoE/eNOS <sup>-/-</sup> DKO mice. <i>Clinical and Experimental Pharmacology and Physiology</i> , 2018, 45, 711-719.	0.9	2
653	Cell Immunopeptidomes Reveal Cell Subtype Surface Markers Derived From Intracellular Proteins. <i>Proteomics</i> , 2018, 18, e1700410.	1.3	15
654	Nanodroplet processing platform for deep and quantitative proteome profiling of 10 <sup>4</sup> -100 mammalian cells. <i>Nature Communications</i> , 2018, 9, 882.	5.8	384
655	Temporal Effects of Combined Birinapant and Paclitaxel on Pancreatic Cancer Cells Investigated via Large-Scale, Ion-Current-Based Quantitative Proteomics (IonStar). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 655-671.	2.5	16
656	Phosphoproteomics Analysis Identifies Novel Candidate Substrates of the Nonreceptor Tyrosine Kinase, Src-related Kinase Lacking C-terminal Regulatory Tyrosine and N-terminal Myristoylation Sites (SRMS). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 925-947.	2.5	16
657	The N-terminal domain of a tick evasin is critical for chemokine binding and neutralization and confers specific binding activity to other evasins. <i>Journal of Biological Chemistry</i> , 2018, 293, 6134-6146.	1.6	19
658	Multi-laboratory analysis of the variability of shipped samples for proteomics following non-cooled international transport. <i>Analytical Biochemistry</i> , 2018, 548, 60-65.	1.1	2
659	PHLDA1 Mediates Drug Resistance in Receptor Tyrosine Kinase-Driven Cancer. <i>Cell Reports</i> , 2018, 22, 2469-2481.	2.9	34

#	ARTICLE	IF	CITATIONS
660	Proteomic characterization of Withaferin A-targeted protein networks for the treatment of monoclonal myeloma gammopathies. <i>Journal of Proteomics</i> , 2018, 179, 17-29.	1.2	21
661	Overexpression of bifunctional fructose-1,6-bisphosphatase/sedoheptulose-1,7-bisphosphatase leads to enhanced photosynthesis and global reprogramming of carbon metabolism in <i>Synechococcus</i> sp. PCC 7002. <i>Metabolic Engineering</i> , 2018, 47, 170-183.	3.6	76
662	Comprehensive Redox Profiling of the Thiol Proteome of <i>Clostridium difficile</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1035-1046.	2.5	21
663	STRENDA DB: enabling the validation and sharing of enzyme kinetics data. <i>FEBS Journal</i> , 2018, 285, 2193-2204.	2.2	38
664	Histological, Physiological, and Comparative Proteomic Analyses Provide Insights into Leaf Rolling in <i>Brassica napus</i> . <i>Journal of Proteome Research</i> , 2018, 17, 1761-1772.	1.8	6
665	Impact of imipramine on proteome of rat primary glial cells. <i>Journal of Neuroimmunology</i> , 2018, 320, 25-37.	1.1	5
666	Proteome-wide analysis of cysteine oxidation reveals metabolic sensitivity to redox stress. <i>Nature Communications</i> , 2018, 9, 1581.	5.8	178
667	Software for Peak Finding and Elemental Composition Assignment for Glycosaminoglycan Tandem Mass Spectra. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1448-1456.	2.5	21
668	Peptidomics dataset: Blood plasma and serum samples of healthy donors fractionated on a set of chromatography sorbents. <i>Data in Brief</i> , 2018, 18, 1204-1211.	0.5	14
669	Development of a Prototype System for Archiving Integrative/Hybrid Structure Models of Biological Macromolecules. <i>Structure</i> , 2018, 26, 894-904.e2.	1.6	81
670	Differences in the bovine milk whey proteome between early pregnancy and the estrous cycle. <i>Theriogenology</i> , 2018, 114, 301-307.	0.9	13
671	Response to "Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra". <i>Journal of Proteome Research</i> , 2018, 17, 1993-1996.	1.8	9
672	Arginine Methylation by PRMT2 Controls the Functions of the Actin Nucleator Cobl. <i>Developmental Cell</i> , 2018, 45, 262-275.e8.	3.1	34
673	Gut microbial functional maturation and succession during human early life. <i>Environmental Microbiology</i> , 2018, 20, 2160-2177.	1.8	30
674	Characterization and non-parametric modeling of the developing serum proteome during infancy and early childhood. <i>Scientific Reports</i> , 2018, 8, 5883.	1.6	13
675	Optimizing Recombinant Protein Production in the <i>Escherichia coli</i> Periplasm Alleviates Stress. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	41
676	A mass spectrometry based predictive strategy reveals ADAP1 is phosphorylated at tyrosine 364. <i>Rapid Communications in Mass Spectrometry</i> , 2018, 32, 1173-1180.	0.7	1
677	Integrated Transcriptomic and Proteomic Analyses Suggest the Participation of Endogenous Protease Inhibitors in the Regulation of Protease Gene Expression in <i>Helicoverpa armigera</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1324-1336.	2.5	14

#	ARTICLE	IF	CITATIONS
678	Proteomic profiling of human cancer pseudopodia for the identification of anti-metastatic drug candidates. <i>Scientific Reports</i> , 2018, 8, 5858.	1.6	8
679	Termite soldiers contribute to social immunity by synthesizing potent oral secretions. <i>Insect Molecular Biology</i> , 2018, 27, 564-576.	1.0	38
680	Foxn1 expression in keratinocytes is stimulated by hypoxia: further evidence of its role in skin wound healing. <i>Scientific Reports</i> , 2018, 8, 5425.	1.6	22
681	Targeted Proteomics Guided by Label-free Quantitative Proteome Analysis in Saliva Reveal Transition Signatures from Health to Periodontal Disease. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1392-1409.	2.5	74
682	Involvement of serum-derived exosomes of elderly patients with bone loss in failure of bone remodeling via alteration of exosomal bone-related proteins. <i>Ageing Cell</i> , 2018, 17, e12758.	3.0	63
683	Insights into Islet Differentiation and Maturation through Proteomic Characterization of a Human iPSC-Derived Pancreatic Endocrine Model. <i>Proteomics - Clinical Applications</i> , 2018, 12, e1600173.	0.8	7
684	The impact of circulating preeclampsia-associated extracellular vesicles on the migratory activity and phenotype of THP-1 monocytic cells. <i>Scientific Reports</i> , 2018, 8, 5426.	1.6	19
685	CRISPR/Cas9-mediated Genomic Editing of Cluap1/IFT38 Reveals a New Role in Actin Arrangement. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1285-1294.	2.5	20
686	Proteotranscriptomic Measurements of E6-Associated Protein (E6AP) Targets in DU145 Prostate Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1170-1183.	2.5	13
687	Proteogenomics of Malignant Melanoma Cell Lines: The Effect of Stringency of Exome Data Filtering on Variant Peptide Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 1801-1811.	1.8	17
688	Proline hydroxylation in collagen supports integrin binding by two distinct mechanisms. <i>Journal of Biological Chemistry</i> , 2018, 293, 7645-7658.	1.6	57
689	Insight into cellular proteome of <i>Lolium multiflorum</i> / <i>Festuca arundinacea</i> introgression forms to decipher crucial mechanisms of cold acclimation in forage grasses. <i>Plant Science</i> , 2018, 272, 22-31.	1.7	17
690	Time-course proteomics dataset to monitor protein-bound methionine oxidation in <i>Bacillus cereus</i> ATCC 14579. <i>Data in Brief</i> , 2018, 18, 394-398.	0.5	2
691	A type VI secretion system effector delivery mechanism dependent on PAAR and a chaperone-co-chaperone complex. <i>Nature Microbiology</i> , 2018, 3, 632-640.	5.9	116
692	Identification of potential urine proteins and microRNA biomarkers for the diagnosis of pulmonary tuberculosis patients. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-13.	3.0	37
693	Cross-talk between monocyte invasion and astrocyte proliferation regulates scarring in brain injury. <i>EMBO Reports</i> , 2018, 19, .	2.0	98
694	A Cost-Effective High-Throughput Plasma and Serum Proteomics Workflow Enables Mapping of the Molecular Impact of Total Pancreatectomy with Islet Autotransplantation. <i>Journal of Proteome Research</i> , 2018, 17, 1983-1992.	1.8	39
695	Parallel reaction monitoring on a Q Exactive mass spectrometer increases reproducibility of phosphopeptide detection in bacterial phosphoproteomics measurements. <i>Journal of Proteomics</i> , 2018, 189, 60-66.	1.2	11

#	ARTICLE	IF	CITATIONS
696	Proteomic analysis of chemosensory organs in the honey bee parasite <i>Varroa destructor</i> : A comprehensive examination of the potential carriers for semiochemicals. <i>Journal of Proteomics</i> , 2018, 181, 131-141.	1.2	26
697	Early onset of disc degeneration in SM/J mice is associated with changes in ion transport systems and fibrotic events. <i>Matrix Biology</i> , 2018, 70, 123-139.	1.5	41
698	Proteomic analysis of pitcher fluid from <i>Nepenthes ventrata</i> . <i>Data in Brief</i> , 2018, 17, 517-519.	0.5	10
699	The SKP1-Cullin-F-box E3 ligase $\hat{I}^2$ TrCP and CDK2 cooperate to control STIL abundance and centriole number. <i>Open Biology</i> , 2018, 8, .	1.5	20
700	Structural and compositional diversity of fibrillin microfibrils in human tissues. <i>Journal of Biological Chemistry</i> , 2018, 293, 5117-5133.	1.6	54
701	The Peptide Repertoire of HLA-B*27 may include Ligands with Lysine at P2 Anchor Position. <i>Proteomics</i> , 2018, 18, e1700249.	1.3	17
702	Comprehensive analysis of the lysine acetylome and its potential regulatory roles in the virulence of <i>Streptococcus pneumoniae</i> . <i>Journal of Proteomics</i> , 2018, 176, 46-55.	1.2	37
703	Fungal Secretome Analysis via PepSAVI-MS: Identification of the Bioactive Peptide KP4 from <i>Ustilago maydis</i> . <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 859-865.	1.2	7
704	TCA precipitation and ethanol/HCl single-step purification evaluation: One-dimensional gel electrophoresis, Bradford assays, spectrofluorometry and Raman spectroscopy data on HSA, Rnase, lysozyme - Mascots and Skyline data. <i>Data in Brief</i> , 2018, 17, 938-953.	0.5	8
705	Systems Signatures Reveal Unique Remission-path of Type 2 Diabetes Following Roux-en-Y Gastric Bypass Surgery. <i>EBioMedicine</i> , 2018, 28, 234-240.	2.7	5
706	Compartmentalization of HP1 Proteins in Pluripotency Acquisition and Maintenance. <i>Stem Cell Reports</i> , 2018, 10, 627-641.	2.3	20
707	Identification of Native and Posttranslationally Modified HLA-B*57:01-Restricted HIV Envelope Derived Epitopes Using Immunoproteomics. <i>Proteomics</i> , 2018, 18, e1700253.	1.3	23
708	Large-scale intact glycopeptide identification by Mascot database search. <i>Scientific Reports</i> , 2018, 8, 2117.	1.6	58
709	The rolB plant oncogene affects multiple signaling protein modules related to hormone signaling and plant defense. <i>Scientific Reports</i> , 2018, 8, 2285.	1.6	24
710	Establishment of Dimethyl Labeling-based Quantitative Acetylproteomics in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1010-1027.	2.5	31
711	N-glycome of the Lysosomal Glycocalyx is Altered in Niemann-Pick Type C Disease (NPC) Model Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 631-642.	2.5	26
712	Enhancing Membrane Protein Identification Using a Simplified Centrifugation and Detergent-Based Membrane Extraction Approach. <i>Analytical Chemistry</i> , 2018, 90, 2434-2439.	3.2	10
713	Tissue-specific changes in apoplast proteins and cell wall structure during cold acclimation of winter wheat crowns. <i>Journal of Experimental Botany</i> , 2018, 69, 1221-1234.	2.4	34



#	ARTICLE	IF	CITATIONS
714	Identification of a Golgi GPI-N-acetylgalactosamine transferase with tandem transmembrane regions in the catalytic domain. <i>Nature Communications</i> , 2018, 9, 405.	5.8	37
715	Protein Tyrosine Phosphatase Receptor Type G (PTPRG) Controls Fibroblast Growth Factor Receptor (FGFR) 1 Activity and Influences Sensitivity to FGFR Kinase Inhibitors. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 850-870.	2.5	30
716	Lipid rafts can form in the inner and outer membranes of <i>Borrelia burgdorferi</i> and have different properties and associated proteins. <i>Molecular Microbiology</i> , 2018, 108, 63-76.	1.2	41
717	Development of a Photo-Cross-Linkable Diaminoquinazoline Inhibitor for Target Identification in <i>Plasmodium falciparum</i> . <i>ACS Infectious Diseases</i> , 2018, 4, 523-530.	1.8	20
718	Bioinformatics Support for Farm Animal Proteomics. , 2018, , 361-386.		0
719	Splicing of platelet resident pre-mRNAs upon activation by physiological stimuli results in functionally relevant proteome modifications. <i>Scientific Reports</i> , 2018, 8, 498.	1.6	65
720	Mapping protein interactions of sodium channel Na <sup>v</sup> 1.7 using epitope-tagged gene-targeted mice. <i>EMBO Journal</i> , 2018, 37, 427-445.	3.5	54
721	Exoproteome Profiling Reveals the Involvement of the Foldase PrsA in the Cell Surface Properties and Pathogenesis of <i>Staphylococcus aureus</i> . <i>Proteomics</i> , 2018, 18, e1700195.	1.3	24
722	ProteomicsDB. <i>Nucleic Acids Research</i> , 2018, 46, D1271-D1281.	6.5	197
723	The function of two type II metacaspases in woody tissues of <i>Populus</i> trees. <i>New Phytologist</i> , 2018, 217, 1551-1565.	3.5	30
724	Long noncoding RNA LISPR1 is required for S1P signaling and endothelial cell function. <i>Journal of Molecular and Cellular Cardiology</i> , 2018, 116, 57-68.	0.9	35
725	Asparagine bioavailability governs metastasis in a model of breast cancer. <i>Nature</i> , 2018, 554, 378-381.	13.7	362
726	Selective Photoaffinity Probe That Enables Assessment of Cannabinoid CB <sub>2</sub> Receptor Expression and Ligand Engagement in Human Cells. <i>Journal of the American Chemical Society</i> , 2018, 140, 6067-6075.	6.6	68
727	Updates on resources, software tools, and databases for plant proteomics in 2016–2017. <i>Electrophoresis</i> , 2018, 39, 1543-1557.	1.3	11
728	Global ubiquitination analysis reveals extensive modification and proteasomal degradation of cowpox virus proteins, but preservation of viral cores. <i>Scientific Reports</i> , 2018, 8, 1807.	1.6	21
729	Peptide Level Turnover Measurements Enable the Study of Proteoform Dynamics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 974-992.	2.5	98
730	Homeolog expression analysis in an allotriploid non-model crop via integration of transcriptomics and proteomics. <i>Scientific Reports</i> , 2018, 8, 1353.	1.6	34
731	Choice of costimulatory domains and of cytokines determines CAR T-cell activity in neuroblastoma. <i>Oncolmmunology</i> , 2018, 7, e1433518.	2.1	120

#	ARTICLE	IF	CITATIONS
732	Human Cervical Mucus Plugs Exhibit Insufficiencies in Antimicrobial Activity Towards Group B Streptococcus. <i>Journal of Infectious Diseases</i> , 2018, 217, 1626-1636.	1.9	19
733	The deep-subsurface sulfate reducer <i>Desulfotomaculum kuznetsovii</i> employs two methanol-degrading pathways. <i>Nature Communications</i> , 2018, 9, 239.	5.8	36
734	T lymphocytes facilitate brain metastasis of breast cancer by inducing Guanylate-Binding Protein 1 expression. <i>Acta Neuropathologica</i> , 2018, 135, 581-599.	3.9	63
735	Comprehensive list of SUMO targets in <i>Caenorhabditis elegans</i> and its implication for evolutionary conservation of SUMO signaling. <i>Scientific Reports</i> , 2018, 8, 1139.	1.6	18
736	The RIG-I-like receptor LGP2 inhibits Dicer-dependent processing of long double-stranded RNA and blocks RNA interference in mammalian cells. <i>EMBO Journal</i> , 2018, 37, .	3.5	94
737	The Sarda Sheep Host Fecal Proteome. <i>Proteomics</i> , 2018, 18, 1700272.	1.3	2
738	Mapping and Quantification of Over 2000 O-linked Glycopeptides in Activated Human T Cells with Isotope-Targeted Glycoproteomics (Isotag). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 764-775.	2.5	138
739	Exploring Biological and Geological Age-related Changes through Variations in Intra- and Intertooth Proteomes of Ancient Dentine. <i>Journal of Proteome Research</i> , 2018, 17, 1000-1013.	1.8	45
740	Serum proteomic pattern in female stress urinary incontinence. <i>Electrophoresis</i> , 2018, 39, 1071-1078.	1.3	8
741	Quantitative Proteomics After Spinal Cord Injury (SCI) in a Regenerative and a Nonregenerative Stage in the Frog <i>Xenopus laevis</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 592-606.	2.5	16
742	Unravelling the differences: comparative proteomic analysis of a clonal virulent and an attenuated <i>Histomonas meleagridis</i> strain. <i>International Journal for Parasitology</i> , 2018, 48, 145-157.	1.3	24
743	Proteome and phosphoproteome analysis of commensally induced dendritic cell maturation states. <i>Journal of Proteomics</i> , 2018, 180, 11-24.	1.2	6
744	Identification of a precursor processing protease from the spider <i>Cupiennius salei</i> essential for venom neurotoxin maturation. <i>Journal of Biological Chemistry</i> , 2018, 293, 2079-2090.	1.6	23
745	Intake of Fish Oil Specifically Modulates Colonic Muc2 Expression in Middle-Aged Rats by Suppressing the Glycosylation Process. <i>Molecular Nutrition and Food Research</i> , 2018, 62, 1700661.	1.5	14
746	Retrovirus-like Gag Protein Arc1 Binds RNA and Traffics across Synaptic Boutons. <i>Cell</i> , 2018, 172, 262-274.e11.	13.5	344
747	Rapid and comprehensive discovery of unreported shellfish allergens using large-scale transcriptomic and proteomic resources. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 1501-1504.e8.	1.5	42
748	Identification of candidate serum biomarkers of childhood-onset growth hormone deficiency using SWATH-MS and feature selection. <i>Journal of Proteomics</i> , 2018, 175, 105-113.	1.2	14
749	Proteome analysis of an <i>Escherichia coli</i> ptsN -null strain under different nitrogen regimes. <i>Journal of Proteomics</i> , 2018, 174, 28-35.	1.2	11

#	ARTICLE	IF	CITATIONS
750	Exploring the molecular complexity of <i>Triatoma dimidiata</i> sialome. <i>Journal of Proteomics</i> , 2018, 174, 47-60.	1.2	17
751	CHIP Regulates Aquaporin-2 Quality Control and Body Water Homeostasis. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 936-948.	3.0	49
752	Biotinylation by antibody recognition—a method for proximity labeling. <i>Nature Methods</i> , 2018, 15, 127-133.	9.0	107
753	Rabbit seminal plasma proteome: The importance of the genetic origin. <i>Animal Reproduction Science</i> , 2018, 189, 30-42.	0.5	17
754	Bifidobacteria or Fiber Protects against Diet-Induced Microbiota-Mediated Colonic Mucus Deterioration. <i>Cell Host and Microbe</i> , 2018, 23, 27-40.e7.	5.1	477
755	Reversible Lysine Derivatization Enabling Improved Arg-C Digestion, a Highly Specific Arg-C Digestion Using Trypsin. <i>Analytical Chemistry</i> , 2018, 90, 1554-1559.	3.2	8
756	Omics Assisted N-terminal Proteoform and Protein Expression Profiling On Methionine Aminopeptidase 1 (MetAP1) Deletion. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 694-708.	2.5	21
757	Mining the Secretome of C2C12 Muscle Cells: Data Dependent Experimental Approach To Analyze Protein Secretion Using Label-Free Quantification and Peptide Based Analysis. <i>Journal of Proteome Research</i> , 2018, 17, 879-890.	1.8	56
758	Combinatorial Omics Analysis Reveals Perturbed Lysosomal Homeostasis in Collagen VII-deficient Keratinocytes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 565-579.	2.5	25
759	Proteome-Wide Characterization of Phosphorylation-Induced Conformational Changes in Breast Cancer. <i>Journal of Proteome Research</i> , 2018, 17, 1129-1137.	1.8	14
760	Mutations in <i>ppe38</i> block PE_PGRS secretion and increase virulence of <i>Mycobacterium tuberculosis</i> . <i>Nature Microbiology</i> , 2018, 3, 181-188.	5.9	112
761	Of mice and men: Traces of life in the death registries of the 1630 plague in Milano. <i>Journal of Proteomics</i> , 2018, 180, 128-137.	1.2	30
762	Advanced aging causes diaphragm functional abnormalities, global proteome remodeling, and loss of mitochondrial cysteine redox flexibility in mice. <i>Experimental Gerontology</i> , 2018, 103, 69-79.	1.2	19
763	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018, 46, D246-D251.	6.5	365
764	Characterization of Detergent Insoluble Proteome in Chronic Traumatic Encephalopathy. <i>Journal of Neuropathology and Experimental Neurology</i> , 2018, 77, 40-49.	0.9	19
765	Transcriptomics-guided bottom-up and top-down venomomics of neonate and adult specimens of the arboreal rear-fanged Brown Treesnake, <i>Boiga irregularis</i> , from Guam. <i>Journal of Proteomics</i> , 2018, 174, 71-84.	1.2	47
766	Proteomic analysis of germinal vesicles in the domestic cat model reveals candidate nuclear proteins involved in oocyte competence acquisition. <i>Molecular Human Reproduction</i> , 2018, 24, 14-26.	1.3	11
767	Large-scale identification and visualization of human liver N-glycome enriched from LO2 cells. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 4195-4202.	1.9	10

#	ARTICLE	IF	CITATIONS
768	The response to neoadjuvant chemoradiotherapy with 5-fluorouracil in locally advanced rectal cancer patients: a predictive proteomic signature. <i>Clinical Proteomics</i> , 2018, 15, 16.	1.1	43
769	New perspectives: systems medicine in cardiovascular disease. <i>BMC Systems Biology</i> , 2018, 12, 57.	3.0	17
770	Reproducible proteomics sample preparation for single FFPE tissue slices using acid-labile surfactant and direct trypsinization. <i>Clinical Proteomics</i> , 2018, 15, 11.	1.1	43
771	A multi-omics approach reveals function of Secretory Carrier-Associated Membrane Proteins in wood formation of <i>Populus</i> trees. <i>BMC Genomics</i> , 2018, 19, 11.	1.2	25
772	Two predominant MUPs, OBP3 and MUP13, are male pheromones in rats. <i>Frontiers in Zoology</i> , 2018, 15, 6.	0.9	14
773	CD74 regulates complexity of tumor cell HLA class II peptidome in brain metastasis and is a positive prognostic marker for patient survival. <i>Acta Neuropathologica Communications</i> , 2018, 6, 18.	2.4	26
774	Comprehensive Peptide Analysis of Mouse Brain Striatum Identifies Novel sORF-Encoded Polypeptides. <i>Proteomics</i> , 2018, 18, e1700218.	1.3	30
775	Nucleolar-nucleoplasmic shuttling of TARG1 and its control by DNA damage-induced poly-ADP-ribosylation and by nucleolar transcription. <i>Scientific Reports</i> , 2018, 8, 6748.	1.6	32
776	Fasting and refeeding induces changes in the mouse hepatic lipid droplet proteome. <i>Journal of Proteomics</i> , 2018, 181, 213-224.	1.2	33
777	Transcriptomic and Neuropeptidomic Analysis of the Stick Insect, <i>Carausius morosus</i> . <i>Journal of Proteome Research</i> , 2018, 17, 2192-2204.	1.8	40
778	Characterization of the Small Intestinal Lesion in Celiac Disease by Label-Free Quantitative Mass Spectrometry. <i>American Journal of Pathology</i> , 2018, 188, 1563-1579.	1.9	12
779	Rb interactome data and its modulations during cell cycle progression in HEK 293 cells. <i>Data in Brief</i> , 2018, 17, 604-609.	0.5	1
780	Quantitative proteomics of <i>Bombyx mori</i> after BmNPV challenge. <i>Journal of Proteomics</i> , 2018, 181, 142-151.	1.2	13
781	Cell Surface MHC Class I Expression Is Limited by the Availability of Peptide-Receptive "Empty" Molecules Rather than by the Supply of Peptide Ligands. <i>Proteomics</i> , 2018, 18, e1700248.	1.3	65
782	Click Chemistry-mediated Biotinylation Reveals a Function for the Protease BACE1 in Modulating the Neuronal Surface Glycoproteome. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1487-1501.	2.5	33
783	Enhancement of red blood cell transfusion compatibility using CRISPR-mediated erythroblast gene editing. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	50
784	EL1-like Casein Kinases Suppress ABA Signaling and Responses by Phosphorylating and Destabilizing the ABA Receptors PYR/PYLs in Arabidopsis. <i>Molecular Plant</i> , 2018, 11, 706-719.	3.9	72
785	Quantitative multiplexed profiling of <i>Penicillium funiculosum</i> secretome grown on polymeric cellulase inducers and glucose. <i>Journal of Proteomics</i> , 2018, 179, 150-160.	1.2	20

#	ARTICLE	IF	CITATIONS
786	Absolute quantification of selected photosynthetic electron transfer proteins in <i>Chlamydomonas reinhardtii</i> in the presence and absence of oxygen. <i>Photosynthesis Research</i> , 2018, 137, 281-293.	1.6	19
787	Proteomic Investigation of the Binding Agent between Liver Glycogen $\hat{I}^2$ Particles. <i>ACS Omega</i> , 2018, 3, 3640-3645.	1.6	35
788	Specter: linear deconvolution for targeted analysis of data-independent acquisition mass spectrometry proteomics. <i>Nature Methods</i> , 2018, 15, 371-378.	9.0	58
789	Identification of long-lived synaptic proteins by proteomic analysis of synaptosome protein turnover. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3827-E3836.	3.3	122
790	Comparison of protein expression between human livers and the hepatic cell lines HepG2, Hep3B, and Huh7 using SWATH and MRM-HR proteomics: Focusing on drug-metabolizing enzymes. <i>Drug Metabolism and Pharmacokinetics</i> , 2018, 33, 133-140.	1.1	42
791	Proteomic profiling of rectal cancer reveals acid ceramidase is implicated in radiation response. <i>Journal of Proteomics</i> , 2018, 179, 53-60.	1.2	17
792	CDK and MAPK Synergistically Regulate Signaling Dynamics via a Shared Multi-site Phosphorylation Region on the Scaffold Protein Ste5. <i>Molecular Cell</i> , 2018, 69, 938-952.e6.	4.5	39
793	Direct Evidence of the Presence of Cross-Linked $\hat{A}^2$ Dimers in the Brains of Alzheimer's Disease Patients. <i>Analytical Chemistry</i> , 2018, 90, 4552-4560.	3.2	37
794	The SystemMHC Atlas project. <i>Nucleic Acids Research</i> , 2018, 46, D1237-D1247.	6.5	119
795	Discovery and Characterization of ZUFSP/ZUP1, a Distinct Deubiquitinase Class Important for Genome Stability. <i>Molecular Cell</i> , 2018, 70, 150-164.e6.	4.5	142
796	Multiplex Fluorescent, Activity-Based Protein Profiling Identifies Active $\hat{I}^{\pm}$ -Glycosidases and Other Hydrolases in Plants. <i>Plant Physiology</i> , 2018, 177, 24-37.	2.3	20
797	Angiogenic and Immunologic Proteins Identified by Deep Proteomic Profiling of Human Retinal and Choroidal Vascular Endothelial Cells: Potential Targets for New Biologic Drugs. <i>American Journal of Ophthalmology</i> , 2018, 193, 197-229.	1.7	23
798	Detection of salivary protein biomarkers of saliva secretion disorder in a primary Sjögren syndrome murine model. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2018, 154, 252-262.	1.4	7
799	Identification of Novel Physiological Substrates of <i>Mycobacterium bovis</i> BCG Protein Kinase G (PknG) by Label-free Quantitative Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1365-1377.	2.5	21
800	Systematic identification of light-regulated cold-responsive proteome in a model cyanobacterium. <i>Journal of Proteomics</i> , 2018, 179, 100-109.	1.2	6
801	Mapping in vivo target interaction profiles of covalent inhibitors using chemical proteomics with label-free quantification. <i>Nature Protocols</i> , 2018, 13, 752-767.	5.5	48
802	Multiple mechanisms drive phage infection efficiency in nearly identical hosts. <i>ISME Journal</i> , 2018, 12, 1605-1618.	4.4	48
803	Protein composition of catalytically active U7-dependent processing complexes assembled on histone pre-mRNA containing biotin and a photo-cleavable linker. <i>Nucleic Acids Research</i> , 2018, 46, 4752-4770.	6.5	21

#	ARTICLE	IF	CITATIONS
804	Translation of neutrally evolving peptides provides a basis for de novo gene evolution. <i>Nature Ecology and Evolution</i> , 2018, 2, 890-896.	3.4	112
805	Environmental allergens induce allergic inflammation through proteolytic maturation of IL-33. <i>Nature Immunology</i> , 2018, 19, 375-385.	7.0	255
806	Protease Activities Triggered by <i>Ralstonia solanacearum</i> Infection in Susceptible and Tolerant Tomato Lines. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1112-1125.	2.5	24
807	Anton Chekhov and Robert Koch Cheek to Cheek: A Proteomic Study. <i>Proteomics</i> , 2018, 18, e1700447.	1.3	20
808	SWATH mass spectrometry as a tool for quantitative profiling of the matrisome. <i>Journal of Proteomics</i> , 2018, 189, 11-22.	1.2	75
809	Proteomic and Biochemical Analyses Reveal a Novel Mechanism for Promoting Protein Ubiquitination and Degradation by UFBP1, a Key Component of Ufmylation. <i>Journal of Proteome Research</i> , 2018, 17, 1509-1520.	1.8	17
810	Benchmarking common quantification strategies for large-scale phosphoproteomics. <i>Nature Communications</i> , 2018, 9, 1045.	5.8	232
811	Genome, transcriptome and proteome: the rise of omics data and their integration in biomedical sciences. <i>Briefings in Bioinformatics</i> , 2018, 19, 286-302.	3.2	498
812	Identification of differentially expressed peptides in high-throughput proteomics data. <i>Briefings in Bioinformatics</i> , 2018, 19, 971-981.	3.2	47
813	Proteomic analysis of the phycobiliprotein antenna of the cryptophyte alga <i>Guillardia theta</i> cultured under different light intensities. <i>Photosynthesis Research</i> , 2018, 135, 149-163.	1.6	19
814	Label-Free Shotgun Proteomics Approach to Characterize Muscle Tissue from Farmed and Wild European Sea Bass ( <i>Dicentrarchus labrax</i> ). <i>Food Analytical Methods</i> , 2018, 11, 292-301.	1.3	15
815	Assessing the impact of protein extraction methods for human gut metaproteomics. <i>Journal of Proteomics</i> , 2018, 180, 120-127.	1.2	115
816	Mitogen-Activated Protein Kinase Kinase 5 Regulates Proliferation and Biosynthetic Processes in Procyclic Forms of <i>Trypanosoma brucei</i> . <i>Journal of Proteome Research</i> , 2018, 17, 108-118.	1.8	5
817	Complement Activation in Peritoneal Dialysis-Induced Arteriopathy. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 268-282.	3.0	45
818	The transcriptome, extracellular proteome and active secretome of agroinfiltrated <i>Nicotiana benthamiana</i> uncover a large, diverse protease repertoire. <i>Plant Biotechnology Journal</i> , 2018, 16, 1068-1084.	4.1	54
819	The online Tabloid Proteome: an annotated database of protein associations. <i>Nucleic Acids Research</i> , 2018, 46, D581-D585.	6.5	6
820	PhoStar: Identifying Tandem Mass Spectra of Phosphorylated Peptides before Database Search. <i>Journal of Proteome Research</i> , 2018, 17, 290-295.	1.8	9
821	Affinity proteomics reveals extensive phosphorylation of the Brassica chromosome axis protein <i>ASYP1</i> and a network of associated proteins at prophase I of meiosis. <i>Plant Journal</i> , 2018, 93, 17-33.	2.8	51

#	ARTICLE	IF	CITATIONS
822	Integrated Proteomic and Transcriptomic Analysis Reveals Long Noncoding RNA HOX Transcript Antisense Intergenic RNA (HOTAIR) Promotes Hepatocellular Carcinoma Cell Proliferation by Regulating Opioid Growth Factor Receptor (OGFr). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 146-159.	2.5	33
823	The E. coli S30 lysate proteome: A prototype for cell-free protein production. <i>New Biotechnology</i> , 2018, 40, 245-260.	2.4	54
824	Insight into the modulation of intestinal proteome of juvenile common carp ( <i>Cyprinus carpio</i> L.) after dietary exposure to ZnO nanoparticles. <i>Science of the Total Environment</i> , 2018, 613-614, 62-71.	3.9	44
825	Comparison of Targeted Mass Spectrometry Techniques with an Immunoassay: A Case Study for HSP90 $\alpha$ . <i>Proteomics - Clinical Applications</i> , 2018, 12, 1700107.	0.8	17
826	Temporal expression profiling of plasma proteins reveals oxidative stress in early stages of Type 1 Diabetes progression. <i>Journal of Proteomics</i> , 2018, 172, 100-110.	1.2	36
827	Comparing intestinal versus diffuse gastric cancer using a PEFf-oriented proteomic pipeline. <i>Journal of Proteomics</i> , 2018, 171, 63-72.	1.2	11
828	A proteomic portrait of dinoflagellate chromatin reveals abundant RNA-binding proteins. <i>Chromosoma</i> , 2018, 127, 29-43.	1.0	13
829	Proline-dependent and basophilic kinases phosphorylate human TRPC6 at serine 14 to control channel activity through increased membrane expression. <i>FASEB Journal</i> , 2018, 32, 208-219.	0.2	6
830	Quantitative phosphoproteomic analysis of acquired cancer drug resistance to pazopanib and dasatinib. <i>Journal of Proteomics</i> , 2018, 170, 130-140.	1.2	27
831	RSK2 is a new Pim2 target with pro-survival functions in FLT3-ITD-positive acute myeloid leukemia. <i>Leukemia</i> , 2018, 32, 597-605.	3.3	22
832	A quantitative assessment of the membrane-integral sub-proteome of a bacterial magnetic organelle. <i>Journal of Proteomics</i> , 2018, 172, 89-99.	1.2	36
833	Comparative proteomic analysis: SclR is importantly involved in carbohydrate metabolism in <i>Aspergillus oryzae</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 319-332.	1.7	8
834	Proteomic Analyses of Cysteine Redox in High-Fat-Fed and Fasted Mouse Livers: Implications for Liver Metabolic Homeostasis. <i>Journal of Proteome Research</i> , 2018, 17, 129-140.	1.8	24
835	Integrative transcriptome and proteome analyses define marked differences between <i>Neospora caninum</i> isolates throughout the tachyzoite lytic cycle. <i>Journal of Proteomics</i> , 2018, 180, 108-119.	1.2	23
836	Netrinomics reveals control of Arabidopsis seed storage proteins and proteases by the Arg/N-end rule pathway. <i>New Phytologist</i> , 2018, 218, 1106-1126.	3.5	44
837	Improved Prediction of Bovine Leucocyte Antigens (BoLA) Presented Ligands by Use of Mass-Spectrometry-Determined Ligand and in Vitro Binding Data. <i>Journal of Proteome Research</i> , 2018, 17, 559-567.	1.8	31
838	Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells. <i>Metabolic Engineering</i> , 2018, 45, 149-157.	3.6	27
839	MS Western, a Method of Multiplexed Absolute Protein Quantification is a Practical Alternative to Western Blotting. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 384-396.	2.5	32

#	ARTICLE	IF	CITATIONS
840	The interactome of intact mitochondria by cross-linking mass spectrometry provides evidence for coexisting respiratory supercomplexes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 216-232.	2.5	142
841	Temporal Proteomics of Inducible RNAi Lines of Clp Protease Subunits Identifies Putative Protease Substrates. <i>Plant Physiology</i> , 2018, 176, 1485-1508.	2.3	37
842	ELMOD1 Stimulates ARF6-GTP Hydrolysis to Stabilize Apical Structures in Developing Vestibular Hair Cells. <i>Journal of Neuroscience</i> , 2018, 38, 843-857.	1.7	16
843	Study of a novel agent for TCA precipitated proteins washing - comprehensive insights into the role of ethanol/HCl on molten globule state by multi-spectroscopic analyses. <i>Journal of Proteomics</i> , 2018, 173, 77-88.	1.2	11
844	Venom-gland transcriptomics and venom proteomics of the Hentz striped scorpion ( <i>Centruroides</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 14-29.	0.8	46
845	Rice Paddy Nitrospirae Carry and Express Genes Related to Sulfate Respiration: Proposal of the New Genus "Candidatus Sulfoibium". <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	83
846	Differential impacts of individual and combined exposures of deoxynivalenol and zearalenone on the HepaRG human hepatic cell proteome. <i>Journal of Proteomics</i> , 2018, 173, 89-98.	1.2	10
847	Nbeal2 interacts with Dock7, Sec16a, and Vac14. <i>Blood</i> , 2018, 131, 1000-1011.	0.6	29
848	Landscape of the regulatory elements for lysine 2-hydroxyisobutyrylation pathway. <i>Cell Research</i> , 2018, 28, 111-125.	5.7	89
849	Spectral Library Based Analysis of Arginine Phosphorylations in <i>Staphylococcus aureus</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 335-348.	2.5	41
850	How many proteins can be identified in a 2DE gel spot within an analysis of a complex human cancer tissue proteome?. <i>Electrophoresis</i> , 2018, 39, 965-980.	1.3	71
851	Lipopolysaccharide Upregulates Palmitoylated Enzymes of the Phosphatidylinositol Cycle: An Insight from Proteomic Studies. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 233-254.	2.5	39
852	Global Proteome Analysis Links Lysine Acetylation to Diverse Functions in <i>Oryza Sativa</i> . <i>Proteomics</i> , 2018, 18, 1700036.	1.3	37
853	Differential Content of Proteins, mRNAs, and miRNAs Suggests that MDSC and Their Exosomes May Mediate Distinct Immune Suppressive Functions. <i>Journal of Proteome Research</i> , 2018, 17, 486-498.	1.8	84
854	Epstein-Barr Virus Protein EB2 Stimulates Translation Initiation of mRNAs through Direct Interactions with both Poly(A)-Binding Protein and Eukaryotic Initiation Factor 4G. <i>Journal of Virology</i> , 2018, 92, .	1.5	15
855	Comprehensive Profiling of Lysine Acetylome in Baculovirus Infected Silkworm ( <i>Bombyx mori</i> ) Cells. <i>Proteomics</i> , 2018, 18, 1700133.	1.3	18
856	Quantitative proteomic analysis of deciduous molars during cap to bell transition in miniature pig. <i>Journal of Proteomics</i> , 2018, 172, 57-67.	1.2	10
857	Marked Differences in the Submandibular Salivary Proteome between Sardinian Alcohol-Preferring and Sardinian Alcohol-Non Preferring Rats Revealed by an Integrated Top-Down "Bottom-Up" Proteomic Platform. <i>Journal of Proteome Research</i> , 2018, 17, 455-469.	1.8	0



#	ARTICLE	IF	CITATIONS
858	Interrogating marine virus-host interactions and elemental transfer with BONCAT and nanoSIMS-based methods. <i>Environmental Microbiology</i> , 2018, 20, 671-692.	1.8	53
859	Spatially-Resolved Top-down Proteomics Bridged to MALDI MS Imaging Reveals the Molecular Physiome of Brain Regions. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 357-372.	2.5	36
860	Comparative Analyses of Data Independent Acquisition Mass Spectrometric Approaches: DIA, WiSIM-DIA, and Untargeted DIA. <i>Proteomics</i> , 2018, 18, 1700304.	1.3	71
861	Comprehensive identification of proteins binding to RNA G-quadruplex motifs in the 5' UTR of tumor-associated mRNAs. <i>Biochimie</i> , 2018, 144, 169-184.	1.3	41
862	Evaluating in Vitro Culture Medium of Gut Microbiome with Orthogonal Experimental Design and a Metaproteomics Approach. <i>Journal of Proteome Research</i> , 2018, 17, 154-163.	1.8	41
863	Proteomic profiling of <i>TGFBI</i> null mouse corneas reveals only minor changes in matrix composition supportive of <i>TGFBI</i> knockdown as therapy against linked corneal dystrophies. <i>FEBS Journal</i> , 2018, 285, 101-114.	2.2	24
864	Competitive Kinase Enrichment Proteomics Reveals that Abemaciclib Inhibits GSK3 $\beta$ and Activates WNT Signaling. <i>Molecular Cancer Research</i> , 2018, 16, 333-344.	1.5	33
865	In silico approaches for unveiling novel glycobiomarkers in cancer. <i>Journal of Proteomics</i> , 2018, 171, 95-106.	1.2	14
866	Quality control in mass spectrometry-based proteomics. <i>Mass Spectrometry Reviews</i> , 2018, 37, 697-711.	2.8	82
867	A mitochondrial proteomics view of complex I deficiency in <i>Candida albicans</i> . <i>Mitochondrion</i> , 2018, 38, 48-57.	1.6	24
868	Towards a one-stop solution for large-scale proteomics data analysis. <i>Science China Life Sciences</i> , 2018, 61, 351-354.	2.3	2
869	Proteomics and multivariate modelling reveal sex-specific alterations in distinct regions of human carotid atheroma. <i>Biology of Sex Differences</i> , 2018, 9, 54.	1.8	12
870	A proteomic dataset of secreted proteins by three <i>Staphylococcus saprophyticus</i> strains. <i>Data in Brief</i> , 2018, 21, 1472-1476.	0.5	0
871	Unbiased Proteomic Approach Identifies Unique and Coincidental Plasma Biomarkers in Repetitive mTBI and AD Pathogenesis. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 405.	1.7	9
872	Olfactory cleft proteome does not reflect olfactory performance in patients with idiopathic and postinfectious olfactory disorder: A pilot study. <i>Scientific Reports</i> , 2018, 8, 17554.	1.6	5
873	Comparison of Two Solid-Phase Extraction (SPE) Methods for the Identification and Quantification of Porcine Retinal Protein Markers by LC-MS/MS. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3847.	1.8	36
874	Coordinated regulation of transcription by CcpA and the <i>Staphylococcus aureus</i> two-component system HptRS. <i>PLoS ONE</i> , 2018, 13, e0207161.	1.1	13
875	Combined multivariate analysis and machine learning reveals a predictive module of metabolic stress response in <i>Arabidopsis thaliana</i> . <i>Molecular Omics</i> , 2018, 14, 437-449.	1.4	15

#	ARTICLE	IF	CITATIONS
876	Mesenchymal stem cells enhance tumorigenic properties of human glioblastoma through independent cell-cell communication mechanisms. <i>Oncotarget</i> , 2018, 9, 24766-24777.	0.8	52
877	TBK1 and IKK $\mu$ prevent TNF-induced cell death by RIPK1 phosphorylation. <i>Nature Cell Biology</i> , 2018, 20, 1389-1399.	4.6	198
878	The development of a new parameter for tracking post-transcriptional regulation allows the detailed map of the <i>Pseudomonas aeruginosa</i> Crc regulon. <i>Scientific Reports</i> , 2018, 8, 16793.	1.6	30
879	Endothelial cell rearrangements during vascular patterning require PI3-kinase-mediated inhibition of actomyosin contractility. <i>Nature Communications</i> , 2018, 9, 4826.	5.8	53
880	Accelerated Barocycler Lysis and Extraction Sample Preparation for Clinical Proteomics by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2019, 18, 399-405.	1.8	14
881	Plasma Functionalization of Polycaprolactone Nanofibers Changes Protein Interactions with Cells, Resulting in Increased Cell Viability. <i>ACS Applied Materials &amp; Interfaces</i> , 2018, 10, 41962-41977.	4.0	37
882	Differences in plasma fibrin clot composition in patients with thrombotic antiphospholipid syndrome compared with venous thromboembolism. <i>Scientific Reports</i> , 2018, 8, 17301.	1.6	25
883	Structural basis for activation of plasma-membrane Ca <sup>2+</sup> -ATPase by calmodulin. <i>Communications Biology</i> , 2018, 1, 206.	2.0	30
884	VDAC2 enables BAX to mediate apoptosis and limit tumor development. <i>Nature Communications</i> , 2018, 9, 4976.	5.8	110
885	Surface Exposure and Packing of Lipoproteins into Outer Membrane Vesicles Are Coupled Processes in <i>Bacteroides</i> . <i>MSphere</i> , 2018, 3, .	1.3	57
886	Specialisation events of fungal metacommunities exposed to a persistent organic pollutant are suggestive of augmented pathogenic potential. <i>Microbiome</i> , 2018, 6, 208.	4.9	16
887	Quantitative Proteomics Reveals Antibiotics Resistance Function of Outer Membrane Proteins in <i>Aeromonas hydrophila</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 390.	1.8	21
888	In-depth analysis of <i>Bacillus subtilis</i> proteome identifies new ORFs and traces the evolutionary history of modified proteins. <i>Scientific Reports</i> , 2018, 8, 17246.	1.6	22
889	Mapping the O $\alpha$ -glycoproteome using site-specific extraction of O $\alpha$ -linked glycopeptides (EXoO). <i>Molecular Systems Biology</i> , 2018, 14, e8486.	3.2	110
890	Proteome Investigation of Rat Lungs subjected to Ex Vivo Perfusion (EVLV). <i>Molecules</i> , 2018, 23, 3061.	1.7	20
891	Proteomic Analysis of Plasmodesmata From <i>Populus</i> Cell Suspension Cultures in Relation With Callose Biosynthesis. <i>Frontiers in Plant Science</i> , 2018, 9, 1681.	1.7	32
892	Protein Profiling of <i>Arabidopsis</i> Roots Treated With Humic Substances: Insights Into the Metabolic and Interactome Networks. <i>Frontiers in Plant Science</i> , 2018, 9, 1812.	1.7	41
893	Quantitative metaproteomics of medieval dental calculus reveals individual oral health status. <i>Nature Communications</i> , 2018, 9, 4744.	5.8	63

#	ARTICLE	IF	CITATIONS
894	Obesity shows preserved plasma proteome in large independent clinical cohorts. <i>Scientific Reports</i> , 2018, 8, 16981.	1.6	45
895	Interactome and Proteome Dynamics Uncover Immune Modulatory Associations of the Pathogen Sensing Factor cGAS. <i>Cell Systems</i> , 2018, 7, 627-642.e6.	2.9	34
896	Genomic and exoproteomic diversity in plant biomass degradation approaches among <i>Aspergilli</i> . <i>Studies in Mycology</i> , 2018, 91, 79-99.	4.5	24
897	SNAREs SYP121 and SYP122 Mediate the Secretion of Distinct Cargo Subsets. <i>Plant Physiology</i> , 2018, 178, 1679-1688.	2.3	56
898	Loss of the Mia40a oxidoreductase leads to hepato-pancreatic insufficiency in zebrafish. <i>PLoS Genetics</i> , 2018, 14, e1007743.	1.5	10
899	Recruitment of Cytosolic J-Proteins by TOM Receptors Promotes Mitochondrial Protein Biogenesis. <i>Cell Reports</i> , 2018, 25, 2036-2043.e5.	2.9	68
900	A Proteomics Approach to Profiling the Temporal Translational Response to Stress and Growth. <i>IScience</i> , 2018, 9, 367-381.	1.9	39
901	Assessing Automated Sample Preparation Technologies for High-Throughput Proteomics of Frozen Well Characterized Tissues from Swedish Biobanks. <i>Journal of Proteome Research</i> , 2019, 18, 548-556.	1.8	18
902	REX1 is the critical target of RNF12 in imprinted X chromosome inactivation in mice. <i>Nature Communications</i> , 2018, 9, 4752.	5.8	32
903	Intelligence Algorithms for Protein Classification by Mass Spectrometry. <i>BioMed Research International</i> , 2018, 2018, 1-11.	0.9	6
904	The Length Distribution and Multiple Specificity of Naturally Presented HLA-I Ligands. <i>Journal of Immunology</i> , 2018, 201, 3705-3716.	0.4	145
905	Food Perception Primes Hepatic ER Homeostasis via Melanocortin-Dependent Control of mTOR Activation. <i>Cell</i> , 2018, 175, 1321-1335.e20.	13.5	86
906	NuRD-interacting protein ZFP296 regulates genome-wide NuRD localization and differentiation of mouse embryonic stem cells. <i>Nature Communications</i> , 2018, 9, 4588.	5.8	22
907	Extraction and biomolecular analysis of dermal interstitial fluid collected with hollow microneedles. <i>Communications Biology</i> , 2018, 1, 173.	2.0	148
908	Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2534-2545.	2.5	602
909	Single Amino Acid Variant Discovery in Small Numbers of Cells. <i>Journal of Proteome Research</i> , 2019, 18, 417-425.	1.8	13
910	HLA-B57 micropolymorphism defines the sequence and conformational breadth of the immunopeptidome. <i>Nature Communications</i> , 2018, 9, 4693.	5.8	31
911	Laboratory strains of <i>Bacillus anthracis</i> exhibit pervasive alteration in expression of proteins related to sporulation under laboratory conditions relative to genetically related wild strains. <i>PLoS ONE</i> , 2018, 13, e0209120.	1.1	8

#	ARTICLE	IF	CITATIONS
912	Arabidopsis thaliana responds to colonisation of Piriformospora indica by secretion of symbiosis-specific proteins. PLoS ONE, 2018, 13, e0209658.	1.1	17
913	An Alliance of Gel-Based and Gel-Free Proteomic Techniques Displays Substantial Insight Into the Proteome of a Virulent and an Attenuated Histomonas meleagridis Strain. Frontiers in Cellular and Infection Microbiology, 2018, 8, 407.	1.8	14
914	Comparative Proteomic Analysis Reveals Elevated Capacity for Photosynthesis in Polyphenol Oxidase Expression-Silenced Clematis terniflora DC. Leaves. International Journal of Molecular Sciences, 2018, 19, 3897.	1.8	10
916	Archiving of Integrative Structural Models. Advances in Experimental Medicine and Biology, 2018, 1105, 261-272.	0.8	6
917	Increased Mitochondrial Protein Levels and Bioenergetics in the <i>Musculus Rectus Femoris</i> of Wfs1-Deficient Mice. Oxidative Medicine and Cellular Longevity, 2018, 2018, 1-12.	1.9	9
918	Iron Regulation in Clostridioides difficile. Frontiers in Microbiology, 2018, 9, 3183.	1.5	49
919	Absolute Quantification of Grapevine Red Blotch Virus in Grapevine Leaf and Petiole Tissues by Proteomics. Frontiers in Plant Science, 2018, 9, 1735.	1.7	10
920	Circadian Proteomic Analysis Uncovers Mechanisms of Post-Transcriptional Regulation in Metabolic Pathways. Cell Systems, 2018, 7, 613-626.e5.	2.9	93
921	Transcriptome and proteome profiling reveals stress-induced expression signatures of imiquimod-treated Tasmanian devil facial tumor disease (DFTD) cells. Oncotarget, 2018, 9, 15895-15914.	0.8	13
922	A quantitative proteomic analysis of cofilin phosphorylation in myeloid cells and its modulation using the LIM kinase inhibitor Pyr1. PLoS ONE, 2018, 13, e0208979.	1.1	11
923	Galectin-8 Favors the Presentation of Surface-Tethered Antigens by Stabilizing the B Cell Immune Synapse. Cell Reports, 2018, 25, 3110-3122.e6.	2.9	18
924	Differential Protein Expression During Growth on Medium Versus Long-Chain Alkanes in the Obligate Marine Hydrocarbon-Degrading Bacterium Thalassolituus oleivorans MIL-1. Frontiers in Microbiology, 2018, 9, 3130.	1.5	36
925	Quantitative Phosphoproteomic and System-Level Analysis of TOR Inhibition Unravel Distinct Organellar Acclimation in Chlamydomonas reinhardtii. Frontiers in Plant Science, 2018, 9, 1590.	1.7	29
926	Associating H <sub>2</sub> O <sub>2</sub> and NO-related changes in the proteome of <i>Mycobacterium smegmatis</i> with enhanced survival in macrophage. Emerging Microbes and Infections, 2018, 7, 1-17.	3.0	13
927	The ER membrane protein complex (EMC) promotes biogenesis of sterol-related enzymes maintaining cholesterol homeostasis. Journal of Cell Science, 2019, 132, .	1.2	73
928	Characterization of the <i>Citrobacter rodentium</i> Cpx regulon and its role in host infection. Molecular Microbiology, 2019, 111, 700-716.	1.2	15
929	Mass Spectrometry-Based Comprehensive Analysis of Pancreatic Cyst Fluids. BioMed Research International, 2018, 2018, 1-12.	0.9	9
930	Proteogenomic Analysis of Burkholderia Species Strains 25 and 46 Isolated from Uraniferous Soils Reveals Multiple Mechanisms to Cope with Uranium Stress. Cells, 2018, 7, 269.	1.8	25

#	ARTICLE	IF	CITATIONS
931	Characterization of the Blister Fluid Proteome for Pediatric Burn Classification. <i>Journal of Proteome Research</i> , 2018, 18, 69-85.	1.8	5
932	A novel lncRNA, TCONS_00006195, represses hepatocellular carcinoma progression by inhibiting enzymatic activity of ENO1. <i>Cell Death and Disease</i> , 2018, 9, 1184.	2.7	43
933	Identification of proteins responding to pathogen-infection in the red alga <i>Pyropia yezoensis</i> using iTRAQ quantitative proteomics. <i>BMC Genomics</i> , 2018, 19, 842.	1.2	12
934	Colonic Proteome Signature in Immunoproteasome-Deficient Stressed Mice and Its Relevance for Irritable Bowel Syndrome. <i>Journal of Proteome Research</i> , 2018, 18, 478-492.	1.8	4
935	Microtubule-Based Control of Motor-Clutch System Mechanics in Glioma Cell Migration. <i>Cell Reports</i> , 2018, 25, 2591-2604.e8.	2.9	37
936	Discovery and Quantification of Nonhuman Proteins in Human Milk. <i>Journal of Proteome Research</i> , 2019, 18, 225-238.	1.8	24
937	Site-Specific K63 Ubiquitinomics Provides Insights into Translation Regulation under Stress. <i>Journal of Proteome Research</i> , 2019, 18, 309-318.	1.8	29
938	Mapping the Proteome of the Synaptic Cleft through Proximity Labeling Reveals New Cleft Proteins. <i>Proteomes</i> , 2018, 6, 48.	1.7	62
939	Ultraviolet Photodissociation of ESI- and MALDI-Generated Protein Ions on a Q-Exactive Mass Spectrometer. <i>Journal of Proteome Research</i> , 2018, 18, 557-564.	1.8	9
940	dbDEPC 3.0: the database of differentially expressed proteins in human cancer with multi-level annotation and drug indication. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, .	1.4	17
941	Proteomic profiling of senescent human diploid fibroblasts treated with gamma-tocotrienol. <i>BMC Complementary and Alternative Medicine</i> , 2018, 18, 314.	3.7	4
942	A pipeline for identifying endogenous neuropeptides from spectral archives. <i>International Journal of Data Mining and Bioinformatics</i> , 2018, 20, 12.	0.1	0
943	A Well-Controlled BioID Design for Endogenous Bait Proteins. <i>Journal of Proteome Research</i> , 2019, 18, 95-106.	1.8	13
944	Xylem Sap Proteomics Reveals Distinct Differences Between R Gene- and Endophyte-Mediated Resistance Against <i>Fusarium Wilt</i> Disease in Tomato. <i>Frontiers in Microbiology</i> , 2018, 9, 2977.	1.5	63
945	A Combination of Proteomic Approaches Identifies A Panel of Circulating Extracellular Vesicle Proteins Related to the Risk of Suffering Cardiovascular Disease in Obese Patients. <i>Proteomics</i> , 2019, 19, e1800248.	1.3	16
946	Toward the Molecular Deciphering of <i>Pomacea canaliculata</i> Immunity: First Proteomic Analysis of Circulating Hemocytes. <i>Proteomics</i> , 2019, 19, e1800314.	1.3	20
947	Proteome and transcriptome profiling of equine myofibrillar myopathy identifies diminished peroxiredoxin 6 and altered cysteine metabolic pathways. <i>Physiological Genomics</i> , 2018, 50, 1036-1050.	1.0	15
948	Generation and Proteome Profiling of PBMC-Originated, iPSC-Derived Corneal Endothelial Cells. , 2018, 59, 2437.		24

#	ARTICLE	IF	CITATIONS
949	Characterization and metabolic synthetic lethal testing in a new model of SDH-loss familial pheochromocytoma and paraganglioma. <i>Oncotarget</i> , 2018, 9, 6109-6127.	0.8	13
950	Filter-Aided Sample Preparation Procedure for Mass Spectrometric Analysis of Plant Histones. <i>Frontiers in Plant Science</i> , 2018, 9, 1373.	1.7	6
951	Growth of Cyanobacteria Is Constrained by the Abundance of Light and Carbon Assimilation Proteins. <i>Cell Reports</i> , 2018, 25, 478-486.e8.	2.9	97
952	glyXtool <sup>MS</sup> : An Open-Source Pipeline for Semiautomated Analysis of Glycopeptide Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2018, 90, 11908-11916.	3.2	35
953	A mitochondrial proteome profile indicative of type 2 diabetes mellitus in skeletal muscles. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-14.	3.2	34
954	Systematic analysis of synergistic proteome modulations in a drug combination of cisplatin and MLN4924. <i>Molecular Omics</i> , 2018, 14, 450-457.	1.4	3
955	Glycoproteomic Alterations in Drug-Resistant Nonsmall Cell Lung Cancer Cells Revealed by Lectin Magnetic Nanoprobe-Based Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 3761-3773.	1.8	26
956	Heterologous expression and characterization of a novel serine protease from <i>Daphnia magna</i> : A possible role in susceptibility to toxic cyanobacteria. <i>Aquatic Toxicology</i> , 2018, 205, 140-147.	1.9	7
957	Differential Proteome Analysis of Human Neuroblastoma Xenograft Primary Tumors and Matched Spontaneous Distant Metastases. <i>Scientific Reports</i> , 2018, 8, 13986.	1.6	7
958	Proteomic analysis identifies highly expressed plasma membrane proteins for detection and therapeutic targeting of specific breast cancer subtypes. <i>Clinical Proteomics</i> , 2018, 15, 30.	1.1	7
959	Global Profiling of Lysine Acetylation in <i>Borrelia burgdorferi</i> B31 Reveals Its Role in Central Metabolism. <i>Frontiers in Microbiology</i> , 2018, 9, 2036.	1.5	29
960	Robust determination of differential abundance in shotgun proteomics using nonparametric statistics. <i>Molecular Omics</i> , 2018, 14, 424-436.	1.4	0
961	Cell Wall and Whole Cell Proteomes Define Flocculation and Fermentation Behavior of Yeast. <i>Fermentation</i> , 2018, 4, 80.	1.4	4
962	Proteome analysis reveals a role of rainbow trout lymphoid organs during <i>Yersinia ruckeri</i> infection process. <i>Scientific Reports</i> , 2018, 8, 13998.	1.6	18
963	Next Steps on in Silico 2DE Analyses of Chromosome 18 Proteoforms. <i>Journal of Proteome Research</i> , 2018, 17, 4085-4096.	1.8	3
964	Repetitive somatic embryogenesis induced cytological and proteomic changes in embryogenic lines of <i>Pseudotsuga menziesii</i> [Mirb.]. <i>BMC Plant Biology</i> , 2018, 18, 164.	1.6	33
965	Microscopic and Proteomic Analysis of Dissected Developing Barley Endosperm Layers Reveals the Starchy Endosperm as Prominent Storage Tissue for ER-Derived Hordeins Alongside the Accumulation of Barley Protein Disulfide Isomerase (HvPDIL1-1). <i>Frontiers in Plant Science</i> , 2018, 9, 1248.	1.7	18
966	Chemical genetic identification of <i>CDKL</i> 5 substrates reveals its role in neuronal microtubule dynamics. <i>EMBO Journal</i> , 2018, 37, .	3.5	57

#	ARTICLE	IF	CITATIONS
967	Nonsense-mediated mRNA decay involves two distinct Upf1-bound complexes. <i>EMBO Journal</i> , 2018, 37, .	3.5	37
968	Methionine supplementation stimulates mitochondrial respiration. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2018, 1865, 1901-1913.	1.9	17
969	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	1.8	47
970	The evolutionary conserved FOXJ1 target gene <i>Fam183b</i> is essential for motile cilia in <i>Xenopus</i> but dispensable for ciliary function in mice. <i>Scientific Reports</i> , 2018, 8, 14678.	1.6	14
971	Quantitative phosphoproteomic analysis identifies novel functional pathways of tumor suppressor DLC1 in estrogen receptor positive breast cancer. <i>PLoS ONE</i> , 2018, 13, e0204658.	1.1	11
972	Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. <i>Journal of Proteome Research</i> , 2018, 17, 4042-4050.	1.8	41
973	Feasibility of a plasma bioassay to assess oxidative protection of low-density lipoproteins by high-density lipoproteins. <i>Journal of Clinical Lipidology</i> , 2018, 12, 1539-1548.	0.6	17
974	Caloric restriction promotes functional changes involving short-chain fatty acid biosynthesis in the rat gut microbiota. <i>Scientific Reports</i> , 2018, 8, 14778.	1.6	57
975	Should I stay or should I go? The settlement-inducing protein complex guides barnacle settlement decisions. <i>Journal of Experimental Biology</i> , 2018, 221, .	0.8	10
976	Comparative proteomics of the two <i>T. brucei</i> PABPs suggests that PABP2 controls bulk mRNA. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006679.	1.3	26
977	Nut Directs p300-Dependent, Genome-Wide H4 Hyperacetylation in Male Germ Cells. <i>Cell Reports</i> , 2018, 24, 3477-3487.e6.	2.9	69
978	Preassembled GPCR signaling complexes mediate distinct cellular responses to ultralow ligand concentrations. <i>Science Signaling</i> , 2018, 11, .	1.6	36
979	Individual Variability of Protein Expression in Human Tissues. <i>Journal of Proteome Research</i> , 2018, 17, 3914-3922.	1.8	15
980	C16-ceramide is a natural regulatory ligand of p53 in cellular stress response. <i>Nature Communications</i> , 2018, 9, 4149.	5.8	76
981	OpenProt: a more comprehensive guide to explore eukaryotic coding potential and proteomes. <i>Nucleic Acids Research</i> , 2019, 47, D403-D410.	6.5	71
982	In-Search Assignment of Monoisotopic Peaks Improves the Identification of Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2018, 17, 3923-3931.	1.8	36
983	PRP4KA, a Putative Spliceosomal Protein Kinase, Is Important for Alternative Splicing and Development in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2018, 210, 1267-1285.	1.2	20
984	<i>Slc7a5</i> regulates <i>Kv1.2</i> channels and modifies functional outcomes of epilepsy-linked channel mutations. <i>Nature Communications</i> , 2018, 9, 4417.	5.8	24

#	ARTICLE	IF	CITATIONS
985	Amplification of the Melanocortin-1 Receptor in Nephrotic Syndrome Identifies a Target for Podocyte Cytoskeleton Stabilization. <i>Scientific Reports</i> , 2018, 8, 15731.	1.6	15
986	Clostridial Butyrate Biosynthesis Enzymes Are Significantly Depleted in the Gut Microbiota of Nonobese Diabetic Mice. <i>MSphere</i> , 2018, 3, .	1.3	22
987	LRP1 (Low-Density Lipoprotein Receptor-Related Protein 1) Regulates Smooth Muscle Contractility by Modulating Ca <sup>2+</sup> Signaling and Expression of Cytoskeleton-Related Proteins. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 2651-2664.	1.1	37
988	Mapping of equine mesenchymal stromal cell surface proteomes for identification of specific markers using proteomics and gene expression analysis: an in vitro cross-sectional study. <i>Stem Cell Research and Therapy</i> , 2018, 9, 288.	2.4	14
989	Proteomic analysis of <i>Lactobacillus casei</i> GCRL163 cell-free extracts reveals a SecB homolog and other biomarkers of prolonged heat stress. <i>PLoS ONE</i> , 2018, 13, e0206317.	1.1	15
990	<sc>FMRP</sc> recruitment of Î²â€œatenin to the translation preâ€œinitiation complex represses translation. <i>EMBO Reports</i> , 2018, 19, .	2.0	15
991	Inhibition of histone methyltransferase EZH2 in <i>Schistosoma mansoni</i> in vitro by GSK343 reduces egg laying and decreases the expression of genes implicated in DNA replication and noncoding RNA metabolism. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006873.	1.3	25
992	Proteome and microbiota analysis reveals alterations of liver-gut axis under different stocking density of Peking ducks. <i>PLoS ONE</i> , 2018, 13, e0198985.	1.1	15
993	Structural dynamics of the E6AP/UBE3A-E6-p53 enzyme-substrate complex. <i>Nature Communications</i> , 2018, 9, 4441.	5.8	52
994	Comparative Glycomics of Immunoglobulin A and G From Saliva and Plasma Reveals Biomarker Potential. <i>Frontiers in Immunology</i> , 2018, 9, 2436.	2.2	59
995	GASP and FASP are Complementary for LCâ€œMS/MS Proteomic Analysis of Drugâ€œMetabolizing Enzymes and Transporters in Pig Liver. <i>Proteomics</i> , 2018, 18, e1800200.	1.3	12
996	Proteomic Profiling of <i>Burkholderia thailandensis</i> During Host Infection Using Bio-Orthogonal Noncanonical Amino Acid Tagging (BONCAT). <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 370.	1.8	10
997	Identification of Potential Plasma Biomarkers for Abdominal Aortic Aneurysm Using Tandem Mass Tag Quantitative Proteomics. <i>Proteomes</i> , 2018, 6, 43.	1.7	9
998	Discovery of RNA-binding proteins and characterization of their dynamic responses by enhanced RNA interactome capture. <i>Nature Communications</i> , 2018, 9, 4408.	5.8	138
999	Characterization of a L-Gulonolactone Oxidase Like Protein in the Floral Nectar of <i>Mucuna sempervirens</i> , Fabaceae. <i>Frontiers in Plant Science</i> , 2018, 9, 1109.	1.7	6
1000	Targeting CDK9 Reactivates Epigenetically Silenced Genes in Cancer. <i>Cell</i> , 2018, 175, 1244-1258.e26.	13.5	182
1001	Raw N-glycan mass spectrometry imaging data on formalin-fixed mouse kidney. <i>Data in Brief</i> , 2018, 21, 185-188.	0.5	4
1002	Disrupted alternative splicing for genes implicated in splicing and ciliogenesis causes PRPF31 retinitis pigmentosa. <i>Nature Communications</i> , 2018, 9, 4234.	5.8	158



#	ARTICLE	IF	CITATIONS
1003	Candidate <i>Treponema pallidum</i> biomarkers uncovered in urine from individuals with syphilis using mass spectrometry. <i>Future Microbiology</i> , 2018, 13, 1497-1510.	1.0	14
1004	Toward the Quantitative Characterization of Arginine Phosphorylations in <i>Staphylococcus aureus</i> . <i>Journal of Proteome Research</i> , 2019, 18, 265-279.	1.8	10
1005	Dishevelled enables casein kinase 1 $\alpha$ -mediated phosphorylation of Frizzled 6 required for cell membrane localization. <i>Journal of Biological Chemistry</i> , 2018, 293, 18477-18493.	1.6	13
1006	Specific Enrichment and Proteomics Analysis of <i>Escherichia coli</i> Persisters from Rifampin Pretreatment. <i>Journal of Proteome Research</i> , 2018, 17, 3984-3996.	1.8	47
1007	Proteome Profiling of Developing Murine Lens Through Mass Spectrometry. , 2018, 59, 100.		21
1008	High-throughput proteomic profiling of the fish liver following bacterial infection. <i>BMC Genomics</i> , 2018, 19, 719.	1.2	68
1009	Transcriptome and Proteome of Fish-Pathogenic <i>Streptococcus agalactiae</i> Are Modulated by Temperature. <i>Frontiers in Microbiology</i> , 2018, 9, 2639.	1.5	21
1010	The proteomic study of serially passaged human skin fibroblast cells uncovers down-regulation of the chromosome condensin complex proteins involved in replicative senescence. <i>Biochemical and Biophysical Research Communications</i> , 2018, 505, 1112-1120.	1.0	6
1011	S-palmitoylation Is Required for the Control of Growth Cone Morphology of DRG Neurons by CNP-Induced cGMP Signaling. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 345.	1.4	13
1012	Ubiquitin-Independent Disassembly by a p97 AAA-ATPase Complex Drives PP1 Holoenzyme Formation. <i>Molecular Cell</i> , 2018, 72, 766-777.e6.	4.5	62
1013	A Metabolic Labeling Strategy for Relative Protein Quantification in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2371.	1.5	4
1014	Acid bone lysate activates TGF $\beta$ 2 signalling in human oral fibroblasts. <i>Scientific Reports</i> , 2018, 8, 16065.	1.6	23
1015	Activated hepatic stellate cells promote epithelial-to-mesenchymal transition in hepatocellular carcinoma through transglutaminase 2-induced pseudohypoxia. <i>Communications Biology</i> , 2018, 1, 168.	2.0	25
1016	Chromatin-mediated regulators of meiotic recombination revealed by proteomics of a recombination hotspot. <i>Epigenetics and Chromatin</i> , 2018, 11, 64.	1.8	20
1017	Aspartyl Protease 5 Matures Dense Granule Proteins That Reside at the Host-Parasite Interface in <i>Toxoplasma gondii</i> . <i>MBio</i> , 2018, 9, .	1.8	46
1018	Peanut Stunt Virus and Its Satellite RNA Trigger Changes in Phosphorylation in <i>N. benthamiana</i> Infected Plants at the Early Stage of the Infection. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3223.	1.8	7
1019	Integrated dataset on acute phase protein response in chicken challenged with <i>Escherichia coli</i> lipopolysaccharide endotoxin. <i>Data in Brief</i> , 2018, 21, 684-699.	0.5	11
1020	Revealing the cellular degradome by mass spectrometry analysis of proteasome-cleaved peptides. <i>Nature Biotechnology</i> , 2018, 36, 1110-1116.	9.4	33

#	ARTICLE	IF	CITATIONS
1021	Environmentâ€driven changes of mRNA and protein levels in <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2018, 20, 3952-3963.	1.8	19
1022	Module-detection approaches for the integration of multilevel omics data highlight the comprehensive response of <i>Aspergillus fumigatus</i> to caspofungin. <i>BMC Systems Biology</i> , 2018, 12, 88.	3.0	11
1023	Knockout of the Hmt1p Arginine Methyltransferase in <i>Saccharomyces cerevisiae</i> Leads to the Dysregulation of Phosphate-associated Genes and Processes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2462-2479.	2.5	8
1024	A comparative analysis of label-free liquid chromatography-mass spectrometry liver proteomic profiles highlights metabolic differences between pig breeds. <i>PLoS ONE</i> , 2018, 13, e0199649.	1.1	13
1025	Proteomics reveals signal peptide features determining the client specificity in human TRAP-dependent ER protein import. <i>Nature Communications</i> , 2018, 9, 3765.	5.8	68
1026	Functional Proteomics and Deep Network Interrogation Reveal a Complex Mechanism of Action of Midostaurin in Lung Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2434-2447.	2.5	17
1027	In vivo cross-linking supports a head-to-tail mechanism for regulation of the plant plasma membrane P-type H <sup>+</sup> -ATPase. <i>Journal of Biological Chemistry</i> , 2018, 293, 17095-17106.	1.6	18
1028	Coupling of bone resorption and formation by RANKL reverse signalling. <i>Nature</i> , 2018, 561, 195-200.	13.7	376
1029	The Cellosaurus, a Cell-Line Knowledge Resource. <i>Journal of Biomolecular Techniques</i> , 2018, 29, 25-38.	0.8	437
1030	Machine Learning Predicts the Yeast Metabolome from the Quantitative Proteome of Kinase Knockouts. <i>Cell Systems</i> , 2018, 7, 269-283.e6.	2.9	80
1031	Proteome Profiling of Primary Pancreatic Ductal Adenocarcinomas Undergoing Additive Chemoradiation Link ALDH1A1 to Early Local Recurrence and Chemoradiation Resistance. <i>Translational Oncology</i> , 2018, 11, 1307-1322.	1.7	19
1032	Oocyte-specific maternal Slbp2 is required for replication-dependent histone storage and early nuclear cleavage in zebrafish oogenesis and embryogenesis. <i>Rna</i> , 2018, 24, 1738-1748.	1.6	16
1033	Metabolic Reprogramming of <i>Clostridioides difficile</i> During the Stationary Phase With the Induction of Toxin Production. <i>Frontiers in Microbiology</i> , 2018, 9, 1970.	1.5	67
1034	Human Dystrophin Structural Changes upon Binding to Anionic Membrane Lipids. <i>Biophysical Journal</i> , 2018, 115, 1231-1239.	0.2	14
1035	Fast Open Modification Spectral Library Searching through Approximate Nearest Neighbor Indexing. <i>Journal of Proteome Research</i> , 2018, 17, 3463-3474.	1.8	69
1036	Partial enzymatic reactions: A missed opportunity in proteomics research. <i>Rapid Communications in Mass Spectrometry</i> , 2018, 32, 2065-2073.	0.7	9
1037	Shotgun Proteomics Analysis of Saliva and Salivary Gland Tissue from the Common Octopus <i>Octopus vulgaris</i> . <i>Journal of Proteome Research</i> , 2018, 17, 3866-3876.	1.8	15
1038	A Golgi UDP-GlcNAc transporter delivers substrates for N-linked glycans and sphingolipids. <i>Nature Plants</i> , 2018, 4, 792-801.	4.7	27

#	ARTICLE	IF	CITATIONS
1039	Comparative Hippocampal Synaptic Proteomes of Rodents and Primates: Differences in Neuroplasticity-Related Proteins. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 364.	1.4	43
1040	Proteomic Response to Thaxtomin Phytotoxin Elicitor Cellobiose and to Deletion of Cellulose Utilization Regulator CebR in <i>Streptomyces scabies</i> . <i>Journal of Proteome Research</i> , 2018, 17, 3837-3852.	1.8	14
1041	A variant NuRD complex containing PWWP2A/B excludes MBD2/3 to regulate transcription at active genes. <i>Nature Communications</i> , 2018, 9, 3798.	5.8	40
1042	Differential Roles of the Thylakoid Luminal Deg Protease Homologs in Chloroplast Proteostasis. <i>Plant Physiology</i> , 2018, 178, 1065-1080.	2.3	22
1043	Phosphoproteomic-based kinase profiling early in influenza virus infection identifies GRK2 as antiviral drug target. <i>Nature Communications</i> , 2018, 9, 3679.	5.8	44
1044	The kinases HipA and HipA7 phosphorylate different substrate pools in <i>Escherichia coli</i> to promote multidrug tolerance. <i>Science Signaling</i> , 2018, 11, .	1.6	52
1045	Characterization of Cerebrospinal Fluid via Data-Independent Acquisition Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 3418-3430.	1.8	27
1046	Evaluation of Unconventional Protein Secretion by <i>Saccharomyces cerevisiae</i> and other Fungi. <i>Cells</i> , 2018, 7, 128.	1.8	43
1047	An Atypical Parvovirus Drives Chronic Tubulointerstitial Nephropathy and Kidney Fibrosis. <i>Cell</i> , 2018, 175, 530-543.e24.	13.5	89
1048	Identification of degraded bone and tooth splinters from arid environments using palaeoproteomics. <i>Palaeogeography, Palaeoclimatology, Palaeoecology</i> , 2018, 511, 472-482.	1.0	14
1049	Label-Free Proteomic Approach to Characterize Protease-Dependent and -Independent Effects of <i>SarA</i> Inactivation on the <i>Staphylococcus aureus</i> Exoproteome. <i>Journal of Proteome Research</i> , 2018, 17, 3384-3395.	1.8	18
1050	Structural determinants of Rab11 activation by the guanine nucleotide exchange factor SH3BP5. <i>Nature Communications</i> , 2018, 9, 3772.	5.8	29
1051	Proteomics Reveals Scope of Mycolactone-mediated Sec61 Blockade and Distinctive Stress Signature. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1750-1765.	2.5	50
1052	Data for Tandem Mass Tag (TMT) proteomic analysis of the pancreas during the early phase of experimental pancreatitis. <i>Data in Brief</i> , 2018, 20, 779-783.	0.5	0
1053	Proteomic Analysis of the Function of a Novel Cold-Regulated Multispanning Transmembrane Protein COR413-PM1 in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2572.	1.8	22
1054	Evaluation of sample preparation methods for mass spectrometry-based proteomic analysis of barley leaves. <i>Plant Methods</i> , 2018, 14, 72.	1.9	31
1055	Large-Scale Reanalysis of Publicly Available HeLa Cell Proteomics Data in the Context of the Human Proteome Project. <i>Journal of Proteome Research</i> , 2018, 17, 4160-4170.	1.8	21
1056	The Protein Coded by a Short Open Reading Frame, Not by the Annotated Coding Sequence, Is the Main Gene Product of the Dual-Coding Gene MIEF1. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2402-2411.	2.5	44

#	ARTICLE	IF	CITATIONS
1057	Argentilactone Molecular Targets in <i>Paracoccidioides brasiliensis</i> Identified by Chemoproteomics. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	10
1058	The NAD <sup>+</sup> Salvage Pathway Supports PHGDH-Driven Serine Biosynthesis. <i>Cell Reports</i> , 2018, 24, 2381-2391.e5.	2.9	47
1059	Species identification of ancient Lithuanian fish remains using collagen fingerprinting. <i>Journal of Archaeological Science</i> , 2018, 98, 102-111.	1.2	33
1060	MT-MAMS: Protein Methyltransferase Motif Analysis by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 3485-3491.	1.8	23
1061	In vivo phosphoproteomics reveals kinase activity profiles that predict treatment outcome in triple-negative breast cancer. <i>Nature Communications</i> , 2018, 9, 3501.	5.8	45
1062	Chemical Crosslinking Mass Spectrometry Reveals the Conformational Landscape of the Activation Helix of PPAR $\beta$ ; a Model for Ligand-Dependent Antagonism. <i>Structure</i> , 2018, 26, 1431-1439.e6.	1.6	24
1063	Quantitative Proteomics Implicates Rictor/mTORC2 in Cell Adhesion. <i>Journal of Proteome Research</i> , 2018, 17, 3360-3369.	1.8	20
1064	Global phosphoproteomic analysis identifies SRMS-regulated secondary signaling intermediates. <i>Proteome Science</i> , 2018, 16, 16.	0.7	10
1065	The BioStudies databaseâ€”one stop shop for all data supporting a life sciences study. <i>Nucleic Acids Research</i> , 2018, 46, D1266-D1270.	6.5	112
1066	Switching off IMMP2L signaling drives senescence via simultaneous metabolic alteration and blockage of cell death. <i>Cell Research</i> , 2018, 28, 625-643.	5.7	37
1067	A bacteriophage enzyme induces bacterial metabolic perturbation that confers a novel promiscuous function. <i>Nature Ecology and Evolution</i> , 2018, 2, 1321-1330.	3.4	19
1068	MTF2 recruits Polycomb Repressive Complex 2 by helical-shape-selective DNA binding. <i>Nature Genetics</i> , 2018, 50, 1002-1010.	9.4	147
1069	The $\beta$ 3 $\alpha$ 1 Integrin endothelial adhesome regulates microtubuleâ€”dependent cell migration. <i>EMBO Reports</i> , 2018, 19, .	2.0	25
1070	Proximity Labeling by a Recombinant APEX2â€”FGF1 Fusion Protein Reveals Interaction of FGF1 with the Proteoglycans CD44 and CSPG4. <i>Biochemistry</i> , 2018, 57, 3807-3816.	1.2	14
1071	SILAC-based phosphoproteomics reveals new PP2A-Cdc55-regulated processes in budding yeast. <i>GigaScience</i> , 2018, 7, .	3.3	24
1072	The BCKDH Kinase and Phosphatase Integrate BCAA and Lipid Metabolism via Regulation of ATP-Citrate Lyase. <i>Cell Metabolism</i> , 2018, 27, 1281-1293.e7.	7.2	222
1073	Ablation of Sirtuin5 in the postnatal mouse heart results in protein succinylation and normal survival in response to chronic pressure overload. <i>Journal of Biological Chemistry</i> , 2018, 293, 10630-10645.	1.6	31
1074	Molecular modularity and asymmetry of the molluscan mantle revealed by a gene expression atlas. <i>GigaScience</i> , 2018, 7, .	3.3	22

#	ARTICLE	IF	CITATIONS
1075	Quantitative proteomics and systems analysis of cultured H9C2 cardiomyoblasts during differentiation over time supports a "function follows form" model of differentiation. <i>Molecular Omics</i> , 2018, 14, 181-196.	1.4	9
1076	LRRK2 is a negative regulator of <i>Mycobacterium tuberculosis</i> phagosome maturation in macrophages. <i>EMBO Journal</i> , 2018, 37, .	3.5	140
1077	Immunopeptidomic Profiling of HLA-A2-Positive Triple Negative Breast Cancer Identifies Potential Immunotherapy Target Antigens. <i>Proteomics</i> , 2018, 18, e1700465.	1.3	37
1078	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018, 9, 1887.	5.8	70
1079	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. <i>Nature</i> , 2018, 557, 739-743.	13.7	169
1080	Nup133 Is Required for Proper Nuclear Pore Basket Assembly and Dynamics in Embryonic Stem Cells. <i>Cell Reports</i> , 2018, 23, 2443-2454.	2.9	23
1081	Glutaredoxin Deletion Shortens Chronological Life Span in <i>Saccharomyces cerevisiae</i> via ROS-Mediated Ras/PKA Activation. <i>Journal of Proteome Research</i> , 2018, 17, 2318-2327.	1.8	16
1082	Functional Proteomic Profiling of Secreted Serine Proteases in Health and Inflammatory Bowel Disease. <i>Scientific Reports</i> , 2018, 8, 7834.	1.6	67
1083	Adipose tissue proteomic analyses to study puberty in Brahman heifers. <i>Journal of Animal Science</i> , 2018, 96, 2392-2398.	0.2	21
1084	The exon-intron gene structure upstream of the initiation codon predicts translation efficiency. <i>Nucleic Acids Research</i> , 2018, 46, 4575-4591.	6.5	23
1085	Quantitative Assessment of Urea In-Solution Lys-C/Trypsin Digestions Reveals Superior Performance at Room Temperature over Traditional Proteolysis at 37 °C. <i>Journal of Proteome Research</i> , 2018, 17, 2556-2561.	1.8	32
1086	Fermentative <i>Spirochaetes</i> mediate necromass recycling in anoxic hydrocarbon-contaminated habitats. <i>ISME Journal</i> , 2018, 12, 2039-2050.	4.4	74
1087	ProteomeTools: Systematic Characterization of 21 Post-translational Protein Modifications by Liquid Chromatography Tandem Mass Spectrometry (LC-MS/MS) Using Synthetic Peptides. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1850-1863.	2.5	78
1088	Extended investigation of tube-gel sample preparation: a versatile and simple choice for high throughput quantitative proteomics. <i>Scientific Reports</i> , 2018, 8, 8260.	1.6	3
1089	Biochemical Characterization of Isoniazid-resistant <i>Mycobacterium tuberculosis</i> : Can the Analysis of Clonal Strains Reveal Novel Targetable Pathways?. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1685-1701.	2.5	19
1090	Determining the glycation site specificity of human holo-transferrin. <i>Journal of Inorganic Biochemistry</i> , 2018, 186, 95-102.	1.5	4
1091	Secretory kinase Fam20C tunes endoplasmic reticulum redox state via phosphorylation of Ero1. <i>EMBO Journal</i> , 2018, 37, .	3.5	38
1092	Comparative two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) of human milk to identify dysregulated proteins in breast cancer. <i>Electrophoresis</i> , 2018, 39, 1723-1734.	1.3	22

#	ARTICLE	IF	CITATIONS
1093	NuRD and CAF-1-mediated silencing of the D4Z4 array is modulated by DUX4-induced MBD3L proteins. <i>ELife</i> , 2018, 7, .	2.8	47
1094	Label-free quantitative proteomic analysis reveals muscle contraction and metabolism proteins linked to ultimate pH in bovine skeletal muscle. <i>Meat Science</i> , 2018, 145, 209-219.	2.7	38
1095	Activity-Dependent Degradation of the Nascentome by the Neuronal Membrane Proteasome. <i>Molecular Cell</i> , 2018, 71, 169-177.e6.	4.5	61
1096	Rapid Cue-Specific Remodeling of the Nascent Axonal Proteome. <i>Neuron</i> , 2018, 99, 29-46.e4.	3.8	136
1097	Cone Snail Glutaminy Cyclase Sequences from Transcriptomic Analysis and Mass Spectrometric Characterization of Two Pyroglutamyl Conotoxins. <i>Journal of Proteome Research</i> , 2018, 17, 2695-2703.	1.8	10
1098	Ultrafiltration and size exclusion chromatography combined with asymmetrical flow field fractionation for the isolation and characterisation of extracellular vesicles from urine. <i>Journal of Extracellular Vesicles</i> , 2018, 7, 1490143.	5.5	103
1099	Urinary Proteome Analysis Identified Neprilysin and VCAM as Proteins Involved in Diabetic Nephropathy. <i>Journal of Diabetes Research</i> , 2018, 2018, 1-12.	1.0	24
1100	Interrogation of the Gulf toadfish intestinal proteome response to hypersalinity exposure provides insights into osmoregulatory mechanisms and regulation of carbonate mineral precipitation. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 27, 66-76.	0.4	4
1101	Revealing the immune perturbation of black phosphorus nanomaterials to macrophages by understanding the protein corona. <i>Nature Communications</i> , 2018, 9, 2480.	5.8	152
1102	The plant cell wall integrity maintenance and immune signaling systems cooperate to control stress responses in <i>Arabidopsis thaliana</i> . <i>Science Signaling</i> , 2018, 11, .	1.6	178
1103	Novel low-abundance allergens from mango via combinatorial peptide libraries treatment: A proteomics study. <i>Food Chemistry</i> , 2018, 269, 652-660.	4.2	25
1104	Quantifying and Localizing the Mitochondrial Proteome Across Five Tissues in A Mouse Population. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1766-1777.	2.5	50
1105	Temperature-induced changes in the wheat phosphoproteome reveal temperature-regulated interconversion of phosphoforms. <i>Journal of Experimental Botany</i> , 2018, 69, 4609-4624.	2.4	30
1106	Inner ear exosomes and their potential use as biomarkers. <i>PLoS ONE</i> , 2018, 13, e0198029.	1.1	25
1107	Dissecting ribosomal particles throughout the kingdoms of life using advanced hybrid mass spectrometry methods. <i>Nature Communications</i> , 2018, 9, 2493.	5.8	67
1108	Spatially Resolved Proteome Mapping of Laser Capture Microdissected Tissue with Automated Sample Transfer to Nanodroplets. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1864-1874.	2.5	105
1109	Embryogenic Competence Acquisition in Sugar Cane Callus Is Associated with Differential H <sup>+</sup> -Pump Abundance and Activity. <i>Journal of Proteome Research</i> , 2018, 17, 2767-2779.	1.8	21
1111	Time- and polarity-dependent proteomic changes associated with homeostatic scaling at central synapses. <i>ELife</i> , 2018, 7, .	2.8	49

#	ARTICLE	IF	CITATIONS
1112	Proteomic analysis of S-nitrosylated nuclear proteins in rat cortical neurons. <i>Science Signaling</i> , 2018, 11, .	1.6	22
1113	Mitochondrial CoQ deficiency is a common driver of mitochondrial oxidants and insulin resistance. <i>ELife</i> , 2018, 7, .	2.8	91
1114	Cluster-assembled zirconia substrates promote long-term differentiation and functioning of human islets of Langerhans. <i>Scientific Reports</i> , 2018, 8, 9979.	1.6	37
1115	A System-wide Approach to Monitor Responses to Synergistic BRAF and EGFR Inhibition in Colorectal Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1892-1908.	2.5	13
1116	High Cell Density Perfusion Culture has a Maintained Exoproteome and Metabolome. <i>Biotechnology Journal</i> , 2018, 13, e1800036.	1.8	18
1117	Patients with early-stage oropharyngeal cancer can be identified with label-free serum proteomics. <i>British Journal of Cancer</i> , 2018, 119, 200-212.	2.9	11
1118	Proteomic Analysis of Hippocampus in a Mouse Model of Depression Reveals Neuroprotective Function of Ubiquitin C-terminal Hydrolase L1 (UCH-L1) via Stress-induced Cysteine Oxidative Modifications. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1803-1823.	2.5	20
1119	Quantitative Crotonylome Analysis Expands the Roles of p300 in the Regulation of Lysine Crotonylation Pathway. <i>Proteomics</i> , 2018, 18, e1700230.	1.3	63
1120	FBP17 and CIP4 recruit SHIP2 and lamellipodin to prime the plasma membrane for fast endophilin-mediated endocytosis. <i>Nature Cell Biology</i> , 2018, 20, 1023-1031.	4.6	79
1121	Utilities for Mass Spectrometry Analysis of Proteins (UMSAP): Fast post-processing of mass spectrometry data. <i>Rapid Communications in Mass Spectrometry</i> , 2018, 32, 1659-1667.	0.7	2
1122	Dose- and time-dependent effects of triethylene glycol dimethacrylate on the proteome of human THP-1 monocytes. <i>European Journal of Oral Sciences</i> , 2018, 126, 345-358.	0.7	8
1123	Computational Approaches in Reproductomics. , 2018, , 347-383.		0
1124	Extensive Characterization of the Human Salivary Basic Proline-Rich Protein Family by Top-Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 3292-3307.	1.8	10
1125	ATR-mediated proteome remodeling is a major determinant of homologous recombination capacity in cancer cells. <i>Nucleic Acids Research</i> , 2018, 46, 8311-8325.	6.5	45
1126	In-depth proteomic analyses of <i>Haliotis laevigata</i> (greenlip abalone) nacre and prismatic organic shell matrix. <i>Proteome Science</i> , 2018, 16, 11.	0.7	33
1127	Obesity-mediated regulation of cardiac protein acetylation: parallel analysis of total and acetylated proteins via TMT-tagged mass spectrometry. <i>Bioscience Reports</i> , 2018, 38, .	1.1	26
1128	Species comparison of liver proteomes reveals links to naked mole-rat longevity and human aging. <i>BMC Biology</i> , 2018, 16, 82.	1.7	55
1129	A secretome profile indicative of oleate-induced proliferation of HepG2 hepatocellular carcinoma cells. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-14.	3.2	12

#	ARTICLE	IF	CITATIONS
1130	Glycomic Profiling Highlights Increased Fucosylation in Pseudomyxoma Peritonei. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2107-2118.	2.5	8
1131	Development of in Planta Chemical Cross-Linking-Based Quantitative Interactomics in <i>Arabidopsis</i> . <i>Journal of Proteome Research</i> , 2018, 17, 3195-3213.	1.8	20
1132	Proteomic and Bioinformatic Studies for the Characterization of Response to Pemetrexed in Platinum Drug Resistant Ovarian Cancer. <i>Frontiers in Pharmacology</i> , 2018, 9, 454.	1.6	7
1133	The Transcription Factor Hif-1 Enhances the Radio-Resistance of Mouse MSCs. <i>Frontiers in Physiology</i> , 2018, 9, 439.	1.3	20
1134	Antennal Protein Profile in Honeybees: Caste and Task Matter More Than Age. <i>Frontiers in Physiology</i> , 2018, 9, 748.	1.3	18
1135	Proteomic Analysis of Kiwifruit in Response to the Postharvest Pathogen, <i>Botrytis cinerea</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 158.	1.7	37
1136	Early Cold-Induced Peroxidases and Aquaporins Are Associated With High Cold Tolerance in Dajiao ( <i>Musa spp.</i> "Dajiao"). <i>Frontiers in Plant Science</i> , 2018, 9, 282.	1.7	38
1137	Quantitative Tandem Affinity Purification, an Effective Tool to Investigate Protein Complex Composition in Plant Hormone Signaling: Strigolactones in the Spotlight. <i>Frontiers in Plant Science</i> , 2018, 9, 528.	1.7	13
1138	Using RT-qPCR, Proteomics, and Microscopy to Unravel the Spatio-Temporal Expression and Subcellular Localization of Hordoindolines Across Development in Barley Endosperm. <i>Frontiers in Plant Science</i> , 2018, 9, 775.	1.7	26
1139	Sex-Dependent Variation of Pumpkin ( <i>Cucurbita maxima</i> cv. Big Max) Nectar and Nectaries as Determined by Proteomics and Metabolomics. <i>Frontiers in Plant Science</i> , 2018, 9, 860.	1.7	17
1140	iTRAQ-Based Quantitative Proteomic Analysis of Chemically Induced <i>Aquilaria sinensis</i> Provides Insights into Agarwood Formation Mechanism. <i>Proteomics</i> , 2018, 18, e1800023.	1.3	7
1141	The type VI secretion system deploys antifungal effectors against microbial competitors. <i>Nature Microbiology</i> , 2018, 3, 920-931.	5.9	199
1142	Comparison of Nuclear Matrix and Mitotic Chromosome Scaffold Proteins in <i>Drosophila</i> S2 Cells—Transmission of Hallmarks of Nuclear Organization Through Mitosis. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1965-1978.	2.5	19
1143	The Sperm Proteome of the Echiuran <i>Urechis unicinctus</i> (Annelida, Echiura). <i>Proteomics</i> , 2018, 18, e1800107.	1.3	6
1144	The Proteomic Landscape in the Vitreous of Patients With Age-Related and Diabetic Retinal Disease. , 2018, 59, AMD31.		43
1145	SWATH-MS based quantitative proteomics analysis reveals that curcumin alters the metabolic enzyme profile of CML cells by affecting the activity of miR-22/IPO7/HIF-1 $\alpha$ axis. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 170.	3.5	30
1146	Glutamate receptor $\gamma$ 2 serum antibodies in pediatric opsoclonus myoclonus ataxia syndrome. <i>Neurology</i> , 2018, 91, e714-e723.	1.5	43
1147	The Disordered Landscape of the 20S Proteasome Substrates Reveals Tight Association with Phase Separated Granules. <i>Proteomics</i> , 2018, 18, e1800076.	1.3	32



#	ARTICLE	IF	CITATIONS
1148	Deoxynivalenol induces structural alterations in epidermoid carcinoma cells A431 and impairs the response to biomechanical stimulation. <i>Scientific Reports</i> , 2018, 8, 11351.	1.6	16
1149	Insight into the global regulation of <i>laeA</i> in <i>Aspergillus flavus</i> based on proteomic profiling. <i>International Journal of Food Microbiology</i> , 2018, 284, 11-21.	2.1	49
1150	A novel USP9X substrate TTK contributes to tumorigenesis in non-small-cell lung cancer. <i>Theranostics</i> , 2018, 8, 2348-2360.	4.6	46
1151	Comparative proteomic analysis of mouse models of pathological and physiological cardiac hypertrophy, with selection of biomarkers of pathological hypertrophy by integrative proteogenomics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 1043-1054.	1.1	3
1152	A proteomics of gills approach to understanding salinity adaptation of <i>Scylla paramamosain</i> . <i>Gene</i> , 2018, 677, 119-131.	1.0	27
1153	Base-excision repair deficiency alone or combined with increased oxidative stress does not increase mtDNA point mutations in mice. <i>Nucleic Acids Research</i> , 2018, 46, 6642-6669.	6.5	58
1154	SILAC-based quantitative proteomic analysis of the livers of spontaneous obese and diabetic rhesus monkeys. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2018, 315, E294-E306.	1.8	12
1155	Quantitative proteomics reveals proteins involved in the progression from non-cancerous lesions to gastric cancer. <i>Journal of Proteomics</i> , 2018, 186, 15-27.	1.2	23
1156	The Role of Cadaverine Synthesis on Pneumococcal Capsule and Protein Expression. <i>Medical Sciences (Basel, Switzerland)</i> , 2018, 6, 8.	1.3	17
1157	Constitutional absence of epithelial integrin $\beta 3$ impacts the composition of the cellular microenvironment of ILNEB keratinocytes. <i>Matrix Biology</i> , 2018, 74, 62-76.	1.5	11
1158	Additional oxidative stress reroutes the global response of <i>Aspergillus fumigatus</i> to iron depletion. <i>BMC Genomics</i> , 2018, 19, 357.	1.2	41
1159	An overview of Phoneutria nigriventer spider venom using combined transcriptomic and proteomic approaches. <i>PLoS ONE</i> , 2018, 13, e0200628.	1.1	46
1160	The Global Acetylome of the Human Pathogen <i>Vibrio cholerae</i> V52 Reveals Lysine Acetylation of Major Transcriptional Regulators. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 537.	1.8	20
1161	The Use of CRISPR/Cas9 Gene Editing to Confirm Congenic Contaminations in Host-Pathogen Interaction Studies. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 87.	1.8	3
1162	FSPP: A Tool for Genome-Wide Prediction of smORF-Encoded Peptides and Their Functions. <i>Frontiers in Genetics</i> , 2018, 9, 96.	1.1	17
1163	Expression of Siglec-E Alters the Proteome of Lipopolysaccharide (LPS)-Activated Macrophages but Does Not Affect LPS-Driven Cytokine Production or Toll-Like Receptor 4 Endocytosis. <i>Frontiers in Immunology</i> , 2017, 8, 1926.	2.2	22
1164	Quantitative Proteomic Analysis of Four Developmental Stages of <i>Saprolegnia parasitica</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2658.	1.5	21
1165	Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. <i>Frontiers in Microbiology</i> , 2018, 9, 680.	1.5	36

#	ARTICLE	IF	CITATIONS
1166	Changed Expression of Cytoskeleton Proteins During Lung Injury in a Mouse Model of Streptococcus pneumoniae Infection. <i>Frontiers in Microbiology</i> , 2018, 9, 928.	1.5	3
1167	Comparative Proteomics of Three Species of Ammonia-Oxidizing Bacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 938.	1.5	47
1168	Proteomic Analysis of Zika Virus Infected Primary Human Fetal Neural Progenitors Suggests a Role for Doublecortin in the Pathological Consequences of Infection in the Cortex. <i>Frontiers in Microbiology</i> , 2018, 9, 1067.	1.5	37
1169	Multi-Omics and Targeted Approaches to Determine the Role of Cellular Proteases in Streptomyces Protein Secretion. <i>Frontiers in Microbiology</i> , 2018, 9, 1174.	1.5	29
1170	Induction by Bradyrhizobium diazoefficiens of Different Pathways for Growth in D-mannitol or L-arabinose Leading to Pronounced Differences in CO <sub>2</sub> Fixation, O <sub>2</sub> Consumption, and Lateral-Flagellum Production. <i>Frontiers in Microbiology</i> , 2018, 9, 1189.	1.5	10
1171	Characterization of Plasmodium vivax Proteins in Plasma-Derived Exosomes From Malaria-Infected Liver-Chimeric Humanized Mice. <i>Frontiers in Microbiology</i> , 2018, 9, 1271.	1.5	43
1172	Microbial Community Structure–Function Relationships in Yaquina Bay Estuary Reveal Spatially Distinct Carbon and Nitrogen Cycling Capacities. <i>Frontiers in Microbiology</i> , 2018, 9, 1282.	1.5	48
1173	Proteomic Dissection of Nanotopography-Sensitive Mechanotransductive Signaling Hubs that Foster Neuronal Differentiation in PC12 Cells. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 417.	1.8	39
1174	Characterization of the caprolactam degradation pathway in Pseudomonas jessenii using mass spectrometry-based proteomics. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 6699-6711.	1.7	24
1175	Integrated Analysis of Quantitative Proteome and Transcriptional Profiles Reveals the Dynamic Function of Maternally Expressed Proteins After Parthenogenetic Activation of Buffalo Oocyte. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1875-1891.	2.5	14
1176	The Impact of Oncogenic EGFRvIII on the Proteome of Extracellular Vesicles Released from Glioblastoma Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1948-1964.	2.5	116
1177	Effects of manganese toxicity on the protein profile of tomato ( Solanum lycopersicum ) roots as revealed by two complementary proteomic approaches, two-dimensional electrophoresis and shotgun analysis. <i>Journal of Proteomics</i> , 2018, 185, 51-63.	1.2	17
1178	Multifunctional Activity-Based Protein Profiling of the Developing Lung. <i>Journal of Proteome Research</i> , 2018, 17, 2623-2634.	1.8	9
1179	Evolutionary trade-offs associated with loss of PmrB function in host-adapted Pseudomonas aeruginosa. <i>Nature Communications</i> , 2018, 9, 2635.	5.8	28
1180	Chloroplast Acetyltransferase NSI Is Required for State Transitions in Arabidopsis thaliana. <i>Plant Cell</i> , 2018, 30, 1695-1709.	3.1	59
1181	Architectural Features of Human Mitochondrial Cysteine Desulfurase Complexes from Crosslinking Mass Spectrometry and Small-Angle X-Ray Scattering. <i>Structure</i> , 2018, 26, 1127-1136.e4.	1.6	20
1182	Influenza A Virus Induces Autophagosomal Targeting of Ribosomal Proteins. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1909-1921.	2.5	22
1183	Phosphoproteomics of Retinoblastoma: A Pilot Study Identifies Aberrant Kinases. <i>Molecules</i> , 2018, 23, 1454.	1.7	12

#	ARTICLE	IF	CITATIONS
1184	Pilot Study on Mass Spectrometryâ€“Based Analysis of the Proteome of CD34+CD123+ Progenitor Cells for the Identification of Potential Targets for Immunotherapy in Acute Myeloid Leukemia. <i>Proteomes</i> , 2018, 6, 11.	1.7	10
1185	Nrf2-Mediated Fibroblast Reprogramming Drives Cellular Senescence by Targeting the Matrisome. <i>Developmental Cell</i> , 2018, 46, 145-161.e10.	3.1	126
1186	Genome-centric view of carbon processing in thawing permafrost. <i>Nature</i> , 2018, 560, 49-54.	13.7	337
1187	A Cobalamin Activity-Based Probe Enables Microbial Cell Growth and Finds New Cobalamin-Protein Interactions across Domains. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	15
1188	Therapy-induced stress response is associated with downregulation of pre-mRNA splicing in cancer cells. <i>Genome Medicine</i> , 2018, 10, 49.	3.6	40
1189	Proteomic analysis of Medulloblastoma reveals functional biology with translational potential. <i>Acta Neuropathologica Communications</i> , 2018, 6, 48.	2.4	35
1190	Radio-sensitizing effects of VE-821 and beyond: Distinct phosphoproteomic and metabolomic changes after ATR inhibition in irradiated MOLT-4 cells. <i>PLoS ONE</i> , 2018, 13, e0199349.	1.1	8
1191	Discrimination of Isoleucine and Leucine by Dimethylation-Assisted MS3. <i>Analytical Chemistry</i> , 2018, 90, 9055-9059.	3.2	11
1192	Triflic Acid Treatment Enables LC-MS/MS Analysis of Insoluble Bacterial Biomass. <i>Journal of Proteome Research</i> , 2018, 17, 2978-2986.	1.8	5
1193	p38-mediated phosphorylation at T367 induces EZH2 cytoplasmic localization to promote breast cancer metastasis. <i>Nature Communications</i> , 2018, 9, 2801.	5.8	87
1194	Nanowell-mediated two-dimensional liquid chromatography enables deep proteome profiling of <math>\lt; 1000</math> mammalian cells. <i>Chemical Science</i> , 2018, 9, 6944-6951.	3.7	33
1195	Obesity-induced protein carbonylation in murine adipose tissue regulates the DNA-binding domain of nuclear zinc finger proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 13464-13476.	1.6	15
1196	Exploring bioactive peptides from bacterial secretomes using Pep<sup>SAVI</sup>-MS: identification and characterization of Bacâ€“21 from <i>Enterococcus faecalis</i> pPD<sup>1</sup>. <i>Microbial Biotechnology</i> , 2018, 11, 943-951.	2.0	7
1197	Exportin Crm1 is repurposed as a docking protein to generate microtubule organizing centers at the nuclear pore. <i>ELife</i> , 2018, 7, .	2.8	15
1198	Histone variant H2A.Z deposition and acetylation directs the canonical Notch signaling response. <i>Nucleic Acids Research</i> , 2018, 46, 8197-8215.	6.5	44
1199	IKK promotes cytokine-induced and cancer-associated AMPK activity and attenuates phenformin-induced cell death in LKB1-deficient cells. <i>Science Signaling</i> , 2018, 11, .	1.6	21
1200	Three-Dimensional Cell Culture Conditions Affect the Proteome of Cancer-Associated Fibroblasts. <i>Journal of Proteome Research</i> , 2018, 17, 2780-2789.	1.8	19
1201	MS analysis of a dilution series of bacteria:phytoplankton to improve detection of low abundance bacterial peptides. <i>Scientific Reports</i> , 2018, 8, 9276.	1.6	4

#	ARTICLE	IF	CITATIONS
1202	The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018, 28, 2348-2355.e9.	1.8	39
1203	Proteomic Analysis of NCK1/2 Adaptors Uncovers Paralog-specific Interactions That Reveal a New Role for NCK2 in Cell Abscission During Cytokinesis. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1979-1990.	2.5	21
1204	Lys-C/Arg-C, a More Specific and Efficient Digestion Approach for Proteomics Studies. <i>Analytical Chemistry</i> , 2018, 90, 9700-9707.	3.2	28
1205	Abnormal RNA stability in amyotrophic lateral sclerosis. <i>Nature Communications</i> , 2018, 9, 2845.	5.8	113
1206	Extracellular Vesicle Subtypes Released From Activated or Apoptotic T-Lymphocytes Carry a Specific and Stimulus-Dependent Protein Cargo. <i>Frontiers in Immunology</i> , 2018, 9, 534.	2.2	88
1207	OsNOA1 functions in a threshold-dependent manner to regulate chloroplast proteins in rice at lower temperatures. <i>BMC Plant Biology</i> , 2018, 18, 44.	1.6	10
1208	Proteomic Analyses of Human Regulatory T Cells Reveal Adaptations in Signaling Pathways that Protect Cellular Identity. <i>Immunity</i> , 2018, 48, 1046-1059.e6.	6.6	108
1209	Label-Free Proteomics of Tilapia Fillets and Their Relationship with Meat Texture During Post-Mortem Storage. <i>Food Analytical Methods</i> , 2018, 11, 3023-3033.	1.3	21
1210	Comparative Characterization of Osteoclasts Derived From Murine Bone Marrow Macrophages and RAW 264.7 Cells Using Quantitative Proteomics. <i>JBMR Plus</i> , 2018, 2, 328-340.	1.3	35
1211	Proteomic characterization of high-density lipoprotein particles in patients with non-alcoholic fatty liver disease. <i>Clinical Proteomics</i> , 2018, 15, 10.	1.1	23
1212	Fc gamma receptors are expressed in the developing rat brain and activate downstream signaling molecules upon cross-linking with immune complex. <i>Journal of Neuroinflammation</i> , 2018, 15, 7.	3.1	20
1213	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. <i>Genome Biology</i> , 2018, 19, 12.	3.8	21
1214	Systematic quantitative analysis of H2A and H2B variants by targeted proteomics. <i>Epigenetics and Chromatin</i> , 2018, 11, 2.	1.8	17
1215	Linking FOXO3, NCOA3, and TCF7L2 to Ras pathway phenotypes through a genome-wide forward genetic screen in human colorectal cancer cells. <i>Genome Medicine</i> , 2018, 10, 2.	3.6	6
1216	Integrated multi-omic analysis of host-microbiota interactions in acute oak decline. <i>Microbiome</i> , 2018, 6, 21.	4.9	49
1217	Proteomics-based insights into mitogen-activated protein kinase inhibitor resistance of cerebral melanoma metastases. <i>Clinical Proteomics</i> , 2018, 15, 13.	1.1	17
1218	iTRAQ-based quantitative proteomic analysis reveals the lateral meristem developmental mechanism for branched spike development in tetraploid wheat ( <i>Triticum turgidum</i> L.). <i>BMC Genomics</i> , 2018, 19, 228.	1.2	12
1219	Lipid accumulation in human breast cancer cells injured by iron depletors. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 75.	3.5	17

#	ARTICLE	IF	CITATIONS
1220	A tandem mass tag (TMT) proteomic analysis during the early phase of experimental pancreatitis reveals new insights in the disease pathogenesis. <i>Journal of Proteomics</i> , 2018, 181, 190-200.	1.2	10
1221	BoxCar acquisition method enables single-shot proteomics at a depth of 10,000 proteins in 100 minutes. <i>Nature Methods</i> , 2018, 15, 440-448.	9.0	303
1222	IonStar enables high-precision, low-missing-data proteomics quantification in large biological cohorts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4767-E4776.	3.3	76
1223	Enhanced Quantitative LC-MS/MS Analysis of N-linked Glycans Derived from Glycoproteins Using Sodium Deoxycholate Detergent. <i>Journal of Proteome Research</i> , 2018, 17, 2668-2678.	1.8	19
1224	Metabolic Reprogramming of <i>Vibrio cholerae</i> Impaired in Respiratory NADH Oxidation Is Accompanied by Increased Copper Sensitivity. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	9
1225	Computational Methods for Understanding Mass Spectrometry-Based Shotgun Proteomics Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 207-234.	2.8	108
1226	MAPK Reliance via Acquired CDK4/6 Inhibitor Resistance in Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 4201-4214.	3.2	77
1227	An Integrated, High-Throughput Strategy for Multiomic Systems Level Analysis. <i>Journal of Proteome Research</i> , 2018, 17, 3396-3408.	1.8	32
1228	Proteomic Analysis of Urine from California Sea Lions ( <i>Zalophus californianus</i> ): A Resource for Urinary Biomarker Discovery. <i>Journal of Proteome Research</i> , 2018, 17, 3281-3291.	1.8	11
1229	S-Trap, an Ultrafast Sample-Preparation Approach for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2917-2924.	1.8	215
1230	Rab18 is not necessary for lipid droplet biogenesis or turnover in human mammary carcinoma cells. <i>Molecular Biology of the Cell</i> , 2018, 29, 2045-2054.	0.9	34
1231	Spatially Resolved Proteome Profiling of <math>200</math> Cells from Tomato Fruit Pericarp by Integrating Laser-Capture Microdissection with Nanodroplet Sample Preparation. <i>Analytical Chemistry</i> , 2018, 90, 11106-11114.	3.2	31
1232	Protein half-life determines expression of proteostatic networks in podocyte differentiation. <i>FASEB Journal</i> , 2018, 32, 4696-4713.	0.2	15
1233	Transcriptomic and proteomic responses of the oceanic diatom <i>Pseudo-nitzschia granii</i> to iron limitation. <i>Environmental Microbiology</i> , 2018, 20, 3109-3126.	1.8	39
1234	<i>Clostridium sordellii</i> outer spore proteins maintain spore structural integrity and promote bacterial clearance from the gastrointestinal tract. <i>PLoS Pathogens</i> , 2018, 14, e1007004.	2.1	11
1235	TMEM41B is a novel regulator of autophagy and lipid mobilization. <i>EMBO Reports</i> , 2018, 19, .	2.0	134
1236	A Novel Iron Transporter SPD_1590 in <i>Streptococcus pneumoniae</i> Contributing to Bacterial Virulence Properties. <i>Frontiers in Microbiology</i> , 2018, 9, 1624.	1.5	15
1237	Metabolic oscillations on the circadian time scale in <i>Drosophila</i> cells lacking clock genes. <i>Molecular Systems Biology</i> , 2018, 14, e8376.	3.2	38

#	ARTICLE	IF	CITATIONS
1238	Proteome Profiles of Head Kidney and Spleen of Rainbow Trout ( <i>Oncorhynchus Mykiss</i> ). <i>Proteomics</i> , 2018, 18, e1800101.	1.3	18
1239	A proximity-tagging system to identify membrane protein-protein interactions. <i>Nature Methods</i> , 2018, 15, 715-722.	9.0	148
1240	Proteomic distinction of renal oncocytomas and chromophobe renal cell carcinomas. <i>Clinical Proteomics</i> , 2018, 15, 25.	1.1	8
1241	Predicting Antigen Presentation-What Could We Learn From a Million Peptides?. <i>Frontiers in Immunology</i> , 2018, 9, 1716.	2.2	159
1242	LXR/RXR signaling and neutrophil phenotype following myocardial infarction classify sex differences in remodeling. <i>Basic Research in Cardiology</i> , 2018, 113, 40.	2.5	86
1243	Mass spectrometry evaluation of a neuroblastoma SH-SY5Y cell culture protocol. <i>Analytical Biochemistry</i> , 2018, 559, 51-54.	1.1	2
1244	The exoproteome profiles of three <i>Staphylococcus saprophyticus</i> strains reveal diversity in protein secretion contents. <i>Microbiological Research</i> , 2018, 216, 85-96.	2.5	6
1245	Integrated Dissection of Cysteine Oxidative Post-translational Modification Proteome During Cardiac Hypertrophy. <i>Journal of Proteome Research</i> , 2018, 17, 4243-4257.	1.8	17
1246	The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates. <i>Nature Communications</i> , 2018, 9, 3411.	5.8	81
1247	<i>Xenopus</i> . <i>Methods in Molecular Biology</i> , 2018, , .	0.4	3
1248	Determining Allele-Specific Protein Expression (ASPE) Using a Novel Quantitative Concatamer Based Proteomics Method. <i>Journal of Proteome Research</i> , 2018, 17, 3606-3612.	1.8	20
1249	Quantitative Proteomics for <i>Xenopus</i> Embryos II, Data Analysis. <i>Methods in Molecular Biology</i> , 2018, 1865, 195-215.	0.4	13
1250	Balancing sufficiency and impact in reporting standards for mass spectrometry imaging experiments. <i>GigaScience</i> , 2018, 7, .	3.3	11
1251	The <i>Phytophthora infestans</i> Haustorium Is a Site for Secretion of Diverse Classes of Infection-Associated Proteins. <i>MBio</i> , 2018, 9, .	1.8	54
1252	Recapitulation of Human Neural Microenvironment Signatures in iPSC-Derived NPC 3D Differentiation. <i>Stem Cell Reports</i> , 2018, 11, 552-564.	2.3	59
1253	Microscale Reversed-Phase Liquid Chromatography/Capillary Zone Electrophoresis-Tandem Mass Spectrometry for Deep and Highly Sensitive Bottom-Up Proteomics: Identification of 7500 Proteins with Five Micrograms of an MCF7 Proteome Digest. <i>Analytical Chemistry</i> , 2018, 90, 10479-10486.	3.2	35
1254	Protein encoded in human telomerase RNA is involved in cell protective pathways. <i>Nucleic Acids Research</i> , 2018, 46, 8966-8977.	6.5	37
1255	Differentially abundant proteins associated with heterosis in the primary roots of popcorn. <i>PLoS ONE</i> , 2018, 13, e0197114.	1.1	13

#	ARTICLE	IF	CITATIONS
1256	Proteomic Characterization of the Heart and Skeletal Muscle Reveals Widespread Arginine ADP-Ribosylation by the ARTC1 Ectoenzyme. <i>Cell Reports</i> , 2018, 24, 1916-1929.e5.	2.9	55
1257	An ancient family of mobile genomic islands introducing cephalosporinase and carbapenemase genes in <i>Enterobacteriaceae</i> . <i>Virulence</i> , 2018, 9, 1377-1389.	1.8	9
1258	A novel STRIPAK complex component mediates hyphal fusion and fruiting body development in filamentous fungi. <i>Molecular Microbiology</i> , 2018, 110, 513-532.	1.2	19
1259	Absolute two-point quantification of proteins using dimethylated proteotypic peptides. <i>Analyst</i> , The, 2018, 143, 4359-4365.	1.7	1
1260	Top-down proteomic profiling of human saliva in multiple sclerosis patients. <i>Journal of Proteomics</i> , 2018, 187, 212-222.	1.2	40
1261	Venom-gland transcriptomics and venom proteomics of the giant Florida blue centipede, <i>Scolopendra viridis</i> . <i>Toxicon</i> , 2018, 152, 121-136.	0.8	19
1262	Temporal Proteomic Analysis of Pancreatic Î²-Cells in Response to Lipotoxicity and Glucolipotoxicity. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2119-2131.	2.5	25
1263	<i>Bordetella pertussis</i> and <i>Bordetella bronchiseptica</i> filamentous hemagglutinins are processed at different sites. <i>FEBS Open Bio</i> , 2018, 8, 1256-1266.	1.0	4
1264	N-terminal phosphorylation of glutaminase C decreases its enzymatic activity and cancer cell migration. <i>Biochimie</i> , 2018, 154, 69-76.	1.3	9
1265	Cerebrospinal fluid from Alzheimer patients affects cell-mediated nerve growth factor production and cell survival in vitro. <i>Experimental Cell Research</i> , 2018, 371, 175-184.	1.2	11
1266	Photosynthetic and Stress Responsive Proteins Are Altered More Effectively in <i>Nicotiana benthamiana</i> Infected with Plum pox virus Aggressive PPV-CR versus Mild PPV-C Cherry-Adapted Isolates. <i>Journal of Proteome Research</i> , 2018, 17, 3114-3127.	1.8	12
1267	GM-CSF driven myeloid cells in adipose tissue link weight gain and insulin resistance via formation of 2-aminoadipate. <i>Scientific Reports</i> , 2018, 8, 11485.	1.6	18
1268	Neurochondrin interacts with the SMN protein suggesting a novel mechanism for Spinal Muscular Atrophy pathology. <i>Journal of Cell Science</i> , 2018, 131, .	1.2	14
1269	A comprehensive analysis of <i>Candida albicans</i> phosphoproteome reveals dynamic changes in phosphoprotein abundance during hyphal morphogenesis. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9731-9743.	1.7	6
1270	STAT3 associates with vacuolar H <sup>+</sup> -ATPase and regulates cytosolic and lysosomal pH. <i>Cell Research</i> , 2018, 28, 996-1012.	5.7	77
1271	A Methodological Assessment and Characterization of Genetically-Driven Variation in Three Human Phosphoproteomes. <i>Scientific Reports</i> , 2018, 8, 12106.	1.6	2
1272	Proteome-Wide Analysis of <i>Trypanosoma cruzi</i> Exponential and Stationary Growth Phases Reveals a Subcellular Compartment-Specific Regulation. <i>Genes</i> , 2018, 9, 413.	1.0	32
1273	SPOP promotes transcriptional expression of DNA repair and replication factors to prevent replication stress and genomic instability. <i>Nucleic Acids Research</i> , 2018, 46, 9484-9495.	6.5	39

#	ARTICLE	IF	CITATIONS
1274	p62-Dependent Phase Separation of Patient-Derived KEAP1 Mutations and NRF2. <i>Molecular and Cellular Biology</i> , 2018, 38, .	1.1	51
1275	Mutation of the Surface Layer Protein SlpB Has Pleiotropic Effects in the Probiotic <i>Propionibacterium freudenreichii</i> CIRM-BIA 129. <i>Frontiers in Microbiology</i> , 2018, 9, 1807.	1.5	10
1276	Chemical Proteomic Analysis of Serine Hydrolase Activity in Niemann-Pick Type C Mouse Brain. <i>Frontiers in Neuroscience</i> , 2018, 12, 440.	1.4	11
1277	MARCH6 and TRC8 facilitate the quality control of cytosolic and tail-anchored proteins. <i>EMBO Reports</i> , 2018, 19, .	2.0	65
1278	Identification of MOSPD2, a novel scaffold for endoplasmic reticulum membrane contact sites. <i>EMBO Reports</i> , 2018, 19, .	2.0	85
1279	CharmRT: Boosting Peptide Identifications by Chimeric Spectra Identification and Retention Time Prediction. <i>Journal of Proteome Research</i> , 2018, 17, 2581-2589.	1.8	57
1280	HTRA1-Dependent Cell Cycle Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2679-2694.	1.8	11
1281	LC-MS/MS characterization of xyloside-primed glycosaminoglycans with cytotoxic properties reveals structural diversity and novel glycan modifications. <i>Journal of Biological Chemistry</i> , 2018, 293, 10202-10219.	1.6	12
1282	Lgl reduces endosomal vesicle acidification and Notch signaling by promoting the interaction between Vap33 and the V-ATPase complex. <i>Science Signaling</i> , 2018, 11, .	1.6	21
1283	<i>Enterococcus faecium</i> produces membrane vesicles containing virulence factors and antimicrobial resistance related proteins. <i>Journal of Proteomics</i> , 2018, 187, 28-38.	1.2	74
1284	The prion protein is embedded in a molecular environment that modulates transforming growth factor $\beta^2$ and integrin signaling. <i>Scientific Reports</i> , 2018, 8, 8654.	1.6	14
1285	BioID Reveals Novel Proteins of the <i>Plasmodium</i> Parasitophorous Vacuole Membrane. <i>MSphere</i> , 2018, 3, .	1.3	40
1286	Target Selection Strategies for LC-MS/MS Food Allergen Methods. <i>Journal of AOAC INTERNATIONAL</i> , 2018, 101, 146-151.	0.7	22
1287	Evolutionarily conserved and species-specific glycoproteins in the N-glycoproteomes of diverse insect species. <i>Insect Biochemistry and Molecular Biology</i> , 2018, 100, 22-29.	1.2	10
1288	Quantitative protein profiling and pathway analysis of spinal arteriovenous malformations. <i>Microvascular Research</i> , 2018, 120, 47-54.	1.1	3
1289	Integrative Analysis of Proteome and Ubiquitylome Reveals Unique Features of Lysosomal and Endocytic Pathways in Gefitinib-Resistant Non-Small Cell Lung Cancer Cells. <i>Proteomics</i> , 2018, 18, e1700388.	1.3	20
1290	Proteomic characterization of fresh spermatozoa and supernatant after cryopreservation in relation to freezability of carp ( <i>Cyprinus carpio</i> L) semen. <i>PLoS ONE</i> , 2018, 13, e0192972.	1.1	22
1291	Suppressor of $\text{IKK}\epsilon$ forms direct interactions with cytoskeletal proteins, tubulin and $\text{F-actin}$ , linking innate immunity to the cytoskeleton. <i>FEBS Open Bio</i> , 2018, 8, 1064-1082.	1.0	6



#	ARTICLE	IF	CITATIONS
1292	Serum Proteomic Profiling to Identify Biomarkers of Premature Carotid Atherosclerosis. <i>Scientific Reports</i> , 2018, 8, 9209.	1.6	20
1293	Characterization of the adult <i>Aedes aegypti</i> early midgut peritrophic matrix proteome using LC-MS. <i>PLoS ONE</i> , 2018, 13, e0194734.	1.1	23
1294	Control of seed dormancy and germination by DOG1-AHG1 PP2C phosphatase complex via binding to heme. <i>Nature Communications</i> , 2018, 9, 2132.	5.8	138
1295	Coupling Secretomics with Enzyme Activities To Compare the Temporal Processes of Wood Metabolism among White and Brown Rot Fungi. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	44
1296	Suppression of deetyrosinated microtubules improves cardiomyocyte function in human heart failure. <i>Nature Medicine</i> , 2018, 24, 1225-1233.	15.2	191
1297	Î±-synuclein oligomers interact with ATP synthase and open the permeability transition pore in Parkinson's disease. <i>Nature Communications</i> , 2018, 9, 2293.	5.8	351
1298	Diversity and evolution of the emerging Pandoraviridae family. <i>Nature Communications</i> , 2018, 9, 2285.	5.8	122
1299	Nidogen-1 is a novel extracellular ligand for the NKp44 activating receptor. <i>Oncolmmunology</i> , 2018, 7, e1470730.	2.1	54
1300	Proteomic analysis of the human retina reveals region-specific susceptibilities to metabolic- and oxidative stress-related diseases. <i>PLoS ONE</i> , 2018, 13, e0193250.	1.1	35
1301	Comparison of secretome from osteoblasts derived from sclerotic versus non-sclerotic subchondral bone in OA: A pilot study. <i>PLoS ONE</i> , 2018, 13, e0194591.	1.1	43
1302	Biological Databases. <i>Translational Bioinformatics</i> , 2018, , 303-337.	0.0	0
1303	Surfactant and Chaotropic Agent Assisted Sequential Extraction/On-Pellet Digestion (SCAD) for Enhanced Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2744-2754.	1.8	11
1304	A novel bacterial sulfur oxidation pathway provides a new link between the cycles of organic and inorganic sulfur compounds. <i>ISME Journal</i> , 2018, 12, 2479-2491.	4.4	96
1305	In vivo brain GPCR signaling elucidated by phosphoproteomics. <i>Science</i> , 2018, 360, .	6.0	105
1306	Endogenous Stochastic Decoding of the CUG Codon by Competing Ser- and Leu-tRNAs in <i>Ascoidea asiatica</i> . <i>Current Biology</i> , 2018, 28, 2046-2057.e5.	1.8	22
1307	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. <i>Nature Methods</i> , 2018, 15, 527-530.	9.0	88
1308	In Silico Tools and Databases for Designing Peptide-Based Vaccine and Drugs. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018, 112, 221-263.	1.0	49
1309	Nuclear PTEN safeguards pre-mRNA splicing to link Golgi apparatus for its tumor suppressive role. <i>Nature Communications</i> , 2018, 9, 2392.	5.8	47

#	ARTICLE	IF	CITATIONS
1310	Separable roles for Mec1/ATR in genome maintenance, DNA replication, and checkpoint signaling. <i>Genes and Development</i> , 2018, 32, 822-835.	2.7	30
1311	Proteome Response of a Metabolically Flexible Anoxygenic Phototroph to Fe(II) Oxidation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	5
1312	Protein Structure Databases. , 2019, , 460-471.		0
1313	Effect of purification of galactooligosaccharides derived from lactulose with <i>Saccharomyces cerevisiae</i> on their capacity to bind immune cell receptor Dectin-2. <i>Food Research International</i> , 2019, 115, 10-15.	2.9	4
1314	Endogenous Cell Type-Specific Disrupted in Schizophrenia 1 Interactomes Reveal Protein Networks Associated With Neurodevelopmental Disorders. <i>Biological Psychiatry</i> , 2019, 85, 305-316.	0.7	26
1315	Molecular Composition of Vestibular Hair Bundles. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a033209.	2.9	15
1316	Identification of Proteins From Proteomic Analysis. , 2019, , 855-870.		1
1317	Proteomics Data Representation and Databases. , 2019, , 76-83.		0
1318	Quantitative proteomics using tandem mass tags in relation to the acute phase protein response in chicken challenged with <i>Escherichia coli</i> lipopolysaccharide endotoxin. <i>Journal of Proteomics</i> , 2019, 192, 64-77.	1.2	52
1319	Biphasic cellular adaptations and ecological implications of <i>Alteromonas macleodii</i> degrading a mixture of algal polysaccharides. <i>ISME Journal</i> , 2019, 13, 92-103.	4.4	74
1320	Protein replenishment in pitcher fluids of <i>Nepenthes ventrata</i> revealed by quantitative proteomics (SWATH-MS) informed by transcriptomics. <i>Journal of Plant Research</i> , 2019, 132, 681-694.	1.2	13
1321	Cyclosporine A inhibits MRTF-SRF signaling through Na <sup>+</sup> /K <sup>+</sup> ATPase inhibition and actin remodeling. <i>FASEB BioAdvances</i> , 2019, 1, 561-578.	1.3	1
1322	Distinct types of short open reading frames are translated in plant cells. <i>Genome Research</i> , 2019, 29, 1464-1477.	2.4	43
1323	Multi-omics Analyses Reveal Synergistic Carbohydrate Metabolism in <i>Streptococcus mutans</i> - <i>Candida albicans</i> Mixed-Species Biofilms. <i>Infection and Immunity</i> , 2019, 87, .	1.0	71
1324	A Heterochromatin-Specific RNA Export Pathway Facilitates piRNA Production. <i>Cell</i> , 2019, 178, 964-979.e20.	13.5	81
1325	An Insight into the Proteome of Uveal Melanoma-Derived Ectosomes Reveals the Presence of Potentially Useful Biomarkers. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3789.	1.8	24
1326	Parallel Evolution of Complex Centipede Venoms Revealed by Comparative Proteotranscriptomic Analyses. <i>Molecular Biology and Evolution</i> , 2019, 36, 2748-2763.	3.5	24
1327	Proteomics Reveals Cell Surface Urokinase Plasminogen Activator Receptor Expression Impacts Most Hallmarks of Cancer. <i>Proteomics</i> , 2019, 19, e1900026.	1.3	9

#	ARTICLE	IF	CITATIONS
1328	Proteome Analysis of Enriched Heterocysts from Two Hydrogenase Mutants from <i>Anabaena</i> sp. PCC 7120. <i>Proteomics</i> , 2019, 19, e1800332.	1.3	6
1329	Clonal variations in CHO IGF signaling investigated by SILAC-based phosphoproteomics and LFQ-MS. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 8127-8143.	1.7	13
1330	Proteomics and post-secretory content adjustment of <i>Nicotiana tabacum</i> nectar. <i>Planta</i> , 2019, 250, 1703-1715.	1.6	2
1331	Secretome profiling of PC3/nKR cells, a novel highly migrating prostate cancer subline derived from PC3 cells. <i>PLoS ONE</i> , 2019, 14, e0220807.	1.1	3
1332	Identification of Hanks-Type Kinase PknB-Specific Targets in the <i>Streptococcus thermophilus</i> Phosphoproteome. <i>Frontiers in Microbiology</i> , 2019, 10, 1329.	1.5	15
1333	Therapeutic Targeting of RNA Splicing Catalysis through Inhibition of Protein Arginine Methylation. <i>Cancer Cell</i> , 2019, 36, 194-209.e9.	7.7	184
1334	A Novel Pyrazolopyrimidine Ligand of Human PGK1 and Stress Sensor DJ1 Modulates the Shelterin Complex and Telomere Length Regulation. <i>Neoplasia</i> , 2019, 21, 893-907.	2.3	4
1335	Phosphoproteomic analysis reveals plant DNA damage signalling pathways with a functional role for histone H2AX phosphorylation in plant growth under genotoxic stress. <i>Plant Journal</i> , 2019, 100, 1007-1021.	2.8	37
1336	Dataset supporting the proteomic differences found between excretion/secretion products from two isolates of <i>Fasciola hepatica</i> newly excysted juveniles (NEJ) derived from different snail hosts. <i>Data in Brief</i> , 2019, 25, 104272.	0.5	2
1337	Quantitative phosphoproteome and proteome analyses emphasize the influence of phosphorylation events during the nutritional stress of <i>Trypanosoma cruzi</i> : the initial moments of in vitro metacyclogenesis. <i>Cell Stress and Chaperones</i> , 2019, 24, 927-936.	1.2	15
1338	Fecal Metaproteomic Analysis Reveals Unique Changes of the Gut Microbiome Functions After Consumption of Sourdough Carasau Bread. <i>Frontiers in Microbiology</i> , 2019, 10, 1733.	1.5	26
1339	Kinome profiling of non-Hodgkin lymphoma identifies Tyro3 as a therapeutic target in primary effusion lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16541-16550.	3.3	16
1340	The nascent RNA binding complex SFINX licenses piRNA-guided heterochromatin formation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 720-731.	3.6	75
1341	Taxonomic and functional characterization of a microbial community from a volcanic englacial ecosystem in Deception Island, Antarctica. <i>Scientific Reports</i> , 2019, 9, 12158.	1.6	34
1342	Differential Protein Expression Profiles of Bronchoalveolar Lavage Fluid Following Lipopolysaccharide-Induced Direct and Indirect Lung Injury in Mice. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3401.	1.8	17
1343	Application of Bioactive Thermal Proteome Profiling to Decipher the Mechanism of Action of the Lipid Lowering 132-Hydroxy-pheophytin Isolated from a Marine Cyanobacteria. <i>Marine Drugs</i> , 2019, 17, 371.	2.2	15
1344	Development of an Analytical Method for the Metaproteomic Investigation of Bioaerosol from Work Environments. <i>Proteomics</i> , 2019, 19, e1900152.	1.3	6
1345	Chronic shisha exposure alters phosphoproteome of oral keratinocytes. <i>Journal of Cell Communication and Signaling</i> , 2019, 13, 281-289.	1.8	4

#	ARTICLE	IF	CITATIONS
1346	Analysis of the equine œcumulome reveals major metabolic aberrations after maturation in vitro. BMC Genomics, 2019, 20, 588.	1.2	20
1347	Multiple C2 domains and transmembrane region proteins ( MCTP s) tether membranes at plasmodesmata. EMBO Reports, 2019, 20, e47182.	2.0	92
1348	Non-coding RNA Transcription in Tetrahymena Meiotic Nuclei Requires Dedicated Mediator Complex-Associated Proteins. Current Biology, 2019, 29, 2359-2370.e5.	1.8	9
1349	PTMProphet: Fast and Accurate Mass Modification Localization for the Trans-Proteomic Pipeline. Journal of Proteome Research, 2019, 18, 4262-4272.	1.8	80
1350	Citrulline Effect Is a Characteristic Feature of Deiminated Peptides in Tandem Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2019, 30, 1586-1591.	1.2	11
1351	Oxygen-dependent bond formation with FIH regulates the activity of the client protein OTUB1. Redox Biology, 2019, 26, 101265.	3.9	16
1352	Lamin A molecular compression and sliding as mechanisms behind nucleoskeleton elasticity. Nature Communications, 2019, 10, 3056.	5.8	41
1353	Discovery and Qualification of Serum Protein Biomarker Candidates for Cholangiocarcinoma Diagnosis. Journal of Proteome Research, 2019, 18, 3305-3316.	1.8	18
1354	A Chemical Proteomic Analysis of Illudin Interacting Proteins. Chemistry - A European Journal, 2019, 25, 12644-12651.	1.7	7
1355	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. Nature Chemical Biology, 2019, 15, 803-812.	3.9	97
1356	Evolutionary Proteomics Reveals Distinct Patterns of Complexity and Divergence between Lepidopteran Sperm Morphs. Genome Biology and Evolution, 2019, 11, 1838-1846.	1.1	12
1357	Inhibiting ubiquitination causes an accumulation of SUMOylated newly synthesized nuclear proteins at PML bodies. Journal of Biological Chemistry, 2019, 294, 15218-15234.	1.6	37
1358	The Farmed Atlantic Salmon (Salmo salar) Skin Mucus Proteome and Its Nutrient Potential for the Resident Bacterial Community. Genes, 2019, 10, 515.	1.0	26
1359	Degradomics in Biomarker Discovery. Proteomics - Clinical Applications, 2019, 13, e1800138.	0.8	9
1360	Neutrophil extracellular traps (NET) induced by different stimuli: A comparative proteomic analysis. PLoS ONE, 2019, 14, e0218946.	1.1	137
1361	The role of small proteins in Burkholderia cenocepacia J2315 biofilm formation, persistence and intracellular growth. Biofilm, 2019, 1, 100001.	1.5	7
1362	High-throughput mass spectrometry and bioinformatics analysis of breast cancer proteomic data. Data in Brief, 2019, 25, 104125.	0.5	5
1363	Dual strategy for reduced signal suppression effects in matrix-assisted laser desorption/ionization mass spectrometry imaging. Rapid Communications in Mass Spectrometry, 2019, 33, 1711-1721.	0.7	5

#	ARTICLE	IF	CITATIONS
1364	Shotgun proteomic analysis of <i>Bordetella parapertussis</i> provides insights into the physiological response to iron starvation and potential new virulence determinants absent in <i>Bordetella pertussis</i> . <i>Journal of Proteomics</i> , 2019, 206, 103448.	1.2	4
1365	Temporal map of the pig polytrauma plasma proteome with fluid resuscitation and intravenous vitamin C treatment. <i>Journal of Thrombosis and Haemostasis</i> , 2019, 17, 1827-1837.	1.9	8
1366	Use of recombinant proteins as a simple and robust normalization method for untargeted proteomics screening: exhaustive performance assessment. <i>Talanta</i> , 2019, 205, 120163.	2.9	17
1367	Towards a standardized bioinformatics infrastructure for N- and O-glycomics. <i>Nature Communications</i> , 2019, 10, 3275.	5.8	70
1368	Multibatch TMT Reveals False Positives, Batch Effects and Missing Values. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1967-1980.	2.5	128
1369	Bayesian Confidence Intervals for Multiplexed Proteomics Integrate Ion-statistics with Peptide Quantification Concordance*[S]. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2108-2120.	2.5	23
1370	N-terminal $\beta$ -strand underpins biochemical specialization of an ATG8 isoform. <i>PLoS Biology</i> , 2019, 17, e3000373.	2.6	47
1371	PARK2 Mutation Causes Metabolic Disturbances and Impaired Survival of Human iPSC-Derived Neurons. <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 297.	1.8	47
1372	Proteomic Data Integration Highlights Central Actors Involved in Einkorn ( <i>Triticum monococcum</i> ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 T Science, 2019, 10, 832.	1.7	2
1373	MS2â€Deisotoper: A Tool for Deisotoping Highâ€Resolution MS/MS Spectra in Normal and Heavy Isotopeâ€Labelled Samples. <i>Proteomics</i> , 2019, 19, 1800444.	1.3	4
1374	Addressing Complex Matrix Interference Improves Multiplex Food Allergen Detection by Targeted LCâ€MS/MS. <i>Analytical Chemistry</i> , 2019, 91, 9760-9769.	3.2	24
1375	Proteomic Analysis of <i>Plasmodium</i> Merosomes: The Link between Liver and Blood Stages in Malaria. <i>Journal of Proteome Research</i> , 2019, 18, 3404-3418.	1.8	29
1376	A Systems-level Characterization of the Differentiation of Human Embryonic Stem Cells into Mesenchymal Stem Cells*[S]. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1950-1966.	2.5	13
1377	Charge-Mediated Pyrin Oligomerization Nucleates Antiviral IFI16 Sensing of Herpesvirus DNA. <i>MBio</i> , 2019, 10, .	1.8	25
1378	Flower bud proteome reveals modulation of sex-biased proteins potentially associated with sex expression and modification in dioecious <i>Coccinia grandis</i> . <i>BMC Plant Biology</i> , 2019, 19, 330.	1.6	10
1379	Data on the expression of SRPK1a in mammals. <i>Data in Brief</i> , 2019, 25, 104210.	0.5	0
1380	Modulation of posterior intestinal mucosal proteome in rainbow trout ( <i>Oncorhynchus mykiss</i> ) after <i>Yersinia ruckeri</i> infection. <i>Veterinary Research</i> , 2019, 50, 54.	1.1	12
1381	Unveiling the Mechanisms for the Plant Volatile Organic Compound Linalool To Control Gray Mold on Strawberry Fruits. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9265-9276.	2.4	63

#	ARTICLE	IF	CITATIONS
1382	Defining Protein Pattern Differences Among Molecular Subtypes of Diffuse Gliomas Using Mass Spectrometry*[S]. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2029-2043.	2.5	19
1383	PathwayMatcher: proteoform-centric network construction enables fine-granularity multiomics pathway mapping. <i>GigaScience</i> , 2019, 8, .	3.3	4
1384	Rapid Aldosterone-Mediated Signaling in the DCT Increases Activity of the Thiazide-Sensitive NaCl Cotransporter. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 1454-1470.	3.0	49
1385	Enhanced trypsin on a budget: Stabilization, purification and high-temperature application of inexpensive commercial trypsin for proteomics applications. <i>PLoS ONE</i> , 2019, 14, e0218374.	1.1	28
1386	Low-Background Acyl-Biotinyl Exchange Largely Eliminates the Coisolation of Non- <i>S</i> -Acylated Proteins and Enables Deep <i>S</i> -Acylproteomic Analysis. <i>Analytical Chemistry</i> , 2019, 91, 9858-9866.	3.2	32
1387	Quantitative proteomics and single-nucleus transcriptomics of the sinus node elucidates the foundation of cardiac pacemaking. <i>Nature Communications</i> , 2019, 10, 2889.	5.8	84
1388	Division of labour in the black garden ant ( <i>Lasius niger</i> ) leads to three distinct proteomes. <i>Journal of Insect Physiology</i> , 2019, 117, 103907.	0.9	12
1389	Outlining the Grb2 interactome data and its interacting partners in HEK293 cells in absence and presence of epidermal growth factor. <i>Data in Brief</i> , 2019, 25, 104082.	0.5	3
1390	Pressure cycling technology for challenging proteomic sample processing: application to barnacle adhesive. <i>Integrative Biology (United Kingdom)</i> , 2019, 11, 235-247.	0.6	20
1391	The Effects of Spaceflight Factors on the Human Plasma Proteome, Including Both Real Space Missions and Ground-Based Experiments. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3194.	1.8	25
1392	Divergent Polypharmacology-Driven Cellular Activity of Structurally Similar Multi-Kinase Inhibitors through Cumulative Effects on Individual Targets. <i>Cell Chemical Biology</i> , 2019, 26, 1240-1252.e11.	2.5	15
1393	Dynamic remodeling of the interactomes of <i>Nematostella vectensis</i> Hsp70 isoforms under heat shock. <i>Journal of Proteomics</i> , 2019, 206, 103416.	1.2	12
1394	Separating Golgi Proteins from <i>Cis</i> to <i>Trans</i> Reveals Underlying Properties of Cisternal Localization. <i>Plant Cell</i> , 2019, 31, 2010-2034.	3.1	40
1395	Proteomic Analysis of the Lake Trout ( <i>Salvelinus namaycush</i> ) Liver Identifies Proteins from Evolutionarily Close and Distant Fish Relatives. <i>Proteomics</i> , 2019, 19, e1800429.	1.3	8
1396	Characterization under quasi-native conditions of the capsanthin/capsorubin synthase from <i>Capsicum annuum</i> L. <i>Plant Physiology and Biochemistry</i> , 2019, 143, 165-175.	2.8	8
1397	An Energy Efficient AdaBoost Cascade Method for Long-Term Seizure Detection in Portable Neurostimulators. <i>IEEE Transactions on Neural Systems and Rehabilitation Engineering</i> , 2019, 27, 2274-2283.	2.7	12
1398	Proteomic Analysis of Endothelial Cells Exposed to Ultrasmall Nanoparticles Reveals Disruption in Paracellular and Transcellular Transport. <i>Proteomics</i> , 2019, 19, e1800228.	1.3	4
1399	Characterization of a novel glycosylated glutathione transferase of <i>Onchocerca ochengi</i> , closest relative of the human river blindness parasite. <i>Parasitology</i> , 2019, 146, 1773-1784.	0.7	2

#	ARTICLE	IF	CITATIONS
1400	Different Modes of Action of Genetic and Chemical Downregulation of Histone Deacetylases with Respect to Plant Development and Histone Modifications. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5093.	1.8	14
1401	Dataset of <i>Nematostella vectensis</i> Hsp70 isoform interactomes upon heat shock. <i>Data in Brief</i> , 2019, 27, 104580.	0.5	3
1402	Sweet google Oâ€™ mineâ€™”The importance of online search engines for MS-facilitated, database-independent identification of peptide-encoded book prefaces. <i>EuPA Open Proteomics</i> , 2019, 22-23, 14-18.	2.5	0
1403	MHCquant: Automated and Reproducible Data Analysis for Immunopeptidomics. <i>Journal of Proteome Research</i> , 2019, 18, 3876-3884.	1.8	35
1404	XPO1 is a critical player for bortezomib resistance in multiple myeloma: A quantitative proteomic approach. <i>Journal of Proteomics</i> , 2019, 209, 103504.	1.2	44
1405	Functional Genomics of the Retina to Elucidate its Construction and Deconstruction. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4922.	1.8	7
1406	Novel Mechanistic Insights into Bacterial Fluoroquinolone Resistance. <i>Journal of Proteome Research</i> , 2019, 18, 3955-3966.	1.8	20
1407	Proteomic and N-Terminomic TAILS Analyses of Human Alveolar Bone Proteins: Improved Protein Extraction Methodology and LysargiNase Digestion Strategies Increase Proteome Coverage and Missing Protein Identification. <i>Journal of Proteome Research</i> , 2019, 18, 4167-4179.	1.8	21
1408	Sleep-wake cycles drive daily dynamics of synaptic phosphorylation. <i>Science</i> , 2019, 366, .	6.0	181
1409	Meningeal Î³ T cellâ€™ derived IL-17 controls synaptic plasticity and short-term memory. <i>Science Immunology</i> , 2019, 4, .	5.6	184
1410	Animal fibre use in the Keriya valley (Xinjiang, China) during the Bronze and Iron Ages: A proteomic approach. <i>Journal of Archaeological Science</i> , 2019, 110, 104996.	1.2	13
1411	Robust prediction of HLA class II epitopes by deep motif deconvolution of immunopeptidomes. <i>Nature Biotechnology</i> , 2019, 37, 1283-1286.	9.4	208
1412	HAX1 impact on collective cell migration, cell adhesion, and cell shape is linked to the regulation of actomyosin contractility. <i>Molecular Biology of the Cell</i> , 2019, 30, 3024-3036.	0.9	13
1413	Lost and found: market access and public debt dynamics. <i>Oxford Economic Papers</i> , 2019, 71, 445-471.	0.7	17
1414	Trans-Synaptic Signaling through the Glutamate Receptor Delta-1 Mediates Inhibitory Synapse Formation in Cortical Pyramidal Neurons. <i>Neuron</i> , 2019, 104, 1081-1094.e7.	3.8	70
1415	Effects of Simulated Space Radiations on the Tomato Root Proteome. <i>Frontiers in Plant Science</i> , 2019, 10, 1334.	1.7	12
1416	Ageing and amyloidosis underlie the molecular and pathological alterations of tau in a mouse model of familial Alzheimerâ€™s disease. <i>Scientific Reports</i> , 2019, 9, 15758.	1.6	27
1417	<sc>STK</sc> 38 kinase acts as <sc>XPO</sc> 1 gatekeeper regulating the nuclear export of autophagy proteins and other cargoes. <i>EMBO Reports</i> , 2019, 20, e48150.	2.0	34

#	ARTICLE	IF	CITATIONS
1418	Proteomic analysis of eleven tissues in the Chinese giant salamander ( <i>Andrias davidianus</i> ). <i>Scientific Reports</i> , 2019, 9, 16415.	1.6	5
1419	The olfactory secretome varies according to season in female sheep and goat. <i>BMC Genomics</i> , 2019, 20, 794.	1.2	7
1420	Proteomic changes in the milk of water buffaloes ( <i>Bubalus bubalis</i> ) with subclinical mastitis due to intramammary infection by <i>Staphylococcus aureus</i> and by non-aureus staphylococci. <i>Scientific Reports</i> , 2019, 9, 15850.	1.6	26
1421	A Robust and Universal Metaproteomics Workflow for Research Studies and Routine Diagnostics Within 24 h Using Phenol Extraction, FASP Digest, and the MetaProteomeAnalyzer. <i>Frontiers in Microbiology</i> , 2019, 10, 1883.	1.5	66
1422	Transcription-coupled nucleotide excision repair is coordinated by ubiquitin and SUMO in response to ultraviolet irradiation. <i>Nucleic Acids Research</i> , 2020, 48, 231-248.	6.5	10
1423	Biological plasticity rescues target activity in CRISPR knock outs. <i>Nature Methods</i> , 2019, 16, 1087-1093.	9.0	159
1424	The Interactome analysis of the Respiratory Syncytial Virus protein M2-1 suggests a new role in viral mRNA metabolism post-transcription. <i>Scientific Reports</i> , 2019, 9, 15258.	1.6	14
1425	SWATH-based proteomics reveals processes associated with immune evasion and metastasis in poor prognosis colorectal tumours. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 8219-8232.	1.6	15
1426	Strong anion exchange-mediated phosphoproteomics reveals extensive human non-canonical phosphorylation. <i>EMBO Journal</i> , 2019, 38, e100847.	3.5	118
1427	Metallopeptidase inhibitor 1 (TIMP1) promotes receptor tyrosine kinase c-Kit signaling in colorectal cancer. <i>Molecular Oncology</i> , 2019, 13, 2646-2662.	2.1	11
1428	Recent Technological Advances in the Mass Spectrometry-based Nanomedicine Studies: An Insight from Nanoproteomics. <i>Current Pharmaceutical Design</i> , 2019, 25, 1536-1553.	0.9	1
1429	Proteomic analysis discovers the differential expression of novel proteins and phosphoproteins in meningioma including NEK9, HK2 and SET and deregulation of RNA metabolism. <i>EBioMedicine</i> , 2019, 40, 77-91.	2.7	54
1430	Male Fertility Potential Molecular Mechanisms Revealed by iTRAQ-Based Quantitative Proteomic Analysis of the Epididymis from Wip1 <sup>-/-</sup> Mice. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 54-66.	1.0	7
1431	Phellem Cell-Wall Components Are Discriminants of Cork Quality in <i>Quercus suber</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 944.	1.7	10
1432	Limited Oxidative Stress Favors Resistance to Skeletal Muscle Atrophy in Hibernating Brown Bears ( <i>Ursus Arctos</i> ). <i>Antioxidants</i> , 2019, 8, 334.	2.2	15
1433	Identification of Msp1-Induced Signaling Components in Rice Leaves by Integrated Proteomic and Phosphoproteomic Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4135.	1.8	30
1434	Early defects in translation elongation factor E1 levels at excitatory synapses in $\alpha$ -synucleinopathy. <i>Acta Neuropathologica</i> , 2019, 138, 971-986.	3.9	14
1435	Divergent allocation of sperm and the seminal proteome along a competition gradient in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17925-17933.	3.3	76



#	ARTICLE	IF	CITATIONS
1436	Customizing Functionalized Cofactor Mimics to Study the Human Pyridoxal 5â€²-Phosphate-Binding Proteome. <i>Cell Chemical Biology</i> , 2019, 26, 1461-1468.e7.	2.5	13
1437	Extremely Fast and Accurate Open Modification Spectral Library Searching of High-Resolution Mass Spectra Using Feature Hashing and Graphics Processing Units. <i>Journal of Proteome Research</i> , 2019, 18, 3792-3799.	1.8	39
1438	Polyubiquitin Chains Linked by Lysine Residue 48 (K48) Selectively Target Oxidized Proteins<i> In Vivo</i>. <i>Antioxidants and Redox Signaling</i> , 2019, 31, 1133-1149.	2.5	22
1439	Predictive modeling of therapeutic response to chondroitin sulfate/glucosamine hydrochloride in knee osteoarthritis. <i>Therapeutic Advances in Chronic Disease</i> , 2019, 10, 204062231987001.	1.1	11
1440	An integrative approach to cisplatin chronic toxicities in mice reveals importance of organic cation-transporter-dependent protein networks for renoprotection. <i>Archives of Toxicology</i> , 2019, 93, 2835-2848.	1.9	16
1441	Challenges of big data integration in the life sciences. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 6791-6800.	1.9	22
1442	LED lamps enhance somatic embryo maturation in association with the differential accumulation of proteins in the <i>Carica papaya</i> L. â€œGoldenâ€™™ embryogenic callus. <i>Plant Physiology and Biochemistry</i> , 2019, 143, 109-118.	2.8	10
1443	Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitrification anammox reactor using integrated multi-omics. <i>Microbiome</i> , 2019, 7, 122.	4.9	65
1444	Comparative proteomics analysis reveals the difference during antler regeneration stage between red deer and sika deer. <i>PeerJ</i> , 2019, 7, e7299.	0.9	9
1445	Cell-type-specific profiling of brain mitochondria reveals functional and molecular diversity. <i>Nature Neuroscience</i> , 2019, 22, 1731-1742.	7.1	181
1446	Palaeoproteomic identification of breast milk protein residues from the archaeological skeletal remains of a neonatal dog. <i>Scientific Reports</i> , 2019, 9, 12841.	1.6	11
1447	Navigating in vitro bioactivity data by investigating available resources using model compounds. <i>Scientific Data</i> , 2019, 6, 45.	2.4	1
1448	A dataset describing a suite of novel antibody reagents for the RAS signaling network. <i>Scientific Data</i> , 2019, 6, 160.	2.4	4
1449	HDL flux is higher in patients with nonalcoholic fatty liver disease. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 317, E852-E862.	1.8	26
1450	Perturbations in RhoA signalling cause altered migration and impaired neuritogenesis in human iPSC-derived neural cells with PARK2 mutation. <i>Neurobiology of Disease</i> , 2019, 132, 104581.	2.1	32
1451	Next-generation computational tools for interrogating cancer immunity. <i>Nature Reviews Genetics</i> , 2019, 20, 724-746.	7.7	131
1452	p38Î± MAPK proximity assay reveals a regulatory mechanism of alternative splicing in cardiomyocytes. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2019, 1866, 118557.	1.9	14
1453	A human endogenous retrovirus encoded protease potentially cleaves numerous cellular proteins. <i>Mobile DNA</i> , 2019, 10, 36.	1.3	9

#	ARTICLE	IF	CITATIONS
1454	Regulation of the endosomal SNX27-retromer by OTULIN. <i>Nature Communications</i> , 2019, 10, 4320.	5.8	34
1455	Ligand-dependent spatiotemporal signaling profiles of the $\mu$ -opioid receptor are controlled by distinct protein-interaction networks. <i>Journal of Biological Chemistry</i> , 2019, 294, 16198-16213.	1.6	17
1456	DNA Damage Changes Distribution Pattern and Levels of HP1 Protein Isoforms in the Nucleolus and Increases Phosphorylation of HP1 <sup>S2</sup> -Ser88. <i>Cells</i> , 2019, 8, 1097.	1.8	10
1457	A shared core microbiome in soda lakes separated by large distances. <i>Nature Communications</i> , 2019, 10, 4230.	5.8	75
1458	Liver proteome dataset of <i>Sparus aurata</i> exposed to low temperatures. <i>Data in Brief</i> , 2019, 26, 104419.	0.5	5
1459	The ubiquitin-like modifier FAT10 interferes with SUMO activation. <i>Nature Communications</i> , 2019, 10, 4452.	5.8	29
1460	Dissecting the Shared and Context-Dependent Pathways Mediated by the p140Cap Adaptor Protein in Cancer and in Neurons. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 222.	1.8	7
1461	The Core Proteome of Biofilm-Grown Clinical <i>Pseudomonas aeruginosa</i> Isolates. <i>Cells</i> , 2019, 8, 1129.	1.8	26
1462	Proteome Profiling of the Exhaled Breath Condensate after Long-Term Spaceflights. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4518.	1.8	11
1463	Sample Preservation and Storage Significantly Impact Taxonomic and Functional Profiles in Metaproteomics Studies of the Human Gut Microbiome. <i>Microorganisms</i> , 2019, 7, 367.	1.6	32
1464	Sex-based venom variation in the eastern bark centipede ( <i>Hemiscolopendra marginata</i> ). <i>Toxicon</i> , 2019, 169, 45-58.	0.8	9
1465	Mice depleted for Exchange Proteins Directly Activated by cAMP (Epac) exhibit irregular liver regeneration in response to partial hepatectomy. <i>Scientific Reports</i> , 2019, 9, 13789.	1.6	8
1466	PepSAVI-MS Reveals a Proline-rich Antimicrobial Peptide in <i>Amaranthus tricolor</i> . <i>Journal of Natural Products</i> , 2019, 82, 2744-2753.	1.5	16
1467	The muscular, hepatic and adipose tissues proteomes in muskox ( <i>Ovibos moschatus</i> ): Differences between males and females. <i>Journal of Proteomics</i> , 2019, 208, 103480.	1.2	9
1468	Changes in the microsomal proteome of tomato fruit during ripening. <i>Scientific Reports</i> , 2019, 9, 14350.	1.6	17
1469	A homology-guided, genome-based proteome for improved proteomics in the allopolyploid <i>Nicotiana benthamiana</i> . <i>BMC Genomics</i> , 2019, 20, 722.	1.2	50
1470	A small molecule interacts with VDAC2 to block mouse BAK-driven apoptosis. <i>Nature Chemical Biology</i> , 2019, 15, 1057-1066.	3.9	30
1471	Mass spectrometric identification of candidate RNA-binding proteins associated with Transition Nuclear Protein mRNA in the mouse testis. <i>Scientific Reports</i> , 2019, 9, 13618.	1.6	5

#	ARTICLE	IF	CITATIONS
1472	Proteomic analysis of the rice ( <i>Oryza officinalis</i> ) provides clues on molecular tagging of proteins for brown planthopper resistance. <i>BMC Plant Biology</i> , 2019, 19, 30.	1.6	13
1473	Redox Proteomic Analysis Reveals Oxidative Modifications of Proteins by Increased Levels of Intracellular Reactive Oxygen Species during Hypoxia Adaptation of <i>Aspergillus fumigatus</i> . <i>Proteomics</i> , 2019, 19, e1800339.	1.3	4
1474	Stage-specific testes proteomics of <i>Drosophila melanogaster</i> identifies essential proteins for male fertility. <i>European Journal of Cell Biology</i> , 2019, 98, 103-115.	1.6	14
1475	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , 2019, 10, 331.	5.8	146
1476	BAP1 complex promotes transcription by opposing PRC1-mediated H2A ubiquitylation. <i>Nature Communications</i> , 2019, 10, 348.	5.8	105
1477	Multimomics resolution of molecular events during a day in the life of <i>Chlamydomonas</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2374-2383.	3.3	133
1478	Multi-isotype Glycoproteomic Characterization of Serum Antibody Heavy Chains Reveals Isotype- and Subclass-Specific N-Glycosylation Profiles. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 686-703.	2.5	44
1479	Use of rare-earth elements in the phyllosphere colonizer <i>Methylobacterium extorquens</i> PA1. <i>Molecular Microbiology</i> , 2019, 111, 1152-1166.	1.2	88
1480	Systemic analysis of tyrosine kinase signaling reveals a common adaptive response program in a HER2-positive breast cancer. <i>Science Signaling</i> , 2019, 12, .	1.6	26
1481	Dilute-and-shoot analysis of therapeutic monoclonal antibody variants in fermentation broth: a method capability study. <i>MAbs</i> , 2019, 11, 569-582.	2.6	15
1482	Proteogenomics Uncovers Critical Elements of Host Response in Bovine Soft Palate Epithelial Cells Following In Vitro Infection with Foot-And-Mouth Disease Virus. <i>Viruses</i> , 2019, 11, 53.	1.5	13
1483	Identification and Characterization of Canine Ligament Progenitor Cells and Their Extracellular Matrix Niche. <i>Journal of Proteome Research</i> , 2019, 18, 1328-1339.	1.8	7
1484	Plasma Proteomics Analysis Reveals Dysregulation of Complement Proteins and Inflammation in Acquired Obesity—A Study on Rare BMI-Discordant Monozygotic Twin Pairs. <i>Proteomics - Clinical Applications</i> , 2019, 13, 1800173.	0.8	11
1485	Post-translational Regulation of FNIP1 Creates a Rheostat for the Molecular Chaperone Hsp90. <i>Cell Reports</i> , 2019, 26, 1344-1356.e5.	2.9	38
1486	Optimized Fragmentation Improves the Identification of Peptides Cross-Linked by MS-Cleavable Reagents. <i>Journal of Proteome Research</i> , 2019, 18, 1363-1370.	1.8	55
1487	Integrated Phosphoproteome and Transcriptome Analysis Reveals Chlamydia-Induced Epithelial-to-Mesenchymal Transition in Host Cells. <i>Cell Reports</i> , 2019, 26, 1286-1302.e8.	2.9	46
1488	Proteomes of Paired Human Cerebrospinal Fluid and Plasma: Relation to Blood-Brain Barrier Permeability in Older Adults. <i>Journal of Proteome Research</i> , 2019, 18, 1162-1174.	1.8	40
1489	Cytological, Biochemical and Molecular Events of the Embryogenic State in Douglas-fir ( <i>Pseudotsuga</i> ) Tj ETQq1 1 0,784314 rgBT /Overl 1.7 18	1.7	18

#	ARTICLE	IF	CITATIONS
1490	Off-target based drug repurposing opportunities for tivantinib in acute myeloid leukemia. <i>Scientific Reports</i> , 2019, 9, 606.	1.6	21
1491	Plasmodium male gametocyte development and transmission are critically regulated by the two putative deadenylases of the CAF1/CCR4/NOT complex. <i>PLoS Pathogens</i> , 2019, 15, e1007164.	2.1	28
1492	Peptimapper: proteogenomics workflow for the expert annotation of eukaryotic genomes. <i>BMC Genomics</i> , 2019, 20, 56.	1.2	10
1493	The Schistosomiasis SpleenOME: Unveiling the Proteomic Landscape of Splenomegaly Using Label-Free Mass Spectrometry. <i>Frontiers in Immunology</i> , 2018, 9, 3137.	2.2	8
1494	PIM1 kinase promotes gallbladder cancer cell proliferation via inhibition of proline-rich Akt substrate of 40ÅkDa (PRAS40). <i>Journal of Cell Communication and Signaling</i> , 2019, 13, 163-177.	1.8	12
1495	Multi-omic Analyses Reveal Minimal Impact of the CRISPR-Cas9 Nuclease on Cultured Human Cells. <i>Journal of Proteome Research</i> , 2019, 18, 1054-1063.	1.8	2
1496	Proteo-Transcriptomic Dynamics of Cellular Response to HIV-1 Infection. <i>Scientific Reports</i> , 2019, 9, 213.	1.6	24
1497	Triplet-pore structure of a highly divergent TOM complex of hydrogenosomes in <i>Trichomonas vaginalis</i> . <i>PLoS Biology</i> , 2019, 17, e3000098.	2.6	33
1498	First Viruses Infecting the Marine Diatom <i>Guinardia delicatula</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3235.	1.5	37
1499	Sampling of Tissues with Laser Ablation for Proteomics: Comparison of Picosecond Infrared Laser and Microsecond Infrared Laser. <i>Journal of Proteome Research</i> , 2019, 18, 1451-1457.	1.8	8
1500	Mice exposed to maternal androgen excess and diet-induced obesity have altered phosphorylation of catechol-O-methyltransferase in the placenta and fetal liver. <i>International Journal of Obesity</i> , 2019, 43, 2176-2188.	1.6	16
1501	Metabolic reconstruction of the genome of candidate <i>Desulfatiglans</i> TRIP_1 and identification of key candidate enzymes for anaerobic phenanthrene degradation. <i>Environmental Microbiology</i> , 2019, 21, 1267-1286.	1.8	31
1502	CoExpresso: assess the quantitative behavior of protein complexes in human cells. <i>BMC Bioinformatics</i> , 2019, 20, 17.	1.2	9
1503	Increased growth rate and productivity following stable depletion of miR-7 in a mAb producing CHO cell line causes an increase in proteins associated with the Akt pathway and ribosome biogenesis. <i>Journal of Proteomics</i> , 2019, 195, 23-32.	1.2	12
1504	Comparison of the performance of 1D SDS-PAGE with nondenaturing 2DE on the analysis of proteins from human bronchial smooth muscle cells using quantitative LC-MS/MS. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2019, 1105, 193-202.	1.2	7
1505	Detection of Six Commercially Processed Soy Ingredients in an Incurred Food Matrix Using Parallel Reaction Monitoring. <i>Journal of Proteome Research</i> , 2019, 18, 995-1005.	1.8	13
1506	A Novel Truncated Form of Nephronectin Is Present in Small Extracellular Vesicles Isolated from 66cl4 Cells. <i>Journal of Proteome Research</i> , 2019, 18, 1237-1247.	1.8	7
1507	Metaproteomics reveals potential mechanisms by which dietary resistant starch supplementation attenuates chronic kidney disease progression in rats. <i>PLoS ONE</i> , 2019, 14, e0199274.	1.1	25

#	ARTICLE	IF	CITATIONS
1508	Characterization of the Src-regulated kinome identifies SGK1 as a key mediator of Src-induced transformation. <i>Nature Communications</i> , 2019, 10, 296.	5.8	23
1509	Proteomic insight into the pathogenesis of CAPN5-vitreoretinopathy. <i>Scientific Reports</i> , 2019, 9, 7608.	1.6	9
1510	Label-free serum proteomics and multivariate data analysis identifies biomarkers and expression trends that differentiate Intraductal papillary mucinous neoplasia from pancreatic adenocarcinoma and healthy controls. <i>Translational Medicine Communications</i> , 2019, 4, .	0.5	2
1511	Bioinformatics Workflow for Gonococcal Proteomics. <i>Methods in Molecular Biology</i> , 2019, 1997, 185-205.	0.4	2
1512	Proteomic analysis of goat milk kefir: Profiling the fermentation-time dependent protein digestion and identification of potential peptides with biological activity. <i>Food Chemistry</i> , 2019, 295, 456-465.	4.2	55
1513	High-quality MS/MS spectrum prediction for data-dependent and data-independent acquisition data analysis. <i>Nature Methods</i> , 2019, 16, 519-525.	9.0	194
1514	Combined transcriptomic and proteomic analysis reveals a diversity of venom-related and toxin-like peptides expressed in the mat anemone <i>Zoanthus natalensis</i> (Cnidaria, Hexacorallia). <i>Archives of Toxicology</i> , 2019, 93, 1745-1767.	1.9	14
1515	The intrinsic and regulated proteomes of barley seeds in response to fungal infection. <i>Analytical Biochemistry</i> , 2019, 580, 30-35.	1.1	46
1516	A three-pronged "Pitchfork" strategy enables an extensive description of the human membrane proteome and the identification of missing proteins. <i>Journal of Proteomics</i> , 2019, 204, 103411.	1.2	3
1517	Multi omics analysis of fibrotic kidneys in two mouse models. <i>Scientific Data</i> , 2019, 6, 92.	2.4	26
1518	Proteomic analysis of gemcitabine-resistant pancreatic cancer cells reveals that microtubule-associated protein 2 upregulation associates with taxane treatment. <i>Therapeutic Advances in Medical Oncology</i> , 2019, 11, 175883591984123.	1.4	35
1519	Quantitative Photo-crosslinking Mass Spectrometry Revealing Protein Structure Response to Environmental Changes. <i>Analytical Chemistry</i> , 2019, 91, 9041-9048.	3.2	21
1520	<i>Shigella</i> promotes major alteration of gut epithelial physiology and tissue invasion by shutting off host intracellular transport. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13582-13591.	3.3	23
1521	Novel interconnections of HOG signaling revealed by combined use of two proteomic software packages. <i>Cell Communication and Signaling</i> , 2019, 17, 66.	2.7	9
1522	Histopathological and proteomic analyses identify integrin- $\beta$ 1 as a potential mediator of phleboscrosis in uremic patients. <i>Clinical and Experimental Nephrology</i> , 2019, 23, 1100-1108.	0.7	1
1523	The glycan CA19-9 promotes pancreatitis and pancreatic cancer in mice. <i>Science</i> , 2019, 364, 1156-1162.	6.0	166
1524	Rotary substates of mitochondrial ATP synthase reveal the basis of flexible F <sub>1</sub> -F <sub>o</sub> coupling. <i>Science</i> , 2019, 364, .	6.0	160
1525	Serine-Threonine Kinases Encoded by Split <i>hipA</i> Homologs Inhibit Tryptophanyl-tRNA Synthetase. <i>MBio</i> , 2019, 10, .	1.8	25

#	ARTICLE	IF	CITATIONS
1526	A Mass Spectrometry Survey of Chromatin-Associated Proteins in Pluripotency and Early Lineage Commitment. <i>Proteomics</i> , 2019, 19, 1900047.	1.3	16
1527	Multi-omics insights into functional alterations of the liver in insulin-deficient diabetes mellitus. <i>Molecular Metabolism</i> , 2019, 26, 30-44.	3.0	26
1528	Proteomic signatures of neuroinflammation in Alzheimer's disease, multiple sclerosis and ischemic stroke. <i>Expert Review of Proteomics</i> , 2019, 16, 601-611.	1.3	14
1529	Interactome of Glyceraldehyde-3-Phosphate Dehydrogenase Points to the Existence of Metabolons in <i>Paracoccidioides lutzii</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1537.	1.5	26
1530	DEG10 contributes to mitochondrial proteostasis, root growth, and seed yield in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 5423-5436.	2.4	13
1531	Convergent recruitment of adamalysin-like metalloproteases in the venom of the red bark centipede ( <i>Scolopocryptops sexspinosus</i> ). <i>Toxicon</i> , 2019, 168, 1-15.	0.8	8
1532	Urinary tract colonization is enhanced by a plasmid that regulates uropathogenic <i>Acinetobacter baumannii</i> chromosomal genes. <i>Nature Communications</i> , 2019, 10, 2763.	5.8	80
1533	C/EBP $\beta$ -LIP induces cancer-type metabolic reprogramming by regulating the let-7/LIN28B circuit in mice. <i>Communications Biology</i> , 2019, 2, 208.	2.0	13
1534	Analysis of the <i>Escherichia coli</i> extracellular vesicle proteome identifies markers of purity and culture conditions. <i>Journal of Extracellular Vesicles</i> , 2019, 8, 1632099.	5.5	79
1535	Mass spectrometric characterization of the zein protein composition in maize flour extracts upon protein separation by SDS-PAGE and 2D gel electrophoresis. <i>Electrophoresis</i> , 2019, 40, 2747-2758.	1.3	15
1536	A Proteomic Analysis of GSD-1a in Mouse Livers: Evidence for Metabolic Reprogramming, Inflammation, and Macrophage Polarization. <i>Journal of Proteome Research</i> , 2019, 18, 2965-2978.	1.8	8
1537	Oxyfunctionalization of nonsteroidal anti-inflammatory drugs by filamentous fungi. <i>Journal of Applied Microbiology</i> , 2019, 127, 724-738.	1.4	5
1538	Two intracellular and cell type-specific bacterial symbionts in the placozoan <i>Trichoplax H2</i> . <i>Nature Microbiology</i> , 2019, 4, 1465-1474.	5.9	57
1539	Multi-omics of the gut microbial ecosystem in inflammatory bowel diseases. <i>Nature</i> , 2019, 569, 655-662.	13.7	1,638
1540	Proteomic Analysis of Vocal Fold Fibroblasts Exposed to Cigarette Smoke Extract: Exploring the Pathophysiology of Reinke's Edema*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1511-1525.	2.5	20
1541	Triazine Probes Target Ascorbate Peroxidases in Plants. <i>Plant Physiology</i> , 2019, 180, 1848-1859.	2.3	5
1542	CerS6-Derived Sphingolipids Interact with Mff and Promote Mitochondrial Fragmentation in Obesity. <i>Cell</i> , 2019, 177, 1536-1552.e23.	13.5	183
1543	Multi-omics characterization of the necrotrophic mycoparasite <i>Saccharomycopsis schoenii</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007692.	2.1	18

#	ARTICLE	IF	CITATIONS
1544	Plasmodium pseudo-Tyrosine Kinase-like binds PP1 and SERA5 and is exported to host erythrocytes. Scientific Reports, 2019, 9, 8120.	1.6	9
1545	Clinical biomarker discovery by SWATH-MS based label-free quantitative proteomics: impact of criteria for identification of differentiators and data normalization method. Journal of Translational Medicine, 2019, 17, 184.	1.8	16
1546	Proteases Underground: Analysis of the Maize Root Apoplast Identifies Organ Specific Papain-Like Cysteine Protease Activity. Frontiers in Plant Science, 2019, 10, 473.	1.7	15
1547	A Label-free Mass Spectrometry Method to Predict Endogenous Protein Complex Composition*. Molecular and Cellular Proteomics, 2019, 18, 1588-1606.	2.5	28
1548	Posttranslational Modifications Drive Protein Stability to Control the Dynamic Beer Brewing Proteome. Molecular and Cellular Proteomics, 2019, 18, 1721-1731.	2.5	35
1549	Plant-derived virus-like particle vaccines drive cross-presentation of influenza A hemagglutinin peptides by human monocyte-derived macrophages. Npj Vaccines, 2019, 4, 17.	2.9	23
1550	Proteomics of Bordetella pertussis whole-cell and acellular vaccines. BMC Research Notes, 2019, 12, 329.	0.6	4
1551	A chronic hypoxic response in photoreceptors alters the vitreous proteome in mice. Experimental Eye Research, 2019, 185, 107690.	1.2	3
1552	Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. Genes and Development, 2019, 33, 1031-1047.	2.7	83
1553	Individual Physiological Adaptations Enable Selected Bacterial Taxa To Prevail during Long-Term Incubations. Applied and Environmental Microbiology, 2019, 85, .	1.4	4
1554	Proteomic Profiling, Transcription Factor Modeling, and Genomics of Evolved Tolerant Strains Elucidate Mechanisms of Vanillin Toxicity in Escherichia coli. MSystems, 2019, 4, .	1.7	28
1555	Multiple solvent elution, a method to counter the effects of coelution and ion suppression in LC-MS analysis in bottom up proteomics. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2019, 1124, 256-264.	1.2	2
1556	Pharmacoproteomics reveal novel protective activity of bromodomain containing 4 inhibitors on vascular homeostasis in TLR3-mediated airway remodeling. Journal of Proteomics, 2019, 205, 103415.	1.2	24
1557	Proteomic signatures of brain regions affected by tau pathology in early and late stages of Alzheimer's disease. Neurobiology of Disease, 2019, 130, 104509.	2.1	46
1558	Alteration of Proteomes in First-Generation Cultures of Bacillus pumilus Spores Exposed to Outer Space. MSystems, 2019, 4, .	1.7	8
1559	Sum of peak intensities outperforms peak area integration in iTRAQ protein expression measurement by LC-MS/MS using a TripleTOF 5600+ platform. Bioscience Reports, 2019, 39, .	1.1	7
1560	Label-free cervicovaginal fluid proteome profiling reflects the cervix neoplastic transformation. Journal of Mass Spectrometry, 2019, 54, 693-703.	0.7	17
1561	Physiological responses and proteomic changes reveal insights into Stylosanthes response to manganese toxicity. BMC Plant Biology, 2019, 19, 212.	1.6	38

#	ARTICLE	IF	CITATIONS
1562	Role of AcrAB-TolC multidrug efflux pump in drug-resistance acquisition by plasmid transfer. <i>Science</i> , 2019, 364, 778-782.	6.0	176
1563	Identification of a USP9X Substrate NFX1-123 by SILAC-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 2654-2665.	1.8	13
1564	Light-dependent N-terminal phosphorylation of LHCSR3 and LHCB4 are interlinked in <i>Chlamydomonas reinhardtii</i> . <i>Plant Journal</i> , 2019, 99, 877-894.	2.8	20
1565	A Colorful Palette of B-Phycoerythrin Proteoforms Exposed by a Multimodal Mass Spectrometry Approach. <i>CheM</i> , 2019, 5, 1302-1317.	5.8	10
1566	Integrated proteomics and metabolomics analysis reveals differential lipid metabolism in human umbilical vein endothelial cells under high and low shear stress. <i>American Journal of Physiology - Cell Physiology</i> , 2019, 317, C326-C338.	2.1	21
1567	Exosomal Transport of Hepatocyte-Derived Drug-Modified Proteins to the Immune System. <i>Hepatology</i> , 2019, 70, 1732-1749.	3.6	33
1568	Effects of temperature changes in the transcriptional profile of the emerging fish pathogen <i>Francisella noatunensis</i> subsp. <i>orientalis</i> . <i>Microbial Pathogenesis</i> , 2019, 133, 103548.	1.3	4
1569	SETD1A Methyltransferase Is Physically and Functionally Linked to the DNA Damage Repair Protein RAD18. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1428-1436.	2.5	17
1570	A comparative analysis of egg provisioning using mass spectrometry during rapid life history evolution in sea urchins. <i>Evolution &amp; Development</i> , 2019, 21, 188-204.	1.1	20
1571	The synovial fluid proteome differentiates between septic and nonseptic articular pathologies. <i>Journal of Proteomics</i> , 2019, 202, 103370.	1.2	13
1572	iTRAQ comparison of proteomic profiles of endometrial receptivity. <i>Journal of Proteomics</i> , 2019, 203, 103381.	1.2	16
1573	Glycoproteogenomics: A Frequent Gene Polymorphism Affects the Glycosylation Pattern of the Human Serum Fetuin/±2-HS-Glycoprotein. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1479-1490.	2.5	37
1574	<i>Campylobacter jejuni</i> Demonstrates Conserved Proteomic and Transcriptomic Responses When Co-cultured With Human INT 407 and Caco-2 Epithelial Cells. <i>Frontiers in Microbiology</i> , 2019, 10, 755.	1.5	19
1575	Mono(2-ethylhexyl) phthalate (MEHP) induces transcriptomic alterations in oocytes and their derived blastocysts. <i>Toxicology</i> , 2019, 421, 59-73.	2.0	32
1576	In Vivo Proteome of <i>Pseudomonas aeruginosa</i> in Airways of Cystic Fibrosis Patients. <i>Journal of Proteome Research</i> , 2019, 18, 2601-2612.	1.8	23
1577	Interactive Peptide Spectral Annotator: A Versatile Web-based Tool for Proteomic Applications. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S193-S201.	2.5	97
1578	The Ser/Thr Kinase PrkC Participates in Cell Wall Homeostasis and Antimicrobial Resistance in <i>Clostridium difficile</i> . <i>Infection and Immunity</i> , 2019, 87, .	1.0	28
1579	Quantitative proteomic analyses of CD4+ and CD8+ T cells reveal differentially expressed proteins in multiple sclerosis patients and healthy controls. <i>Clinical Proteomics</i> , 2019, 16, 19.	1.1	24



#	ARTICLE	IF	CITATIONS
1580	Cryo-Electron Tomography and Proteomics studies of centrosomes from differentiated quiescent thymocytes. <i>Scientific Reports</i> , 2019, 9, 7187.	1.6	6
1581	Metabolic reprogramming involving glycolysis in the hibernating brown bear skeletal muscle. <i>Frontiers in Zoology</i> , 2019, 16, 12.	0.9	34
1582	Proteomic Characterization of Immunoglobulin Content in Dermal Interstitial Fluid. <i>Journal of Proteome Research</i> , 2019, 18, 2381-2384.	1.8	11
1583	Nucleoporin Nup155 is part of the p53 network in liver cancer. <i>Nature Communications</i> , 2019, 10, 2147.	5.8	29
1584	Capillary Zone Electrophoresis-Tandem Mass Spectrometry with Activated Ion Electron Transfer Dissociation for Large-scale Top-down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2470-2479.	1.2	17
1585	Accurate peptide fragmentation predictions allow data driven approaches to replace and improve upon proteomics search engine scoring functions. <i>Bioinformatics</i> , 2019, 35, 5243-5248.	1.8	52
1586	Proteomic and Metabolomic Profiling of <i>Deinococcus radiodurans</i> Recovering After Exposure to Simulated Low Earth Orbit Vacuum Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 909.	1.5	23
1587	GlycopeptideGraphMS: Improved Glycopeptide Detection and Identification by Exploiting Graph Theoretical Patterns in Mass and Retention Time. <i>Analytical Chemistry</i> , 2019, 91, 7236-7244.	3.2	46
1588	Proteome-wide detection of S-nitrosylation targets and motifs using bioorthogonal cleavable-linker-based enrichment and switch technique. <i>Nature Communications</i> , 2019, 10, 2195.	5.8	66
1589	Systems Biology and Multi-Omics Integration: Viewpoints from the Metabolomics Research Community. <i>Metabolites</i> , 2019, 9, 76.	1.3	387
1590	A proteomic comparison of excretion/secretion products in <i>Fasciola hepatica</i> newly excysted juveniles (NEJ) derived from <i>Lymnaea viatrix</i> or <i>Pseudosuccinea columella</i> . <i>Experimental Parasitology</i> , 2019, 201, 11-20.	0.5	10
1591	Circadian Analysis of the Mouse Cerebellum Proteome. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1852.	1.8	10
1592	Influence of surface chemistry on the formation of a protein corona on nanodiamonds. <i>Journal of Materials Chemistry B</i> , 2019, 7, 3383-3389.	2.9	15
1593	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. <i>Expert Review of Proteomics</i> , 2019, 16, 375-390.	1.3	86
1594	Quantitative proteomic analysis of venom from Southern India common krait ( <i>Bungarus</i> ) commercial antivenom. <i>Expert Review of Proteomics</i> , 2019, 16, 457-469.	1.3	39
1595	Palaeoproteomics of bird bones for taxonomic classification. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 650-665.	1.0	15
1596	Relationship of <i>GUN1</i> to <i>FUG1</i> in chloroplast protein homeostasis. <i>Plant Journal</i> , 2019, 99, 521-535.	2.8	35
1597	Molecular Mechanisms of Tungsten Toxicity Differ for <i>Glycine max</i> Depending on Nitrogen Regime. <i>Frontiers in Plant Science</i> , 2019, 10, 367.	1.7	8

#	ARTICLE	IF	CITATIONS
1598	More than a Toxin: Protein Inventory of Clostridium tetani Toxoid Vaccines. <i>Proteomes</i> , 2019, 7, 15.	1.7	17
1599	The Plant <sc>PTM</sc> Viewer, a central resource for exploring plant protein modifications. <i>Plant Journal</i> , 2019, 99, 752-762.	2.8	97
1600	Deciphering the Roles of N-Glycans on Collagen-Platelet Interactions. <i>Journal of Proteome Research</i> , 2019, 18, 2467-2477.	1.8	14
1601	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
1602	PROTEOFORMER 2.0: Further Developments in the Ribosome Profiling-assisted Proteogenomic Hunt for New Proteoforms. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S126-S140.	2.5	43
1603	<i>Toxoplasma</i> Controls Host Cyclin E Expression through the Use of a Novel MYR1-Dependent Effector Protein, HCE1. <i>MBio</i> , 2019, 10, .	1.8	49
1604	Novel <sc>CSF</sc> biomarkers in genetic frontotemporal dementia identified by proteomics. <i>Annals of Clinical and Translational Neurology</i> , 2019, 6, 698-707.	1.7	42
1605	Multi-Enzymatic Limited Digestion: The Next-Generation Sequencing for Proteomics?. <i>Journal of Proteome Research</i> , 2019, 18, 2501-2513.	1.8	29
1606	Depletion of the RNA binding protein HNRNP D impairs homologous recombination by inhibiting DNA-end resection and inducing R-loop accumulation. <i>Nucleic Acids Research</i> , 2019, 47, 4068-4085.	6.5	41
1607	Photocatalytic Protein Damage by Silver Nanoparticles Circumvents Bacterial Stress Response and Multidrug Resistance. <i>MSphere</i> , 2019, 4, .	1.3	23
1608	Comprehensive proteome and phosphoproteome profiling shows negligible influence of RNA later on protein abundance and phosphorylation. <i>Clinical Proteomics</i> , 2019, 16, 18.	1.1	6
1609	Metaproteome analysis reveals that syntrophy, competition, and phage-host interaction shape microbial communities in biogas plants. <i>Microbiome</i> , 2019, 7, 69.	4.9	88
1610	Liver proteomics of gilthead sea bream ( <i>Sparus aurata</i> ) exposed to cold stress. <i>Journal of Thermal Biology</i> , 2019, 82, 234-241.	1.1	14
1611	An Interaction Network of the Human SEPT9 Established by Quantitative Mass Spectrometry. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1869-1880.	0.8	15
1612	Proteomics of diphtheria toxoid vaccines reveals multiple proteins that are immunogenic and may contribute to protection of humans against <i>Corynebacterium diphtheriae</i> . <i>Vaccine</i> , 2019, 37, 3061-3070.	1.7	25
1613	The interactome of a family of potential methyltransferases in HeLa cells. <i>Scientific Reports</i> , 2019, 9, 6584.	1.6	52
1614	Mass Spectrometry-Based Proteomics Analyses Using the OpenProt Database to Unveil Novel Proteins Translated from Non-Canonical Open Reading Frames. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	8
1615	Enrichment of ATP Binding Proteins Unveils Proteomic Alterations in Human Macrophage Cell Death, Inflammatory Response, and Protein Synthesis after Interaction with <i>Candida albicans</i>. <i>Journal of Proteome Research</i> , 2019, 18, 2139-2159.	1.8	3

#	ARTICLE	IF	CITATIONS
1616	Dark metabolism: a molecular insight into how the Antarctic sea-ice diatom <i>Fragilariopsis cylindrus</i> survives long-term darkness. <i>New Phytologist</i> , 2019, 223, 675-691.	3.5	40
1617	A Protein-Linger Strategy Keeps the Plant On-Hold After Rehydration of Drought-Stressed <i>Beta vulgaris</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 381.	1.7	10
1618	Quantitative proteomic analysis of prostate tissue specimens identifies deregulated protein complexes in primary prostate cancer. <i>Clinical Proteomics</i> , 2019, 16, 15.	1.1	15
1619	Identification of O-GlcNacetylated Proteins in <i>Trypanosoma cruzi</i> . <i>Frontiers in Endocrinology</i> , 2019, 10, 199.	1.5	9
1620	Vps11 and Vps18 of Vps-C membrane traffic complexes are E3 ubiquitin ligases and fine-tune signalling. <i>Nature Communications</i> , 2019, 10, 1833.	5.8	26
1621	Elevated carbon dioxide levels lead to proteome-wide alterations for optimal growth of a fast-growing cyanobacterium, <i>Synechococcus elongatus</i> PCC 11801. <i>Scientific Reports</i> , 2019, 9, 6257.	1.6	21
1622	Exploring the Potential Role of Moonlighting Function of the Surface-Associated Proteins From <i>Mycobacterium bovis</i> BCG Moreau and Pasteur by Comparative Proteomic. <i>Frontiers in Immunology</i> , 2019, 10, 716.	2.2	10
1623	Brain Citrullination Patterns and T Cell Reactivity of Cerebrospinal Fluid-Derived CD4+ T Cells in Multiple Sclerosis. <i>Frontiers in Immunology</i> , 2019, 10, 540.	2.2	31
1624	Dysregulation of Myosin Complex and Striated Muscle Contraction Pathway in the Brains of ALS-SOD1 Model Mice. <i>ACS Chemical Neuroscience</i> , 2019, 10, 2408-2417.	1.7	15
1625	Capturing site-specific heterogeneity with large-scale N-glycoproteome analysis. <i>Nature Communications</i> , 2019, 10, 1311.	5.8	180
1626	A post-translational modification of human Norovirus capsid protein attenuates glycan binding. <i>Nature Communications</i> , 2019, 10, 1320.	5.8	50
1627	Proteomes of Leaf-Growing Zones in Rice Genotypes with Contrasting Drought Tolerance. <i>Proteomics</i> , 2019, 19, 1800310.	1.3	9
1628	Significant Down-Regulation of Urea Cycle Generates Clinically Relevant Proteomic Signature in Hepatocellular Carcinoma Patients with Macrovascular Invasion. <i>Journal of Proteome Research</i> , 2019, 18, 2032-2044.	1.8	18
1629	A Pathogen and a Non-pathogen Spotted Fever Group Rickettsia Trigger Differential Proteome Signatures in Macrophages. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 43.	1.8	23
1630	Combining Rapid Data Independent Acquisition and CRISPR Gene Deletion for Studying Potential Protein Functions: A Case of HMG1. <i>Proteomics</i> , 2019, 19, e1800438.	1.3	31
1631	Chemoproteomic Selectivity Profiling of PIKK and PI3K Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2019, 14, 655-664.	1.6	21
1632	MDC1 Interacts with TOPBP1 to Maintain Chromosomal Stability during Mitosis. <i>Molecular Cell</i> , 2019, 74, 571-583.e8.	4.5	97
1633	Cationic gold nanoparticles elicit mitochondrial dysfunction: a multi-omics study. <i>Scientific Reports</i> , 2019, 9, 4366.	1.6	54

#	ARTICLE	IF	CITATIONS
1634	Nitric oxide-dependent anaerobic ammonium oxidation. <i>Nature Communications</i> , 2019, 10, 1244.	5.8	103
1635	Multiplex targeted mass spectrometry assay for one-shot flavivirus diagnosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6754-6759.	3.3	18
1636	Lysosomal targeting of the ABC transporter TAPL is determined by membrane-localized charged residues. <i>Journal of Biological Chemistry</i> , 2019, 294, 7308-7323.	1.6	15
1637	Molecular analysis of somatic embryogenesis through proteomic approach and optimization of protocol in recalcitrant <i>Musa</i> spp.. <i>Physiologia Plantarum</i> , 2019, 167, 282-301.	2.6	16
1638	Physical Activity Associated Proteomics of Skeletal Muscle: Being Physically Active in Daily Life May Protect Skeletal Muscle From Aging. <i>Frontiers in Physiology</i> , 2019, 10, 312.	1.3	70
1639	Human chorionic gonadotrophin pharmaceutical formulations of urinary origin display high levels of contaminant proteins—A label-free quantitation proteomics study. <i>Electrophoresis</i> , 2019, 40, 1622-1629.	1.3	5
1640	Mitochondrial protein-induced stress triggers a global adaptive transcriptional programme. <i>Nature Cell Biology</i> , 2019, 21, 442-451.	4.6	146
1641	The chaperone ERp29 is required for tunneling nanotube formation by stabilizing MSec. <i>Journal of Biological Chemistry</i> , 2019, 294, 7177-7193.	1.6	22
1642	Quantitative Proteomics Links the Intermediate Filament Nestin to Resistance to Targeted BRAF Inhibition in Melanoma Cells. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1096-1109.	2.5	25
1643	Heterogeneous clinical phenotypes and cerebral malformations reflected by rotatin cellular dynamics. <i>Brain</i> , 2019, 142, 867-884.	3.7	22
1644	Anti $\alpha$ -enolase antibody is a novel autoimmune biomarker for unexplained recurrent miscarriages. <i>EBioMedicine</i> , 2019, 41, 610-622.	2.7	17
1645	Microsampling Capillary Electrophoresis Mass Spectrometry Enables Single-Cell Proteomics in Complex Tissues: Developing Cell Clones in Live <i>Xenopus laevis</i> and Zebrafish Embryos. <i>Analytical Chemistry</i> , 2019, 91, 4797-4805.	3.2	97
1646	Chromatin capture links the metabolic enzyme AHCY to stem cell proliferation. <i>Science Advances</i> , 2019, 5, eaav2448.	4.7	38
1647	Differential miRNA expression profile and proteome in plasma exosomes from patients with paroxysmal nocturnal hemoglobinuria. <i>Scientific Reports</i> , 2019, 9, 3611.	1.6	13
1648	Autocrine motility factor promotes endometrial cancer progression by targeting GPER-1. <i>Cell Communication and Signaling</i> , 2019, 17, 22.	2.7	22
1649	Deprivation of the Periplasmic Chaperone SurA Reduces Virulence and Restores Antibiotic Susceptibility of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 100.	1.5	31
1650	<i>Neisseria gonorrhoeae</i> MlaA influences gonococcal virulence and membrane vesicle production. <i>PLoS Pathogens</i> , 2019, 15, e1007385.	2.1	40
1651	Pro-inflammatory Cytokines Alter the Immunopeptidome Landscape by Modulation of HLA-B Expression. <i>Frontiers in Immunology</i> , 2019, 10, 141.	2.2	38

#	ARTICLE	IF	CITATIONS
1652	YESdb: integrative analysis of environmental stress in yeast. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	1
1653	The temporal profile of activity-dependent presynaptic phospho-signalling reveals long-lasting patterns of poststimulus regulation. PLoS Biology, 2019, 17, e3000170.	2.6	29
1654	Plasma proteome profiling discovers novel proteins associated with non-alcoholic fatty liver disease. Molecular Systems Biology, 2019, 15, e8793.	3.2	176
1655	Urinary Proteomics Profiles Are Useful for Detection of Cancer Biomarkers and Changes Induced by Therapeutic Procedures. Molecules, 2019, 24, 794.	1.7	25
1656	Quantitative proteomic analyses of dynamic signalling events in cortical neurons undergoing excitotoxic cell death. Cell Death and Disease, 2019, 10, 213.	2.7	16
1657	Dynamic pigmentary and structural coloration within cephalopod chromatophore organs. Nature Communications, 2019, 10, 1004.	5.8	105
1658	Molecular characterization of <i>Histomonas meleagridis</i> exoproteome with emphasis on protease secretion and parasite-bacteria interaction. PLoS ONE, 2019, 14, e0212429.	1.1	6
1659	Label-free absolute protein quantification with data-independent acquisition. Journal of Proteomics, 2019, 200, 51-59.	1.2	60
1660	Tick Genomes' organ engagement in lipid metabolism revealed by a combined transcriptomic and proteomic approach. Ticks and Tick-borne Diseases, 2019, 10, 787-797.	1.1	12
1661	Anaerobic oxidation of ethane by archaea from a marine hydrocarbon seep. Nature, 2019, 568, 108-111.	13.7	149
1662	Agonist-selective NOP receptor phosphorylation correlates in vitro and in vivo and reveals differential post-activation signaling by chemically diverse agonists. Science Signaling, 2019, 12, .	1.6	36
1663	Caught in a Trap? Proteomic Analysis of Neutrophil Extracellular Traps in Rheumatoid Arthritis and Systemic Lupus Erythematosus. Frontiers in Immunology, 2019, 10, 423.	2.2	136
1664	Ubiquitin C-terminal hydrolase L1 (UCH-L1) loss causes neurodegeneration by altering protein turnover in the first postnatal weeks. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7963-7972.	3.3	36
1665	Silencing of carbonic anhydrase I enhances the malignant potential of exosomes secreted by prostatic tumour cells. Journal of Cellular and Molecular Medicine, 2019, 23, 3641-3655.	1.6	7
1666	Combined Transcriptome and Proteome Analysis of Immortalized Human Keratinocytes Expressing Human Papillomavirus 16 (HPV16) Oncogenes Reveals Novel Key Factors and Networks in HPV-Induced Carcinogenesis. MSphere, 2019, 4, .	1.3	23
1667	A Study into the ADP-Ribosylome of IFN- $\beta$ -Stimulated THP-1 Human Macrophage-like Cells Identifies ARTD8/PARP14 and ARTD9/PARP9 ADP-Ribosylation. Journal of Proteome Research, 2019, 18, 1607-1622.	1.8	21
1668	Thylakoid Localized Type 2 NAD(P)H Dehydrogenase NdbA Optimizes Light-Activated Heterotrophic Growth of <i>Synechocystis</i> sp. PCC 6803. Plant and Cell Physiology, 2019, 60, 1386-1399.	1.5	9
1669	Identification of a non-canonical chondroitin sulfate linkage region trisaccharide. Glycobiology, 2019, 29, 366-371.	1.3	16

#	ARTICLE	IF	CITATIONS
1670	Structural and functional differentiation of the light-harvesting protein Lhcb4 during land plant diversification. <i>Physiologia Plantarum</i> , 2019, 166, 336-350.	2.6	14
1671	IsoProt: A Complete and Reproducible Workflow To Analyze iTRAQ/TMT Experiments. <i>Journal of Proteome Research</i> , 2019, 18, 1751-1759.	1.8	11
1672	A homopolymeric adenosine tract in the promoter region of nspA influences factor H-mediated serum resistance in <i>Neisseria meningitidis</i> . <i>Scientific Reports</i> , 2019, 9, 2736.	1.6	4
1673	Life history shapes variation in egg composition in the blue tit <i>Cyanistes caeruleus</i> . <i>Communications Biology</i> , 2019, 2, 6.	2.0	18
1674	Binding Specificity of Native Odorant-Binding Protein Isoforms Is Driven by Phosphorylation and O-N-Acetylglucosaminylation in the Pig <i>Sus scrofa</i> . <i>Frontiers in Endocrinology</i> , 2019, 9, 816.	1.5	14
1675	Histone serotonylation is a permissive modification that enhances TFIID binding to H3K4me3. <i>Nature</i> , 2019, 567, 535-539.	13.7	292
1676	Proteomic analysis reveals that sugar and fatty acid metabolisms play a central role in sterility of the male-sterile line 1355A of cotton. <i>Journal of Biological Chemistry</i> , 2019, 294, 7057-7067.	1.6	13
1677	Time-resolved dissection of the molecular crosstalk driving <i>Fusarium</i> head blight in wheat provides new insights into host susceptibility determinism. <i>Plant, Cell and Environment</i> , 2019, 42, 2291-2308.	2.8	18
1678	The Foliar Endophyte <i>Phialocephala scopiformis</i> DAOMC 229536 Proteome When Grown on Wood Used as the Sole Carbon Source. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
1679	More Is Not Always Better: Evaluation of 1D and 2D-LC-MS/MS Methods for Metaproteomics. <i>Frontiers in Microbiology</i> , 2019, 10, 238.	1.5	55
1680	Differential View on the Bile Acid Stress Response of <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 258.	1.5	24
1681	Proteomic Analysis of <i>Arabidopsis</i> <i>pld1</i> Mutants Revealed an Important Role of Phospholipase D Alpha 1 in Chloroplast Biogenesis. <i>Frontiers in Plant Science</i> , 2019, 10, 89.	1.7	12
1682	LipidII interaction with specific residues of <i>Mycobacterium tuberculosis</i> PknB extracytoplasmic domain governs its optimal activation. <i>Nature Communications</i> , 2019, 10, 1231.	5.8	42
1683	Quantitative proteomic changes in LPS-activated monocyte-derived dendritic cells: A SWATH-MS study. <i>Scientific Reports</i> , 2019, 9, 4343.	1.6	6
1684	Arsenic Trioxide and (â²)-Gossypol Synergistically Target Glioma Stem-Like Cells via Inhibition of Hedgehog and Notch Signaling. <i>Cancers</i> , 2019, 11, 350.	1.7	29
1685	Miniaturised interaction proteomics on a microfluidic platform with ultra-low input requirements. <i>Nature Communications</i> , 2019, 10, 1525.	5.8	29
1686	&lt;p&gt;Plasma protein adsorption on Fe&lt;sub&gt;3&lt;/sub&gt;O&lt;sub&gt;4&lt;/sub&gt;-PEG nanoparticles activates the complement system and induces an inflammatory response&lt;/p&gt;. <i>International Journal of Nanomedicine</i> , 2019, Volume 14, 2055-2067.	3.3	32
1687	A Systematic Workflow for Design and Computational Analysis of Protein Microarrays. , 2019, , 213-222.		1

#	ARTICLE	IF	CITATIONS
1688	Identification, Quantification, and System Analysis of Protein Nâ€¦ Lysine Methylation in Anucleate Blood Platelets. <i>Proteomics</i> , 2019, 19, e1900001.	1.3	7
1689	Mass Spectrometry of Proteins. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	0
1690	Living in future ocean acidification, physiological adaptive responses of the immune system of sea urchins resident at a CO2 vent system. <i>Science of the Total Environment</i> , 2019, 672, 938-950.	3.9	53
1691	Chemosynthetic symbiont with a drastically reduced genome serves as primary energy storage in the marine flatworm <i>Paracatenula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8505-8514.	3.3	49
1692	Comparative proteomics combined with analyses of transgenic plants reveal Zm<sc>REM</sc>1.3 mediates maize resistance to southern corn rust. <i>Plant Biotechnology Journal</i> , 2019, 17, 2153-2168.	4.1	46
1693	Improved Methodology for Sensitive and Rapid Quantitative Proteomic Analysis of Adultâ€Derived Mouse Microglia: Application to a Novel In Vitro Mouse Microglial Cell Model. <i>Proteomics</i> , 2019, 19, 1800469.	1.3	15
1694	Quantitative Proteomics Data in theâ€Public Domain: Challenges and Opportunities. <i>Methods in Molecular Biology</i> , 2019, 1977, 217-235.	0.4	5
1695	Scavenging organic nitrogen and remodelling lipid metabolism are key survival strategies adopted by the endophytic fungi, <i>Serendipita vermifera</i> and <i>Serendipita bescii</i> to alleviate nitrogen and phosphorous starvation in vitro. <i>Environmental Microbiology Reports</i> , 2019, 11, 548-557.	1.0	18
1696	Defining the <sc>RNA</sc> interactome by total <sc>RNA</sc> â€associated protein purification. <i>Molecular Systems Biology</i> , 2019, 15, e8689.	3.2	114
1697	Quantitative Microproteomics Based Characterization of the Central and Peripheral Nervous System of a Mouse Model of Krabbe Disease. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1227-1241.	2.5	25
1698	Proteomics of Asrij Perturbation in Drosophila Lymph Glands for Identification of New Regulators of Hematopoiesis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1171-1182.	2.5	5
1699	EZH1/CXorf67 mimics K27M mutated oncohistones and functions as an intrinsic inhibitor of PRC2 function in aggressive posterior fossa ependymoma. <i>Neuro-Oncology</i> , 2019, 21, 878-889.	0.6	106
1700	The ABCB7-Like Transporter PexA in Rhodobacter capsulatus Is Involved in the Translocation of Reactive Sulfur Species. <i>Frontiers in Microbiology</i> , 2019, 10, 406.	1.5	4
1701	The proteome of <i>Medicago truncatula</i> in response to ammonium and urea nutrition reveals the role of membrane proteins and enzymes of root lignification. <i>Environmental and Experimental Botany</i> , 2019, 162, 168-180.	2.0	13
1702	Metaproteomic and 16S rRNA Gene Sequencing Analysis of the Infant Fecal Microbiome. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1430.	1.8	12
1703	Benzo[ <i>a</i> ]pyrene Induction of Glutathione S-Transferases: An Activity-Based Protein Profiling Investigation. <i>Chemical Research in Toxicology</i> , 2019, 32, 1259-1267.	1.7	13
1704	Proteomics profiling of arginine methylation defines PRMT5 substrate specificity. <i>Science Signaling</i> , 2019, 12, .	1.6	114
1705	Ozone-induced damage of fibrinogen molecules: identification of oxidation sites by high-resolution mass spectrometry. <i>Free Radical Research</i> , 2019, 53, 430-455.	1.5	17

#	ARTICLE	IF	CITATIONS
1706	Light-Controlled Affinity Purification of Protein Complexes Exemplified by the Resting ZAP70 Interactome. <i>Frontiers in Immunology</i> , 2019, 10, 226.	2.2	11
1707	Intestinal Epithelial Cells and the Microbiome Undergo Swift Reprogramming at the Inception of Colonic <i>Citrobacter rodentium</i> Infection. <i>MBio</i> , 2019, 10, .	1.8	38
1708	Analysis of 1508 Plasma Samples by Capillary-Flow Data-Independent Acquisition Profiles Proteomics of Weight Loss and Maintenance. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1242-1254.	2.5	162
1709	Proteomic analysis of the similarities and differences of soil drought and polyethylene glycol stress responses in wheat ( <i>Triticum aestivum</i> L.). <i>Plant Molecular Biology</i> , 2019, 100, 391-410.	2.0	26
1710	Proteomic and Postâ€Translational Modification Profiling of Exosomeâ€Mimetic Nanovesicles Compared to Exosomes. <i>Proteomics</i> , 2019, 19, e1800161.	1.3	49
1711	Proteomic analysis of synovial fluid: current and potential uses to improve clinical outcomes. <i>Expert Review of Proteomics</i> , 2019, 16, 287-302.	1.3	21
1712	Phosphodiesterase beta is the master regulator of cAMP signalling during malaria parasite invasion. <i>PLoS Biology</i> , 2019, 17, e3000154.	2.6	38
1713	Insight into Salivary Gland Proteomes of Two Polyphagous Stink Bugs: <i>Nezara viridula</i> L. and <i>Halyomorpha halys</i> StÅl. <i>Proteomics</i> , 2019, 19, 1800436.	1.3	19
1714	In-Depth Proteome Analysis Highlights HepaRG Cells as a Versatile Cell System Surrogate for Primary Human Hepatocytes. <i>Cells</i> , 2019, 8, 192.	1.8	41
1715	Inhibition of histone methyltransferase DOT1L silences ERÎ± gene and blocks proliferation of antiestrogen-resistant breast cancer cells. <i>Science Advances</i> , 2019, 5, eaav5590.	4.7	70
1716	Fission Yeast NDR/LATS Kinase Orb6 Regulates Exocytosis via Phosphorylation of the Exocyst Complex. <i>Cell Reports</i> , 2019, 26, 1654-1667.e7.	2.9	27
1717	Comparison of Protein Quantification in a Complex Background by DIA and TMT Workflows with Fixed Instrument Time. <i>Journal of Proteome Research</i> , 2019, 18, 1340-1351.	1.8	107
1718	Proteomic study uncovers molecular principles of single-cell-level phenotypic heterogeneity in lipid storage of <i>Nannochloropsis oceanica</i> . <i>Biotechnology for Biofuels</i> , 2019, 12, 21.	6.2	14
1719	Reprogramming of <i>Trypanosoma cruzi</i> metabolism triggered by parasite interaction with the host cell extracellular matrix. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007103.	1.3	23
1720	Folliculin regulates mTORC1/2 and WNT pathways in early human pluripotency. <i>Nature Communications</i> , 2019, 10, 632.	5.8	47
1721	Physiological and comparative proteomic analyses of saline-alkali NaHCO <sub>3</sub> -responses in leaves of halophyte <i>Puccinellia tenuiflora</i> . <i>Plant and Soil</i> , 2019, 437, 137-158.	1.8	41
1722	Proteomic Atlas of the Human Brain in Alzheimerâ€s Disease. <i>Journal of Proteome Research</i> , 2019, 18, 1380-1391.	1.8	42
1723	Extracellular peptide Kratos restricts cell death during vascular development and stress in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 2199-2210.	2.4	11



#	ARTICLE	IF	CITATIONS
1724	Reversible SAHH inhibitor protects against glomerulonephritis in lupus-prone mice by downregulating renal $\beta$ -actinin-4 expression and stabilizing integrin-cytoskeleton linkage. <i>Arthritis Research and Therapy</i> , 2019, 21, 40.	1.6	7
1725	Development of a Sensitive, Scalable Method for Spatial, Cell-Type-Resolved Proteomics of the Human Brain. <i>Journal of Proteome Research</i> , 2019, 18, 1787-1795.	1.8	39
1726	Proteomic Changes in Oral Keratinocytes Chronically Exposed to Shisha (Water Pipe). <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 86-97.	1.0	8
1727	Proteomics and Visual Health Research: Proteome of the Human Sclera Using High-Resolution Mass Spectrometry. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 98-110.	1.0	8
1728	Identification of Early Salinity Stress-Responsive Proteins in <i>Dunaliella salina</i> by isobaric tags for relative and absolute quantitation (iTRAQ)-Based Quantitative Proteomic Analysis. <i>International Journal of Molecular Sciences</i> , 2019, 20, 599.	1.8	22
1729	Characterization of the catabolic pathway of diclofenac in <i>Raoultella</i> sp. KDF8. <i>International Biodeterioration and Biodegradation</i> , 2019, 137, 88-94.	1.9	19
1730	Oxylipins mediate cell-to-cell communication in <i>Pseudomonas aeruginosa</i> . <i>Communications Biology</i> , 2019, 2, 66.	2.0	24
1731	On the characterisation of the porcine gland-specific salivary proteome. <i>Journal of Proteomics</i> , 2019, 196, 92-105.	1.2	10
1732	The Antarctic psychrophiles <i>Chlamydomonas</i> spp. UWO241 and ICE-MDV exhibit differential restructuring of photosystem I in response to iron. <i>Photosynthesis Research</i> , 2019, 141, 209-228.	1.6	26
1733	Synbiotic-driven improvement of metabolic disturbances is associated with changes in the gut microbiome in diet-induced obese mice. <i>Molecular Metabolism</i> , 2019, 22, 96-109.	3.0	102
1734	Signal peptide peptidase-like 2c impairs vesicular transport and cleaves SNARE proteins. <i>EMBO Reports</i> , 2019, 20, .	2.0	22
1735	oxSWATH: An integrative method for a comprehensive redox-centered analysis combined with a generic differential proteomics screening. <i>Redox Biology</i> , 2019, 22, 101130.	3.9	15
1736	A network of chaperones prevents and detects failures in membrane protein lipid bilayer integration. <i>Nature Communications</i> , 2019, 10, 672.	5.8	33
1737	Structure of the complex I-like molecule NDH of $\alpha$ -oxygenic photosynthesis. <i>Nature</i> , 2019, 566, 411-414.	13.7	123
1738	The intramembrane protease <i>SPPL</i> 2c promotes male germ cell development by cleaving $\beta$ -phospholamban. <i>EMBO Reports</i> , 2019, 20, .	2.0	27
1739	The classical NLRP3 inflammasome controls FADD unconventional secretion through microvesicle shedding. <i>Cell Death and Disease</i> , 2019, 10, 190.	2.7	33
1740	Autoantibody Biomarker Discovery in Primary Open Angle Glaucoma Using Serological Proteome Analysis (SERPA). <i>Frontiers in Immunology</i> , 2019, 10, 381.	2.2	32
1741	Unveiling Kiwifruit Metabolite and Protein Changes in the Course of Postharvest Cold Storage. <i>Frontiers in Plant Science</i> , 2019, 10, 71.	1.7	34

#	ARTICLE	IF	CITATIONS
1742	Proteomics Reveals Profound Metabolic Changes in the Alcohol Use Disorder Brain. ACS Chemical Neuroscience, 2019, 10, 2364-2373.	1.7	26
1743	Colonic epithelial cell diversity in health and inflammatory bowel disease. Nature, 2019, 567, 49-55.	13.7	486
1744	Sequential Digestion with Trypsin and Elastase in Cross-Linking Mass Spectrometry. Analytical Chemistry, 2019, 91, 4472-4478.	3.2	26
1745	Coacervation of Lipid Bilayer in Natural Cell Membranes for Extraction, Fractionation, and Enrichment of Proteins in Proteomics Studies. Journal of Proteome Research, 2019, 18, 1595-1606.	1.8	11
1746	Serum biomarkers identification by iTRAQ and verification by MRM: S100A8/S100A9 levels predict tumor-stroma involvement and prognosis in Glioblastoma. Scientific Reports, 2019, 9, 2749.	1.6	33
1747	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. Nature Biotechnology, 2019, 37, 314-322.	9.4	254
1748	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. Molecular Systems Biology, 2019, 15, e8503.	3.2	576
1749	Profiling microalgal protein extraction by microwave burst heating in comparison to spark plasma exposures. Algal Research, 2019, 39, 101416.	2.4	15
1750	Beneficial effects of Coomassie staining on proteomic analysis employing PAGE separation followed with whole-gel slicing, in-gel digestion and quantitative LC-MS/MS. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2019, 1110-1111, 25-35.	1.2	5
1751	Shotgun proteomics provides an insight into pathogenesis-related proteins using anamorphic stage of the biotroph, Erysiphe pisi pathogen of garden pea. Microbiological Research, 2019, 222, 25-34.	2.5	9
1752	The flavonoid 4,4-dimethoxychalcone promotes autophagy-dependent longevity across species. Nature Communications, 2019, 10, 651.	5.8	100
1753	Multiplexed Relative Quantitation with Isobaric Tagging Mass Spectrometry Reveals Class I Major Histocompatibility Complex Ligand Dynamics in Response to Doxorubicin. Analytical Chemistry, 2019, 91, 5106-5115.	3.2	27
1754	The companion of cellulose synthase 1 confers salt tolerance through a Tau-like mechanism in plants. Nature Communications, 2019, 10, 857.	5.8	71
1755	An atypical aspartic protease modulates lateral root development in Arabidopsis thaliana. Journal of Experimental Botany, 2019, 70, 2157-2171.	2.4	24
1756	A rapid methods development workflow for high-throughput quantitative proteomic applications. PLoS ONE, 2019, 14, e0211582.	1.1	17
1757	Pre-fractionation Extends but also Creates a Bias in the Detectable HLA Class I <sup>TM</sup> Ligandome. Journal of Proteome Research, 2019, 18, 1634-1643.	1.8	24
1758	Metabolic, Anti-apoptotic and Immune Evasion Strategies of Primary Human Myeloma Cells Indicate Adaptations to Hypoxia*. Molecular and Cellular Proteomics, 2019, 18, 936-953.	2.5	30
1759	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. Molecular and Cellular Proteomics, 2019, 18, 982a-994.	2.5	91

#	ARTICLE	IF	CITATIONS
1760	Multifaceted activity of cytokinin in leaf development shapes its size and structure in Arabidopsis. <i>Plant Journal</i> , 2019, 97, 805-824.	2.8	74
1761	Systems-Level Analysis of Oxygen Exposure in <i>Zymomonas mobilis</i> : Implications for Isoprenoid Production. <i>MSystems</i> , 2019, 4, .	1.7	27
1762	Proteomic characterization of rabbit ( <i>Oryctolagus cuniculus</i> ) sperm from two different genotypes. <i>Theriogenology</i> , 2019, 128, 140-148.	0.9	8
1763	Identification and characterization of cytochrome P450 1232A24 and 1232F1 from <i>Arthrobacter</i> sp. and their role in the metabolic pathway of papaverine. <i>Journal of Biochemistry</i> , 2019, 166, 51-66.	0.9	9
1764	Modulation of the ATM/autophagy pathway by a G-quadruplex ligand tips the balance between senescence and apoptosis in cancer cells. <i>Nucleic Acids Research</i> , 2019, 47, 2739-2756.	6.5	50
1765	Extrachloroplastic PP7L Functions in Chloroplast Development and Abiotic Stress Tolerance. <i>Plant Physiology</i> , 2019, 180, 323-341.	2.3	30
1766	Visualization and Analysis of Epiproteome Dynamics. <i>Journal of Molecular Biology</i> , 2019, 431, 1519-1539.	2.0	10
1767	Localization of Outer Membrane Proteins in <i>Treponema denticola</i> by Quantitative Proteome Analyses of Outer Membrane Vesicles and Cellular Fractions. <i>Journal of Proteome Research</i> , 2019, 18, 1567-1581.	1.8	11
1768	Identification of several plasma proteins whose levels in colorectal cancer patients differ depending on outcome. <i>FASEB BioAdvances</i> , 2019, 1, 723-730.	1.3	7
1769	Maintenance of spatial gene expression by Polycomb-mediated repression after formation of a vertebrate body plan. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	13
1770	Sensitive Determination of Proteolytic Proteoforms in Limited Microscale Proteome Samples. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2335-2347.	2.5	74
1771	The <i>Arabidopsis thaliana</i> N-recognin E3 ligase PROTEOLYSIS1 influences the immune response. <i>Plant Direct</i> , 2019, 3, e00194.	0.8	12
1772	BMP signaling inhibition in <i>Drosophila</i> secondary cells remodels the seminal proteome and self and rival ejaculate functions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24719-24728.	3.3	29
1773	<i>Candida utilis</i> yeast as a functional protein source for Atlantic salmon ( <i>Salmo salar</i> L.): Local intestinal tissue and plasma proteome responses. <i>PLoS ONE</i> , 2019, 14, e0218360.	1.1	16
1774	Growth phase proteomics of the heterotrophic marine bacterium <i>Ruegeria pomeroyi</i> . <i>Scientific Data</i> , 2019, 6, 303.	2.4	1
1775	Characterization of a human liver reference material fit for proteomics applications. <i>Scientific Data</i> , 2019, 6, 324.	2.4	3
1776	Discovery of increased epidermal DNAH10 expression after regeneration of dermis in a randomized with-in person trial – reflections on psoriatic inflammation. <i>Scientific Reports</i> , 2019, 9, 19136.	1.6	3
1777	Class I HDAC inhibitors enhance YB acetylation and oxidative stress to block sarcoma metastasis. <i>EMBO Reports</i> , 2019, 20, e48375.	2.0	78

#	ARTICLE	IF	CITATIONS
1778	Interplay between the bacterial protein deacetylase CobB and the second messenger cAMP•GMP. EMBO Journal, 2019, 38, e100948.	3.5	28
1779	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus <i>Dichomitus squalens</i> . Applied and Environmental Microbiology, 2019, 85, .	1.4	21
1780	Host-Microbe Interactions in the Chemosynthetic <i>Riftia pachyptila</i> Symbiosis. MBio, 2019, 10, .	1.8	38
1781	Quantitative Proteomics Reveal Peroxiredoxin Perturbation Upon Persistent Lymphocytic Choriomeningitis Virus Infection in Human Cells. Frontiers in Microbiology, 2019, 10, 2438.	1.5	7
1782	Loss of O-Linked Protein Glycosylation in Burkholderia cenocepacia Impairs Biofilm Formation and Siderophore Activity and Alters Transcriptional Regulators. MSphere, 2019, 4, .	1.3	12
1783	DYRK1A Overexpression Alters Cognition and Neural-Related Proteomic Pathways in the Hippocampus That Are Rescued by Green Tea Extract and/or Environmental Enrichment. Frontiers in Molecular Neuroscience, 2019, 12, 272.	1.4	21
1784	Network Analyses and Data Integration of Proteomics and Metabolomics From Leaves of Two Contrasting Varieties of Sugarcane in Response to Drought. Frontiers in Plant Science, 2019, 10, 1524.	1.7	41
1785	A mass spectrometry guided approach for the identification of novel vaccine candidates in gram-negative pathogens. Scientific Reports, 2019, 9, 17401.	1.6	7
1786	Thromboinflammatory changes in plasma proteome of pregnant women with PCOS detected by quantitative label-free proteomics. Scientific Reports, 2019, 9, 17578.	1.6	9
1787	In vitro-digested milk proteins: Evaluation of angiotensin-1-converting enzyme inhibitory and antioxidant activities, peptidomic profile, and mucin gene expression in HT29-MTX cells. Journal of Dairy Science, 2019, 102, 10760-10771.	1.4	16
1788	Proteome Profiling of Cerebral Vessels in Rhesus Macaques: Dysregulation of Antioxidant Activity and Extracellular Matrix Proteins Contributes to Cerebrovascular Aging in Rhesus Macaques. Frontiers in Aging Neuroscience, 2019, 11, 293.	1.7	8
1789	Salivary Protein Panel to Diagnose Systolic Heart Failure. Biomolecules, 2019, 9, 766.	1.8	7
1790	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. Genome Research, 2019, 29, 2073-2087.	2.4	52
1791	ChimST: An Efficient Spectral Library Search Tool for Peptide Identification from Chimeric Spectra in Data-Dependent Acquisition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1416-1425.	1.9	0
1793	The Disulfide Stress Response and Protein S-thioallylation Caused by Allicin and Diallyl Polysulfanes in Bacillus subtilis as Revealed by Transcriptomics and Proteomics. Antioxidants, 2019, 8, 605.	2.2	23
1794	TcellSubC: An Atlas of the Subcellular Proteome of Human T Cells. Frontiers in Immunology, 2019, 10, 2708.	2.2	14
1795	Using Omics Technologies and Systems Biology to Identify Epitope Targets for the Development of Monoclonal Antibodies Against Antibiotic-Resistant Bacteria. Frontiers in Immunology, 2019, 10, 2841.	2.2	11
1796	Accessible and reproducible mass spectrometry imaging data analysis in Galaxy. GigaScience, 2019, 8, .	3.3	22

#	ARTICLE	IF	CITATIONS
1797	Unbalanced Roles of Fungal Aggressiveness and Host Cultivars in the Establishment of the Fusarium Head Blight in Bread Wheat. <i>Frontiers in Microbiology</i> , 2019, 10, 2857.	1.5	22
1798	Co-regulation map of the human proteome enables identification of protein functions. <i>Nature Biotechnology</i> , 2019, 37, 1361-1371.	9.4	106
1799	Proteomic comparison of selective breeding and growth hormone transgenesis in fish: Unique pathways to enhanced growth. <i>Journal of Proteomics</i> , 2019, 192, 114-124.	1.2	31
1800	Changes in the urinary extracellular vesicle proteome are associated with nephronophthisis-related ciliopathies. <i>Journal of Proteomics</i> , 2019, 192, 27-36.	1.2	22
1801	Nrf2 Sequesters Keap1 Preventing Podosome Disassembly: A Quintessential Duet Moonlights in Endothelium. <i>Antioxidants and Redox Signaling</i> , 2019, 30, 1709-1730.	2.5	16
1802	Salicylic acid influences the protease activity and posttranslation modifications of the secreted peptides in the moss <i>Physcomitrella patens</i> . <i>Journal of Peptide Science</i> , 2019, 25, e3138.	0.8	9
1803	Effects of hypoxia-reoxygenation stress on mitochondrial proteome and bioenergetics of the hypoxia-tolerant marine bivalve <i>Crassostrea gigas</i> . <i>Journal of Proteomics</i> , 2019, 194, 99-111.	1.2	62
1804	A specific lipid metabolic profile is associated with the epithelial mesenchymal transition program. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 344-357.	1.2	69
1805	Smell of Infection: A Novel, Noninvasive Method for Detection of Fish Excretory-Secretory Proteins. <i>Journal of Proteome Research</i> , 2019, 18, 1371-1379.	1.8	4
1806	Intricate Crosstalk Between Lipopolysaccharide, Phospholipid and Fatty Acid Metabolism in <i>Escherichia coli</i> Modulates Proteolysis of LpxC. <i>Frontiers in Microbiology</i> , 2018, 9, 3285.	1.5	35
1807	Discerning strain-specific $\beta$ -lactam drug resistance by clonal isolates of multi-drug resistant <i>Pseudomonas aeruginosa</i> using selected reaction monitoring. <i>International Journal of Mass Spectrometry</i> , 2019, 438, 36-43.	0.7	2
1808	A simple approach for restoration of differentiation and function in cryopreserved human hepatocytes. <i>Archives of Toxicology</i> , 2019, 93, 819-829.	1.9	22
1809	Response of the biomining <i>Acidithiobacillus ferrooxidans</i> to high cadmium concentrations. <i>Journal of Proteomics</i> , 2019, 198, 132-144.	1.2	32
1810	Identification of Hybrid Insulin Peptides (HIPs) in Mouse and Human Islets by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2019, 18, 814-825.	1.8	56
1811	Microbial metal-sulfide oxidation in inactive hydrothermal vent chimneys suggested by metagenomic and metaproteomic analyses. <i>Environmental Microbiology</i> , 2019, 21, 682-701.	1.8	50
1812	A multiomic approach to characterize the temporal sequence in Alzheimer's disease-related pathology. <i>Neurobiology of Disease</i> , 2019, 124, 454-468.	2.1	41
1813	A Primer on Data Analytics in Functional Genomics: How to Move from Data to Insight?. <i>Trends in Biochemical Sciences</i> , 2019, 44, 21-32.	3.7	16
1814	Small Extracellular Vesicles in Rat Serum Contain Astrocyte-Derived Protein Biomarkers of Repetitive Stress. <i>International Journal of Neuropsychopharmacology</i> , 2019, 22, 232-246.	1.0	60

#	ARTICLE	IF	CITATIONS
1815	Noncanonical Modulation of the eIF2 Pathway Controls an Increase in Local Translation during Neural Wiring. <i>Molecular Cell</i> , 2019, 73, 474-489.e5.	4.5	70
1816	Glycoproteomic Analysis of MGL-Binding Proteins on Acute T-Cell Leukemia Cells. <i>Journal of Proteome Research</i> , 2019, 18, 1125-1132.	1.8	18
1817	A chemical biology toolbox to study protein methyltransferases and epigenetic signaling. <i>Nature Communications</i> , 2019, 10, 19.	5.8	113
1818	Comprehensive identification of RNA-protein interactions in any organism using orthogonal organic phase separation (OOPS). <i>Nature Biotechnology</i> , 2019, 37, 169-178.	9.4	247
1819	Proteomic analysis and antivenomics study of Western India <i>Naja naja</i> venom: correlation between venom composition and clinical manifestations of cobra bite in this region. <i>Expert Review of Proteomics</i> , 2019, 16, 171-184.	1.3	41
1820	Global Proteomic Profiling of <i>Salmonella</i> Infection by a Giant Phage. <i>Journal of Virology</i> , 2019, 93, .	1.5	18
1821	TCO, a Putative Transcriptional Regulator in Arabidopsis, Is a Target of the Protein Kinase CK2. <i>International Journal of Molecular Sciences</i> , 2019, 20, 99.	1.8	0
1822	Interactome of the yeast RNA polymerase III transcription machinery constitutes several chromatin modifiers and regulators of the genes transcribed by RNA polymerase II. <i>Gene</i> , 2019, 702, 205-214.	1.0	8
1823	Integrative hepatic metabolomics and proteomics reveal insights into the mechanism of different feed efficiency with high or low dietary forage levels in Holstein heifers. <i>Journal of Proteomics</i> , 2019, 194, 1-13.	1.2	15
1824	The mTORC1/4E-BP1 axis represents a critical signaling node during fibrogenesis. <i>Nature Communications</i> , 2019, 10, 6.	5.8	159
1825	Early Response of <i>Sulfolobus acidocaldarius</i> to Nutrient Limitation. <i>Frontiers in Microbiology</i> , 2018, 9, 3201.	1.5	21
1826	Proteome-wide Analysis of Protein Thermal Stability in the Model Higher Plant <i>Arabidopsis thaliana</i> . <i>Molecular and Cellular Proteomics</i> , 2019, 18, 308-319.	2.5	42
1827	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , 2019, 47, D442-D450.	6.5	6,449
1828	Chemical Cross-Linking Enables Drafting ClpXP Proximity Maps and Taking Snapshots of In Situ Interaction Networks. <i>Cell Chemical Biology</i> , 2019, 26, 48-59.e7.	2.5	31
1829	Valorisation of the microalgae <i>Nannochloropsis gaditana</i> biomass by proteomic approach in the context of circular economy. <i>Journal of Proteomics</i> , 2019, 193, 239-242.	1.2	26
1830	Quantification of Calcyclin and Heat Shock Protein 90 in Sera from Women with and without Preeclampsia by Mass Spectrometry. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800181.	0.8	9
1831	Protein Inference Using PIA Workflows and PSI Standard File Formats. <i>Journal of Proteome Research</i> , 2019, 18, 741-747.	1.8	33
1832	MIR sequences recruit zinc finger protein ZNF768 to expressed genes. <i>Nucleic Acids Research</i> , 2019, 47, 700-715.	6.5	14

#	ARTICLE	IF	CITATIONS
1833	The European Nucleotide Archive in 2018. <i>Nucleic Acids Research</i> , 2019, 47, D84-D88.	6.5	103
1834	The global regulator Crc orchestrates the metabolic robustness underlying oxidative stress resistance in <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2019, 21, 898-912.	1.8	27
1835	Identification of Proteomic Markers in Head and Neck Cancer Using MALDI-MS Imaging, LC-MS/MS, and Immunohistochemistry. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1700173.	0.8	34
1836	Varroa chemosensory proteins: some are conserved across Arthropoda but others are arachnid specific. <i>Insect Molecular Biology</i> , 2019, 28, 321-341.	1.0	12
1837	Proteome characterization in various biological fluids of <i>Trypanosoma brucei</i> gambiense-infected subjects. <i>Journal of Proteomics</i> , 2019, 196, 150-161.	1.2	9
1838	Importance of Pyruvate Sensing and Transport for the Resuscitation of Viable but Nonculturable <i>Escherichia coli</i> K-12. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	39
1839	Unipept 4.0: Functional Analysis of Metaproteome Data. <i>Journal of Proteome Research</i> , 2019, 18, 606-615.	1.8	112
1840	ZBTB10 binds the telomeric variant repeat TTGGGG and interacts with TRF2. <i>Nucleic Acids Research</i> , 2019, 47, 1896-1907.	6.5	28
1841	Adding function to the genome of African <i>Salmonella</i> Typhimurium ST313 strain D23580. <i>PLoS Biology</i> , 2019, 17, e3000059.	2.6	62
1842	Floral nectar chitinase is a potential marker for monofloral honey botanical origin authentication: A case study from loquat ( <i>Eriobotrya japonica</i> Lindl.). <i>Food Chemistry</i> , 2019, 282, 76-83.	4.2	17
1843	Affinity chromatography revealed 14-3-3 interactome of tomato ( <i>Solanum lycopersicum</i> L.) during blue light-induced de-etiolation. <i>Journal of Proteomics</i> , 2019, 193, 44-61.	1.2	12
1844	Proteogenomics in the context of the Human Proteome Project (HPP). <i>Expert Review of Proteomics</i> , 2019, 16, 267-275.	1.3	6
1845	Mitochondrial ribosomal protein PTCO3 mutations cause oxidative phosphorylation defects with Leigh syndrome. <i>Neurogenetics</i> , 2019, 20, 9-25.	0.7	46
1846	Proteomic characterization of <i>Aspergillus fumigatus</i> isolated from air and surfaces of the International Space Station. <i>Fungal Genetics and Biology</i> , 2019, 124, 39-46.	0.9	28
1847	Quantitative Proteomic Analysis of Small and Large Extracellular Vesicles (EVs) Reveals Enrichment of Adhesion Proteins in Small EVs. <i>Journal of Proteome Research</i> , 2019, 18, 947-959.	1.8	71
1848	Aqueous raw and ripe Pu-erh tea extracts alleviate obesity and alter cecal microbiota composition and function in diet-induced obese rats. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1823-1835.	1.7	31
1849	Toward a versatile protocol for radiocarbon and proteomics analysis of ancient collagen. <i>Journal of Archaeological Science</i> , 2019, 101, 1-10.	1.2	8
1850	Changes in Synaptic Proteins Precede Neurodegeneration Markers in Preclinical Alzheimer's Disease Cerebrospinal Fluid. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 546-560.	2.5	115

#	ARTICLE	IF	CITATIONS
1851	Predicting peptide presentation by major histocompatibility complex class I: an improved machine learning approach to the immunopeptidome. <i>BMC Bioinformatics</i> , 2019, 20, 7.	1.2	45
1852	Delineation of the pan-proteome of fish-pathogenic <i>Streptococcus agalactiae</i> strains using a label-free shotgun approach. <i>BMC Genomics</i> , 2019, 20, 11.	1.2	23
1853	IQGAP-related protein IqgC suppresses Ras signaling during large-scale endocytosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1289-1298.	3.3	19
1854	Quantitative Proteomics of Potato Leaves Infected with <i>Phytophthora infestans</i> Provides Insights into Coordinated and Altered Protein Expression during Early and Late Disease Stages. <i>International Journal of Molecular Sciences</i> , 2019, 20, 136.	1.8	20
1855	A Case Study and Methodology for OpenSWATH Parameter Optimization Using the ProCan90 Data Set and 45â€810 Computational Analysis Runs. <i>Journal of Proteome Research</i> , 2019, 18, 1019-1031.	1.8	7
1856	Data-independent Acquisition Improves Quantitative Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 786-795.	2.5	31
1857	Label-free and isobaric tandem mass tag (TMT) multiplexed quantitative proteomic data of two contrasting rice cultivars exposed to drought stress and recovery. <i>Data in Brief</i> , 2019, 22, 697-702.	0.5	5
1858	Fibroblast polarization over the myocardial infarction time continuum shifts roles from inflammation to angiogenesis. <i>Basic Research in Cardiology</i> , 2019, 114, 6.	2.5	118
1859	Peptidome profiling dataset of ovarian cancer and non-cancer proximal fluids: Ascites and blood sera. <i>Data in Brief</i> , 2019, 22, 557-562.	0.5	8
1860	Quantitative Proteomics Reveals the Dynamic Protein Landscape during Initiation of Human Th17 Cell Polarization. <i>IScience</i> , 2019, 11, 334-355.	1.9	25
1861	Optimization Workflow for the Analysis of Cross-Linked Peptides Using a Quadrupole Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 2019, 91, 1808-1814.	3.2	10
1862	Comparative Proteomic Analysis of Slime from the Striped Pyjama Squid, <i>Sepioloidea lineolata</i> , and the Southern Bottletail Squid, <i>Sepiadarium austrinum</i> (Cephalopoda: Sepiariidae). <i>Journal of Proteome Research</i> , 2019, 18, 890-899.	1.8	4
1863	Peptidomics Analysis of Milk Protein-Derived Peptides Released over Time in the Preterm Infant Stomach. <i>Journal of Proteome Research</i> , 2019, 18, 912-922.	1.8	35
1864	Macrophage Phosphoproteome Analysis Reveals MINCLE-dependent and -independent Mycobacterial Cord Factor Signaling. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 669-685.	2.5	20
1865	Identification of novel ejaculate proteins in a seed beetle and division of labour across male accessory reproductive glands. <i>Insect Biochemistry and Molecular Biology</i> , 2019, 104, 50-57.	1.2	24
1866	Noncovalently Associated Peptides Observed during Liquid Chromatography-Mass Spectrometry and Their Effect on Cross-Link Analyses. <i>Analytical Chemistry</i> , 2019, 91, 2678-2685.	3.2	19
1867	Capillary Zone Electrophoresisâ€Tandem Mass Spectrometry for Large-Scale Phosphoproteomics with the Production of over 11,000 Phosphopeptides from the Colon Carcinoma HCT116 Cell Line. <i>Analytical Chemistry</i> , 2019, 91, 2201-2208.	3.2	27
1868	Glycoproteomic Profiling Provides Candidate Myocardial Infarction Predictors of Later Progression to Heart Failure. <i>ACS Omega</i> , 2019, 4, 1272-1280.	1.6	10



#	ARTICLE	IF	CITATIONS
1869	Exosomes harbor B cell targets in pancreatic adenocarcinoma and exert decoy function against complement-mediated cytotoxicity. <i>Nature Communications</i> , 2019, 10, 254.	5.8	120
1870	iProX: an integrated proteome resource. <i>Nucleic Acids Research</i> , 2019, 47, D1211-D1217.	6.5	1,001
1871	Molecular changes during extended neoadjuvant letrozole treatment of breast cancer: distinguishing acquired resistance from dormant tumours. <i>Breast Cancer Research</i> , 2019, 21, 2.	2.2	29
1872	Analysis of the Bacterial and Host Proteins along and across the Porcine Gastrointestinal Tract. <i>Proteomes</i> , 2019, 7, 4.	1.7	24
1873	Whole Proteome Profiling of N-Myristoyltransferase Activity and Inhibition Using Sortase A. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 115-126.	2.5	22
1874	<i>Clinical Proteomics</i> , 2019, , 911-925.		0
1875	Quantitative Proteomics of the 2016 WHO Neisseria gonorrhoeae Reference Strains Surveys Vaccine Candidates and Antimicrobial Resistance Determinants. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 127-150.	2.5	35
1876	Proteome-transcriptome analysis and proteome remodeling in mouse lens epithelium and fibers. <i>Experimental Eye Research</i> , 2019, 179, 32-46.	1.2	40
1878	ArrayExpress update “ from bulk to single-cell expression data. <i>Nucleic Acids Research</i> , 2019, 47, D711-D715.	6.5	497
1879	Identification of Protein Abundance Changes in Hepatocellular Carcinoma Tissues Using PCT“SWATH. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1700179.	0.8	32
1880	Functional characterization of RNA fragments using high-throughput interactome screening. <i>Journal of Proteomics</i> , 2019, 193, 173-183.	1.2	6
1881	Transcriptomic and proteomic insight into the mechanism of cyclooctasulfur“versus thiosulfate“oxidation by the chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Environmental Microbiology</i> , 2019, 21, 244-258.	1.8	16
1882	Label-free quantitative proteomic analysis of Panax ginseng leaves upon exposure to heat stress. <i>Journal of Ginseng Research</i> , 2019, 43, 143-153.	3.0	24
1883	FlashPack: Fast and Simple Preparation of Ultrahigh-performance Capillary Columns for LC-MS*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 383-390.	2.5	70
1884	Proteome response of two natural strains of <i>Saccharomyces cerevisiae</i> with divergent lignocellulosic inhibitor stress tolerance. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	19
1885	HCN Regulates Cellular Processes through Posttranslational Modification of Proteins by <i>S</i> -cyanylation. <i>Plant Physiology</i> , 2019, 179, 107-123.	2.3	43
1886	Characterisation of infection associated microRNA and protein cargo in extracellular vesicles of <i>Theileria annulata</i> infected leukocytes. <i>Cellular Microbiology</i> , 2019, 21, e12969.	1.1	25
1887	SWATH proteomic profiling of prostate cancer cells identifies NUSAP1 as a potential molecular target for Galialactone. <i>Journal of Proteomics</i> , 2019, 193, 217-229.	1.2	15

#	ARTICLE	IF	CITATIONS
1888	Development of a Parallel Reaction Monitoring-MS Method To Quantify IGF Proteins in Dogs and a Case of Nonislet Cell Tumor Hypoglycemia. <i>Journal of Proteome Research</i> , 2019, 18, 18-29.	1.8	5
1889	Ribosome profiles and riboproteomes of healthy and Potato virus A and <i>Agrobacterium</i> -infected <i>Nicotiana benthamiana</i> plants. <i>Molecular Plant Pathology</i> , 2019, 20, 392-409.	2.0	13
1890	Quantitative proteomic profiling of immune responses to <i>Ichthyophthirius multifiliis</i> in common carp skin mucus. <i>Fish and Shellfish Immunology</i> , 2019, 84, 834-842.	1.6	36
1891	Quantitative mass spectrometry to identify protein markers for diagnosis of malignant pleural mesothelioma. <i>Journal of Proteomics</i> , 2019, 192, 374-382.	1.2	11
1892	Insight into the sulfur metabolism of <i>Desulfurella amilsii</i> by differential proteomics. <i>Environmental Microbiology</i> , 2019, 21, 209-225.	1.8	57
1893	Fine-tuning of RBOHF activity is achieved by differential phosphorylation and Ca <sup>2+</sup> binding. <i>New Phytologist</i> , 2019, 221, 1935-1949.	3.5	111
1894	Analysis of femurs from mice embarked on board BIONEM1 biosatellite reveals a decrease in immune cell development, including B cells, after 1 wk of recovery on Earth. <i>FASEB Journal</i> , 2019, 33, 3772-3783.	0.2	31
1895	In Vitro and In Vivo Proteomic Comparison of Human Neural Progenitor Cell-induced Photoreceptor Survival. <i>Proteomics</i> , 2019, 19, e1800213.	1.3	8
1896	Altered levels of focal adhesion and extracellular matrix-receptor interacting proteins were identified in Hailey-Hailey disease by quantitative iTRAQ proteome analysis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 3801-3812.	1.2	6
1897	Proteomic Landscape of Cholangiocarcinomas Reveals Three Different Subgroups According to Their Localization and the Aspect of Non-Tumor Liver. <i>Proteomics - Clinical Applications</i> , 2019, 13, 1800128.	0.8	11
1898	Comparative exoproteome profiling of an invasive and a commensal <i>Staphylococcus haemolyticus</i> isolate. <i>Journal of Proteomics</i> , 2019, 197, 106-114.	1.2	16
1899	O-Fucosylation of thrombospondin-like repeats is required for processing of microneme protein 2 and for efficient host cell invasion by <i>Toxoplasma gondii</i> tachyzoites. <i>Journal of Biological Chemistry</i> , 2019, 294, 1967-1983.	1.6	27
1900	Time-resolved interaction proteomics of the GIGANTEA protein under diurnal cycles in <i>Arabidopsis</i> . <i>FEBS Letters</i> , 2019, 593, 319-338.	1.3	35
1901	Exposure to microplastics reduces attachment strength and alters the haemolymph proteome of blue mussels ( <i>Mytilus edulis</i> ). <i>Environmental Pollution</i> , 2019, 246, 423-434.	3.7	150
1902	Protein O-fucosyltransferase 2-mediated O-glycosylation of the adhesin MIC2 is dispensable for <i>Toxoplasma gondii</i> tachyzoite infection. <i>Journal of Biological Chemistry</i> , 2019, 294, 1541-1553.	1.6	20
1903	Dirhodium (II) complex interferes with iron-transport system to exert antibacterial action against <i>Streptococcus pneumoniae</i> . <i>Journal of Proteomics</i> , 2019, 194, 160-167.	1.2	10
1904	Stable-protein Pair Analysis as A Novel Strategy to Identify Proteomic Signatures: Application To Seminal Plasma From Infertile Patients. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S77-S90.	2.5	30
1905	Cohesin-mediated NF- $\kappa$ B signaling limits hematopoietic stem cell self-renewal in aging and inflammation. <i>Journal of Experimental Medicine</i> , 2019, 216, 152-175.	4.2	56

#	ARTICLE	IF	CITATIONS
1906	A High-throughput Bead-based Affinity Assay Enables Analysis of Genital Protein Signatures in Women At Risk of HIV Infection. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 461-476.	2.5	4
1907	Trypanosomes can initiate nuclear export co-transcriptionally. <i>Nucleic Acids Research</i> , 2019, 47, 266-282.	6.5	25
1908	The human allicin-proteome: S-thioallylation of proteins by the garlic defence substance allicin and its biological effects. <i>Free Radical Biology and Medicine</i> , 2019, 131, 144-153.	1.3	61
1909	Using the sORFs.Org Database. <i>Current Protocols in Bioinformatics</i> , 2019, 65, e68.	25.8	9
1910	Proteomics of Uterosacral Ligament Connective Tissue from Women with and without Pelvic Organ Prolapse. <i>Proteomics - Clinical Applications</i> , 2019, 13, 1800086.	0.8	4
1911	Comprehensive Workflow for Integrative Transcriptomics Meta-Analysis. , 2019, , 1-16.		0
1912	The proteome microenvironment determines the protective effect of preconditioning in cisplatin-induced acute kidney injury. <i>Kidney International</i> , 2019, 95, 333-349.	2.6	55
1913	Quantitative Proteomics Identification of Seminal Fluid Proteins in Male <i>Drosophila melanogaster</i> . <i>Molecular and Cellular Proteomics</i> , 2019, 18, S46-S58.	2.5	66
1914	The jPOST environment: an integrated proteomics data repository and database. <i>Nucleic Acids Research</i> , 2019, 47, D1218-D1224.	6.5	94
1915	New substrates and interactors of the mycobacterial Serine/Threonine protein kinase PknG identified by a tailored interactomic approach. <i>Journal of Proteomics</i> , 2019, 192, 321-333.	1.2	30
1916	Targeted Analysis of Lysosomal Directed Proteins and Their Sites of Mannose-6-phosphate Modification. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 16-27.	2.5	36
1917	Antiepileptic drug carbamazepine promotes horizontal transfer of plasmid-borne multi-antibiotic resistance genes within and across bacterial genera. <i>ISME Journal</i> , 2019, 13, 509-522.	4.4	245
1918	Proteasome-mediated remodeling of the proteome and phosphoproteome during kiwifruit pollen germination. <i>Journal of Proteomics</i> , 2019, 192, 334-345.	1.2	13
1919	Ocean acidification increases iodine accumulation in kelp-based coastal food webs. <i>Global Change Biology</i> , 2019, 25, 629-639.	4.2	26
1920	Tape Stripped Stratum Corneum Samples Prove to be Suitable for Comprehensive Proteomic Investigation of Actinic Keratosis. <i>Proteomics - Clinical Applications</i> , 2019, 13, 1800084.	0.8	10
1921	Human follicular fluid proteomic and peptidomic composition quantitative studies by SWATH-MS methodology. Applicability of high pH RP-HPLC fractionation. <i>Journal of Proteomics</i> , 2019, 191, 131-142.	1.2	18
1922	A comprehensive proteomics study on platelet concentrates: Platelet proteome, storage time and Mirasol pathogen reduction technology. <i>Platelets</i> , 2019, 30, 368-379.	1.1	28
1923	The dystrophin isoform Dp71e <sup>71</sup> is involved in neurite outgrowth and neuronal differentiation of PC12 cells. <i>Journal of Proteomics</i> , 2019, 191, 80-87.	1.2	7

#	ARTICLE	IF	CITATIONS
1924	Systematic analysis of the cerebrospinal fluid proteome of fibromyalgia patients. <i>Journal of Proteomics</i> , 2019, 190, 35-43.	1.2	17
1925	Anatomy and evolution of database search engines—a central component of mass spectrometry based proteomic workflows. <i>Mass Spectrometry Reviews</i> , 2020, 39, 292-306.	2.8	97
1926	Distinct editing functions of natural HLA-DM allotypes impact antigen presentation and CD4+ T cell activation. <i>Cellular and Molecular Immunology</i> , 2020, 17, 133-142.	4.8	17
1927	Genetic analysis of Hsp70 phosphorylation sites reveals a role in <i>Candida albicans</i> cell and colony morphogenesis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140135.	1.1	28
1928	ANPELA: analysis and performance assessment of the label-free quantification workflow for metaproteomic studies. <i>Briefings in Bioinformatics</i> , 2020, 21, 621-636.	3.2	151
1929	Proteomic profiles during adventitious rooting of <i>Eucalyptus</i> species relevant to the cellulose industry. <i>New Forests</i> , 2020, 51, 213-241.	0.7	6
1930	A critical assessment of the feature selection methods used for biomarker discovery in current metaproteomics studies. <i>Briefings in Bioinformatics</i> , 2020, 21, 1378-1390.	3.2	34
1931	Neuronal-specific microexon splicing of <i>TAF1</i> mRNA is directly regulated by SRRM4/nSR100. <i>RNA Biology</i> , 2020, 17, 62-74.	1.5	11
1932	Horizontal acquisition of a patchwork Calvin cycle by symbiotic and free-living <i>Campylobacterota</i> (formerly <i>Epsilonproteobacteria</i> ). <i>ISME Journal</i> , 2020, 14, 104-122.	4.4	55
1933	Mass Spectrometry Data Analysis in Proteomics. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	3
1934	Redox homeostasis in the growth zone of the rice leaf plays a key role in cold tolerance. <i>Journal of Experimental Botany</i> , 2020, 71, 1053-1066.	2.4	8
1935	Bioinformatics for animal diseases: focused to major diseases and cancer. , 2020, , 381-405.		0
1936	Genomic, transcriptomic, and proteomic insights into the symbiosis of deep-sea tubeworm holobionts. <i>ISME Journal</i> , 2020, 14, 135-150.	4.4	41
1937	Alterations in rat adipose tissue transcriptome and proteome in response to prolonged fasting. <i>Biological Chemistry</i> , 2020, 401, 389-405.	1.2	9
1938	LAMTOR/Ragulator regulates lipid metabolism in macrophages and foam cell differentiation. <i>FEBS Letters</i> , 2020, 594, 31-42.	1.3	7
1939	Early growth response 1 regulates hematopoietic support and proliferation in human primary bone marrow stromal cells. <i>Haematologica</i> , 2020, 105, 1206-1215.	1.7	11
1940	Proteomics Highlights Common and Distinct Pathophysiological Processes Associated with Ileal and Colonic Ulcers in Crohn's Disease. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 205-215.	0.6	19
1941	Genome-wide functional association networks: background, data & state-of-the-art resources. <i>Briefings in Bioinformatics</i> , 2020, 21, 1224-1237.	3.2	20

#	ARTICLE	IF	CITATIONS
1942	FA-SAT ncRNA interacts with PKM2 protein: depletion of this complex induces a switch from cell proliferation to apoptosis. Cellular and Molecular Life Sciences, 2020, 77, 1371-1386.	2.4	10
1943	Cysteine oxidation triggers amyloid fibril formation of the tumor suppressor p16INK4A. Redox Biology, 2020, 28, 101316.	3.9	17
1944	Lineage-Restricted Regulation of SCD and Fatty Acid Saturation by MITF Controls Melanoma Phenotypic Plasticity. Molecular Cell, 2020, 77, 120-137.e9.	4.5	87
1945	Reproducibility, Specificity and Accuracy of Relative Quantification Using Spectral Library-based Data-independent Acquisition. Molecular and Cellular Proteomics, 2020, 19, 181-197.	2.5	106
1946	Widespread presence of bovine proteins in human cell lines. Journal of Mass Spectrometry, 2020, 55, e4464.	0.7	4
1947	Salivary proteins from dysplastic leukoplakia and oral squamous cell carcinoma and their potential for early detection. Journal of Proteomics, 2020, 212, 103574.	1.2	25
1948	Molecular Diversification of the Seminal Fluid Proteome in a Recently Diverged Passerine Species Pair. Molecular Biology and Evolution, 2020, 37, 488-506.	3.5	38
1949	Quantitative proteomics in development of disease protein biomarkers. , 2020, , 261-288.		3
1950	Simple Method To Characterize the Ciliary Proteome of Multiciliated Cells. Journal of Proteome Research, 2020, 19, 391-400.	1.8	11
1951	Comparative proteomics of related symbiotic mussel species reveals high variability of host-symbiont interactions. ISME Journal, 2020, 14, 649-656.	4.4	15
1952	Serum Small Extracellular Vesicles Proteome of Tuberculosis Patients Demonstrated Deregulated Immune Response. Proteomics - Clinical Applications, 2020, 14, e1900062.	0.8	15
1953	Brain Region-Specific nAChR and Associated Protein Abundance Alterations Following Chronic Nicotine and/or Menthol Exposure. Journal of Proteome Research, 2020, 19, 36-48.	1.8	4
1954	Overexpression of HMG-CoA synthase promotes Arabidopsis root growth and adversely affects glucosinolate biosynthesis. Journal of Experimental Botany, 2020, 71, 272-289.	2.4	10
1955	Mapping of Transglutaminase-2 Sites of Human Salivary Small Basic Proline-Rich Proteins by HPLC-High-Resolution ESI-MS/MS. Journal of Proteome Research, 2020, 19, 300-313.	1.8	4
1956	RP-HPLC-ESI-IT Mass Spectrometry Reveals Significant Variations of the Human Salivary Protein Profile Associated with Predominantly Antibody Deficiencies. Journal of Clinical Immunology, 2020, 40, 329-339.	2.0	8
1957	Proteomic Investigation of Tolerant <i>Escherichia coli</i> Populations from Cyclic Antibiotic Treatment. Journal of Proteome Research, 2020, 19, 900-913.	1.8	39
1958	Nuclear proteome analysis of Chlamydomonas with response to CO2 limitation. Algal Research, 2020, 46, 101765.	2.4	15
1959	Integrative genomics reveal a role for MCP1P1 in adipogenesis and adipocyte metabolism. Cellular and Molecular Life Sciences, 2020, 77, 4899-4919.	2.4	13

#	ARTICLE	IF	CITATIONS
1960	HDAC inhibition improves cardiopulmonary function in a feline model of diastolic dysfunction. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	75
1961	Transcriptomic and Proteomic Responses of the Organohalide-Respiring Bacterium <i>Desulfoluna spongiiphila</i> to Growth with 2,6-Dibromophenol as the Electron Acceptor. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	13
1962	An omics perspective on drug target discovery platforms. <i>Briefings in Bioinformatics</i> , 2020, 21, 1937-1953.	3.2	105
1963	Structural Insights Into PfARO and Characterization of its Interaction With PfAIP. <i>Journal of Molecular Biology</i> , 2020, 432, 878-896.	2.0	21
1964	CFAP43 modulates ciliary beating in mouse and <i>Xenopus</i> . <i>Developmental Biology</i> , 2020, 459, 109-125.	0.9	22
1965	Structure Dependent Determination of Organophosphate Targets in Mammalian Tissues Using Activity-Based Protein Profiling. <i>Chemical Research in Toxicology</i> , 2020, 33, 414-425.	1.7	7
1966	Exploration of the propagation of transpovirons within Mimiviridae reveals a unique example of commensalism in the viral world. <i>ISME Journal</i> , 2020, 14, 727-739.	4.4	22
1967	Phosphorylation-Related Crosstalk Between Distant Regions of the Core Region of the Coat Protein Contributes to Virion Assembly of Plum Pox Virus. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 653-667.	1.4	8
1968	Characterizing Patients with Recurrent Urinary Tract Infections in Vesicoureteral Reflux: A Pilot Study of the Urinary Proteome. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 456-466.	2.5	8
1969	Comparison of the molecular and cellular phenotypes of common mouse syngeneic models with human tumors. <i>BMC Genomics</i> , 2020, 21, 2.	1.2	124
1970	Impact of Na <sup>+</sup> -Translocating NADH:Quinone Oxidoreductase on Iron Uptake and <i>Mn</i> Expression in <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	4
1971	Unravelling the role of long non-coding RNA - LINC01087 in breast cancer. <i>Non-coding RNA Research</i> , 2020, 5, 1-10.	2.4	13
1972	Norovirus infection results in eIF2 $\pm$ independent host translation shut-off and remodels the G3BP1 interactome evading stress granule formation. <i>PLoS Pathogens</i> , 2020, 16, e1008250.	2.1	41
1973	Biochemical and Proteomic Studies of Human Pyridoxal 5 $\alpha$ -Phosphate-Binding Protein (PLPBP). <i>ACS Chemical Biology</i> , 2020, 15, 254-261.	1.6	11
1974	Composition and processing activity of a semi-recombinant holo U7 snRNP. <i>Nucleic Acids Research</i> , 2020, 48, 1508-1530.	6.5	13
1975	The adaptive response to iron involves changes in energetic strategies in the pathogen <i>Candida albicans</i> . <i>MicrobiologyOpen</i> , 2020, 9, e970.	1.2	14
1976	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	9.4	273
1977	High-density chemical cross-linking for modeling protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 93-102.	3.3	56

#	ARTICLE	IF	CITATIONS
1978	Proteomic and transcriptomic changes in rat liver following oral feeding of formaldehyde. <i>Chemosphere</i> , 2020, 245, 125599.	4.2	13
1979	Bisphenol A Activates an Innate Viral Immune Response Pathway. <i>Journal of Proteome Research</i> , 2020, 19, 644-654.	1.8	12
1980	Proteome analysis and differential expression by JA driven elicitation in <i>Andrographis paniculata</i> (Burm. f.) Wall. ex Nees using Q-TOF-MS/MS. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 140, 489-504.	1.2	9
1981	Comparative proteome and metabolome analyses of latex-exuding and non-exuding <i>Taraxacum koksaghyz</i> roots provide insights into laticifer biology. <i>Journal of Experimental Botany</i> , 2020, 71, 1278-1293.	2.4	13
1982	PRMT1-mediated methylation of the microprocessor-associated proteins regulates microRNA biogenesis. <i>Nucleic Acids Research</i> , 2020, 48, 96-115.	6.5	22
1983	Disruption of Acetyl-Lysine Turnover in Muscle Mitochondria Promotes Insulin Resistance and Redox Stress without Overt Respiratory Dysfunction. <i>Cell Metabolism</i> , 2020, 31, 131-147.e11.	7.2	41
1984	Comparative membrane proteomics reveal contrasting adaptation strategies for coastal and oceanic marine <i>Synechococcus</i> cyanobacteria. <i>Environmental Microbiology</i> , 2020, 22, 1816-1828.	1.8	6
1985	Thermotolerance and plasticity of camel somatic cells exposed to acute and chronic heat stress. <i>Journal of Advanced Research</i> , 2020, 22, 105-118.	4.4	43
1986	Colonies of the fungus <i>Aspergillus niger</i> are highly differentiated to adapt to local carbon source variation. <i>Environmental Microbiology</i> , 2020, 22, 1154-1166.	1.8	15
1987	Proteomic Characterization of Host-Pathogen Interactions during Bovine Trophoblast Cell Line Infection by <i>Neospora caninum</i> . <i>Pathogens</i> , 2020, 9, 749.	1.2	7
1988	Xylose Metabolism and the Effect of Oxidative Stress on Lipid and Carotenoid Production in <i>Rhodotorula toruloides</i> : Insights for Future Biorefinery. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 1008.	2.0	49
1989	Systematic genetic and proteomic screens during gametogenesis identify H2BK34 methylation as an evolutionary conserved meiotic mark. <i>Epigenetics and Chromatin</i> , 2020, 13, 35.	1.8	6
1990	Pharmacological and phosphoproteomic approaches to roles of protein kinase C in kappa opioid receptor-mediated effects in mice. <i>Neuropharmacology</i> , 2020, 181, 108324.	2.0	5
1991	Protein Phosphatase-1 Complex Disassembly by p97 is Initiated through Multivalent Recognition of Catalytic and Regulatory Subunits by the p97 SEP-domain Adapters. <i>Journal of Molecular Biology</i> , 2020, 432, 6061-6074.	2.0	20
1992	Thermal Proteome Profiling and Meltome Analysis of a Thermophilic Bacterial Strain, <i>Geobacillus thermoleovorans</i> ARTRW1: Toward Industrial Applications. <i>OMICS A Journal of Integrative Biology</i> , 2020, 24, 756-765.	1.0	5
1993	DIALib-QC an assessment tool for spectral libraries in data-independent acquisition proteomics. <i>Nature Communications</i> , 2020, 11, 5251.	5.8	32
1994	Single-cell derived tumor organoids display diversity in HLA class I peptide presentation. <i>Nature Communications</i> , 2020, 11, 5338.	5.8	41
1995	The reductive glycine pathway allows autotrophic growth of <i>Desulfovibrio desulfuricans</i> . <i>Nature Communications</i> , 2020, 11, 5090.	5.8	152

#	ARTICLE	IF	CITATIONS
1996	Abscisic Acid-Triggered Persulfidation of the Cys Protease ATG4 Mediates Regulation of Autophagy by Sulfide. <i>Plant Cell</i> , 2020, 32, 3902-3920.	3.1	68
1997	Papain-like protease regulates SARS-CoV-2 viral spread and innate immunity. <i>Nature</i> , 2020, 587, 657-662.	13.7	818
1998	A Multi-Omics Approach Identifies Key Regulatory Pathways Induced by Long-Term Zinc Supplementation in Human Primary Retinal Pigment Epithelium. <i>Nutrients</i> , 2020, 12, 3051.	1.7	15
1999	Tumor Cell Attack by Crotalicidin (Ctn) and Its Fragment Ctn[15â€³4]: Insights into Their Dual Membranolytic and Intracellular Targeting Mechanism. <i>ACS Chemical Biology</i> , 2020, 15, 2945-2957.	1.6	10
2000	Inclusion of African American/Black adults in a pilot brain proteomics study of Alzheimer's disease. <i>Neurobiology of Disease</i> , 2020, 146, 105129.	2.1	18
2001	Spatial Transcriptomics Reveals Genes Associated with Dysregulated Mitochondrial Functions and Stress Signaling in Alzheimer Disease. <i>IScience</i> , 2020, 23, 101556.	1.9	61
2002	Comparative Proteomic Profiling of 3T3-L1 Adipocyte Differentiation Using SILAC Quantification. <i>Journal of Proteome Research</i> , 2020, 19, 4884-4900.	1.8	5
2003	Optimized incorporation of an unnatural fluorescent amino acid affords measurement of conformational dynamics governing high-fidelity DNA replication. <i>Journal of Biological Chemistry</i> , 2020, 295, 17265-17280.	1.6	14
2004	Proteome activity landscapes of tumor cell lines determine drug responses. <i>Nature Communications</i> , 2020, 11, 3639.	5.8	47
2005	The Cyclin CYCA3;4 Is a Postprophase Target of the APC/C <sup>CCS52A2</sup> E3-Ligase Controlling Formative Cell Divisions in Arabidopsis. <i>Plant Cell</i> , 2020, 32, 2979-2996.	3.1	22
2006	Radiosensitization by Kinase Inhibition Revealed by Phosphoproteomic Analysis of Pancreatic Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1649-1663.	2.5	7
2007	Label-free proteomics reveals serum proteins whose levels differ between pancreatic ductal adenocarcinoma patients with short or long survival. <i>Tumor Biology</i> , 2020, 42, 101042832093641.	0.8	4
2008	Chromokinesin KIF4A teams up with stathmin 1 to regulate abscission in a SUMO-dependent manner. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	7
2009	The Regulator PltZ Regulates a Putative ABC Transporter System PltIJKNOP of <i>Pseudomonas aeruginosa</i> ATCC 27853 in Response to the Antimicrobial 2,4-Diacetylphloroglucinol. <i>Frontiers in Microbiology</i> , 2020, 11, 1423.	1.5	6
2010	SNAIL Promotes Metastatic Behavior of Rhabdomyosarcoma by Increasing EZRIN and AKT Expression and Regulating MicroRNA Networks. <i>Cancers</i> , 2020, 12, 1870.	1.7	14
2011	Comprehensive proteomics data on whole rice grain of selected pigmented and non-pigmented rice varieties using SWATH-MS approach. <i>Data in Brief</i> , 2020, 31, 105927.	0.5	5
2012	Co-option of Plasmodium falciparum PP1 for egress from host erythrocytes. <i>Nature Communications</i> , 2020, 11, 3532.	5.8	37
2013	FYN and ABL Regulate the Interaction Networks of the DCBLD Receptor Family. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1586-1601.	2.5	6



#	ARTICLE	IF	CITATIONS
2014	Predictive Signatures of 19 Antibiotic-Induced <i>Escherichia coli</i> Proteomes. <i>ACS Infectious Diseases</i> , 2020, 6, 2120-2129.	1.8	8
2015	Proto-Oncogene Serine/Threonine Kinase PIM3 Promotes Cell Migration via Modulating Rho GTPase Signaling. <i>Journal of Proteome Research</i> , 2020, 19, 1298-1309.	1.8	9
2016	<i>Streptococcus pneumoniae</i> metal homeostasis alters cellular metabolism. <i>Metallomics</i> , 2020, 12, 1416-1427.	1.0	13
2017	Na <sub>2</sub> CO <sub>3</sub> -responsive Photosynthetic and ROS Scavenging Mechanisms in Chloroplasts of <i>Alkaligrass</i> Revealed by Phosphoproteomics. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 271-288.	3.0	10
2018	Large-scale site-specific mapping of the O-GalNAc glycoproteome. <i>Nature Protocols</i> , 2020, 15, 2589-2610.	5.5	28
2019	Identification and Characterization of the Heat-Induced Plastidial Stress Granules Reveal New Insight Into <i>Arabidopsis</i> Stress Response. <i>Frontiers in Plant Science</i> , 2020, 11, 595792.	1.7	24
2020	A primary human T-cell spectral library to facilitate large scale quantitative T-cell proteomics. <i>Scientific Data</i> , 2020, 7, 412.	2.4	11
2021	diaPASEF: parallel accumulation <sup>+</sup> serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236.	9.0	387
2022	The Nucleosome Remodeling and Deacetylase Complex Has an Asymmetric, Dynamic, and Modular Architecture. <i>Cell Reports</i> , 2020, 33, 108450.	2.9	37
2023	Molecular Surgery: Proteomics of a Rare Genetic Disease Gives Insight into Common Causes of Blindness. <i>IScience</i> , 2020, 23, 101667.	1.9	9
2024	A comprehensive spectral assay library to quantify the <i>Escherichia coli</i> proteome by DIA/SWATH-MS. <i>Scientific Data</i> , 2020, 7, 389.	2.4	28
2025	Proteomic Characterization of Synaptosomes from Human Substantia Nigra Indicates Altered Mitochondrial Translation in Parkinson <sup>+</sup> s Disease. <i>Cells</i> , 2020, 9, 2580.	1.8	16
2026	A membrane-depolarizing toxin substrate of the <i>Staphylococcus aureus</i> type VII secretion system mediates intraspecies competition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20836-20847.	3.3	57
2027	Identification of Tomato Proteins That Interact With Replication Initiator Protein (Rep) of the Geminivirus TYLCV. <i>Frontiers in Plant Science</i> , 2020, 11, 1069.	1.7	19
2028	Human cytomegalovirus protein pUL36: A dual cell death pathway inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18771-18779.	3.3	42
2029	Integrated Quantitative Proteomics and Metabolome Profiling Reveal MSMEG_6171 Overexpression Perturbing Lipid Metabolism of <i>Mycobacterium smegmatis</i> Leading to Increased Vancomycin Resistance. <i>Frontiers in Microbiology</i> , 2020, 11, 1572.	1.5	7
2030	Identification of Potential Interacting Proteins With the Extracellular Loops of the Neuronal Glycoprotein M6a by TMT/MS. <i>Frontiers in Synaptic Neuroscience</i> , 2020, 12, 28.	1.3	7
2031	Discovery of treatment for nerve agents targeting a new metabolic pathway. <i>Archives of Toxicology</i> , 2020, 94, 3249-3264.	1.9	6

#	ARTICLE	IF	CITATIONS
2032	Proteomic Analysis Reveals a Mitochondrial Remodeling of $\hat{1}^2$ TC3 Cells in Response to Nanotopography. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 508.	1.8	14
2033	Proteomic Study of the Survival and Resuscitation Mechanisms of Filamentous Persisters in an Evolved <i>Escherichia coli</i> Population from Cyclic Ampicillin Treatment. <i>MSystems</i> , 2020, 5, .	1.7	23
2034	Mitochondrial Proteome of Affected Glutamatergic Neurons in a Mouse Model of Leigh Syndrome. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 660.	1.8	11
2035	Cellular response of <i>Brevibacterium casei</i> #NIOSBA88 to arsenic and chromium <sup>VI</sup> a proteomic approach. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 1885-1895.	0.8	12
2036	Rescue of oxytocin response and social behaviour in a mouse model of autism. <i>Nature</i> , 2020, 584, 252-256.	13.7	92
2037	Tumor Classification using MS Spectra Based on Deep Learning. , 2020, , .		0
2038	Mass-Spectrometric Detection of SARS-CoV-2 Virus in Scrapings of the Epithelium of the Nasopharynx of Infected Patients via Nucleocapsid N Protein. <i>Journal of Proteome Research</i> , 2020, 19, 4393-4397.	1.8	87
2039	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation. <i>Molecular Systems Biology</i> , 2020, 16, e9596.	3.2	131
2040	Pharmacodynamic modeling of synergistic birinapant/paclitaxel interactions in pancreatic cancer cells. <i>BMC Cancer</i> , 2020, 20, 1024.	1.1	3
2041	Barley Root Proteome and Metabolome in Response to Cytokinin and Abiotic Stimuli. <i>Frontiers in Plant Science</i> , 2020, 11, 590337.	1.7	25
2042	Identification of Molecular Network Associated with Neuroprotective Effects of Yashtimadhu ( <i>Glycyrrhiza glabra</i> L.) by Quantitative Proteomics of Rotenone-Induced Parkinson's Disease Model. <i>ACS Omega</i> , 2020, 5, 26611-26625.	1.6	22
2043	Proteomic and transcriptomic profiling of aerial organ development in <i>Arabidopsis</i> . <i>Scientific Data</i> , 2020, 7, 334.	2.4	20
2045	Revealing mechanisms of mating plug function under sexual selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27465-27473.	3.3	11
2046	Lost and Found: Re-searching and Re-scoring Proteomics Data Aids Genome Annotation and Improves Proteome Coverage. <i>MSystems</i> , 2020, 5, .	1.7	13
2047	Re-establishment of the epigenetic state and rescue of kinome deregulation in Ts65Dn mice upon treatment with green tea extract and environmental enrichment. <i>Scientific Reports</i> , 2020, 10, 16023.	1.6	15
2048	Constructing and deconstructing GATA2-regulated cell fate programs to establish developmental trajectories. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	28
2049	Triton X-114 Fractionated Subcellular Proteome of <i>Leptospira interrogans</i> Shows Selective Enrichment of Pathogenic and Outer Membrane Proteins in the Detergent Fraction. <i>Proteomics</i> , 2020, 20, e2000170.	1.3	13
2050	<i>Akkermansia muciniphila</i> uses human milk oligosaccharides to thrive in the early life conditions in vitro. <i>Scientific Reports</i> , 2020, 10, 14330.	1.6	96

#	ARTICLE	IF	CITATIONS
2051	Cofilin-1 Is a Mechanosensitive Regulator of Transcription. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 678.	1.8	8
2052	Lipoproteins Contribute to the Anti-inflammatory Capacity of <i>Lactobacillus plantarum</i> WCFS1. <i>Frontiers in Microbiology</i> , 2020, 11, 1822.	1.5	13
2053	Molecular abnormalities in autopsied brain tissue from the inferior horn of the lateral ventricles of nonagenarians and Alzheimer disease patients. <i>BMC Neurology</i> , 2020, 20, 317.	0.8	15
2054	Structure of a nucleotide pyrophosphatase/phosphodiesterase (NPP) from <i>Euphorbia characias</i> latex characterized by small-angle X-ray scattering: clues for the general organization of plant NPPs. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 857-867.	1.1	1
2055	Mitochondrial CaMKII causes adverse metabolic reprogramming and dilated cardiomyopathy. <i>Nature Communications</i> , 2020, 11, 4416.	5.8	54
2056	Development of robust targeted proteomics assays for cerebrospinal fluid biomarkers in multiple sclerosis. <i>Clinical Proteomics</i> , 2020, 17, 33.	1.1	6
2057	Structural and functional studies of <i>Arabidopsis thaliana</i> legumain beta reveal isoform specific mechanisms of activation and substrate recognition. <i>Journal of Biological Chemistry</i> , 2020, 295, 13047-13064.	1.6	24
2058	ITGB3-mediated uptake of small extracellular vesicles facilitates intercellular communication in breast cancer cells. <i>Nature Communications</i> , 2020, 11, 4261.	5.8	92
2059	Viewing Cortical Collecting Duct Function Through Phenotype-guided Single-Tubule Proteomics. <i>Function</i> , 2020, 1, zqaa007.	1.1	2
2060	Machine learning to predict retention time of small molecules in nano-HPLC. <i>Analytical and Bioanalytical Chemistry</i> , 2020, 412, 7767-7776.	1.9	26
2061	Intermittent Hypoxia Promotes Functional Neuroprotection from Retinal Ischemia in Untreated First-Generation Offspring: Proteomic Mechanistic Insights. , 2020, 61, 15.		11
2062	Seminal fluid protein divergence among populations exhibiting postmating prezygotic reproductive isolation. <i>Molecular Ecology</i> , 2020, 29, 4428-4441.	2.0	12
2063	Receptor-independent modulation of cAMP-dependent protein kinase and protein phosphatase signaling in cardiac myocytes by oxidizing agents. <i>Journal of Biological Chemistry</i> , 2020, 295, 15342-15365.	1.6	4
2064	High-Resolution Mass Spectrometry-Based Approaches for the Detection and Quantification of Peptidase Activity in Plasma. <i>Molecules</i> , 2020, 25, 4071.	1.7	10
2065	Immiscible inclusion bodies formed by polyglutamine and poly(glycine-alanine) are enriched with distinct proteomes but converge in proteins that are risk factors for disease and involved in protein degradation. <i>PLoS ONE</i> , 2020, 15, e0233247.	1.1	7
2066	Myocardial proteomic profile in pulmonary arterial hypertension. <i>Scientific Reports</i> , 2020, 10, 14351.	1.6	12
2067	Nocardamine-Dependent Iron Uptake in <i>Pseudomonas aeruginosa</i> : Exclusive Involvement of the FoxA Outer Membrane Transporter. <i>ACS Chemical Biology</i> , 2020, 15, 2741-2751.	1.6	27
2068	Plasma proteins facilitates placental transfer of polystyrene particles. <i>Journal of Nanobiotechnology</i> , 2020, 18, 128.	4.2	38

#	ARTICLE	IF	CITATIONS
2069	Impaired chondrocyte U3 snoRNA expression in osteoarthritis impacts the chondrocyte protein translation apparatus. <i>Scientific Reports</i> , 2020, 10, 13426.	1.6	21
2070	Preparing for Life: Plasma Proteome Changes and Immune System Development During the First Week of Human Life. <i>Frontiers in Immunology</i> , 2020, 11, 578505.	2.2	23
2071	Dataset for proteomic analysis of <i>Chlorella sorokiniana</i> cells under cadmium stress. <i>Data in Brief</i> , 2020, 33, 106544.	0.5	0
2072	State of the Field in Multi-Omics Research: From Computational Needs to Data Mining and Sharing. <i>Frontiers in Genetics</i> , 2020, 11, 610798.	1.1	180
2073	Short-Chain Fatty Acids Modulate Metabolic Pathways and Membrane Lipids in <i>Prevotella bryantii</i> B14. <i>Proteomes</i> , 2020, 8, 28.	1.7	17
2074	Characteristics of the Protein Complexes and Pores Formed by <i>Bacillus cereus</i> Hemolysin BL. <i>Toxins</i> , 2020, 12, 672.	1.5	8
2075	The Cellular Response to Lanthanum Is Substrate Specific and Reveals a Novel Route for Glycerol Metabolism in <i>Pseudomonas putida</i> KT2440. <i>MBio</i> , 2020, 11, .	1.8	17
2076	Immunopeptidomic Analysis Reveals That Deamidated HLA-bound Peptides Arise Predominantly from Deglycosylated Precursors. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1236-1247.	2.5	25
2077	Protein Profiles of Lipid Droplets during the Hypersensitive Defense Response of <i>Arabidopsis</i> against <i>Pseudomonas</i> Infection. <i>Plant and Cell Physiology</i> , 2020, 61, 1144-1157.	1.5	32
2078	Improving Gene Annotation of the Peanut Genome by Integrated Proteogenomics Workflow. <i>Journal of Proteome Research</i> , 2020, 19, 2226-2235.	1.8	7
2079	Non-antibiotic pharmaceuticals enhance the transmission of exogenous antibiotic resistance genes through bacterial transformation. <i>ISME Journal</i> , 2020, 14, 2179-2196.	4.4	133
2080	The FOXJ1 target <i>Cfap206</i> is required for sperm motility, mucociliary clearance of the airways and brain development. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	19
2081	TaxIt: An Iterative Computational Pipeline for Untargeted Strain-Level Identification Using MS/MS Spectra from Pathogenic Single-Organism Samples. <i>Journal of Proteome Research</i> , 2020, 19, 2501-2510.	1.8	11
2082	Thymosin $\beta$ 4 cytoplasmic/nuclear translocation as a new marker of cellular stress. A Caco2 case study. <i>RSC Advances</i> , 2020, 10, 12680-12688.	1.7	7
2083	Development of a novel method for the quantification of tyrosine 39 phosphorylated $\alpha$ - and $\beta$ -synuclein in human cerebrospinal fluid. <i>Clinical Proteomics</i> , 2020, 17, 13.	1.1	10
2084	Label-free plasma proteomics identifies haptoglobin-related protein as candidate marker of idiopathic pulmonary fibrosis and dysregulation of complement and oxidative pathways. <i>Scientific Reports</i> , 2020, 10, 7787.	1.6	12
2085	Phosphoproteomics of CD2 signaling reveals AMPK-dependent regulation of lytic granule polarization in cytotoxic T cells. <i>Science Signaling</i> , 2020, 13, .	1.6	18
2086	Human Neutrophils Produce Antifungal Extracellular Vesicles against <i>Aspergillus fumigatus</i> . <i>MBio</i> , 2020, 11, .	1.8	50

#	ARTICLE	IF	CITATIONS
2087	Engineered anti-inflammatory peptides inspired by mapping an evasin-chemokine interaction. <i>Journal of Biological Chemistry</i> , 2020, 295, 10926-10939.	1.6	9
2088	High-throughput transcriptomic and proteomic profiling of mesenchymal-amoeboid transition in 3D collagen. <i>Scientific Data</i> , 2020, 7, 160.	2.4	15
2089	Comparative tachyzoite proteome analyses among six <i>Neospora caninum</i> isolates with different virulence. <i>International Journal for Parasitology</i> , 2020, 50, 377-388.	1.3	10
2090	OPTN recruitment to a Golgi-proximal compartment regulates immune signalling and cytokine secretion. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	15
2091	Discovering the RNA-Binding Proteome of Plant Leaves with an Improved RNA Interactome Capture Method. <i>Biomolecules</i> , 2020, 10, 661.	1.8	63
2092	Saliva proteomic patterns in patients with molar incisor hypomineralization. <i>Scientific Reports</i> , 2020, 10, 7560.	1.6	11
2093	Natural brominated phenoxyphenols kill persistent and biofilm-incorporated cells of MRSA and other pathogenic bacteria. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 5985-5998.	1.7	5
2094	Quantitative alterations in bovine milk proteome from healthy, subclinical and clinical mastitis during <i>S. aureus</i> infection. <i>Journal of Proteomics</i> , 2020, 223, 103815.	1.2	19
2095	Plasma protein expression differs between colorectal cancer patients depending on primary tumor location. <i>Cancer Medicine</i> , 2020, 9, 5221-5234.	1.3	8
2096	Proteomic datasets of uninfected and <i>Staphylococcus aureus</i> -infected goat milk. <i>Data in Brief</i> , 2020, 30, 105665.	0.5	1
2097	Cancer Burden Is Controlled by Mural Cell-Integrin Regulated Crosstalk with Tumor Cells. <i>Cell</i> , 2020, 181, 1346-1363.e21.	13.5	53
2098	Novel nonclassic progesterone receptor PGRMC1 pulldown-precipitated proteins reveal a key role during human decidualization. <i>Fertility and Sterility</i> , 2020, 113, 1050-1066.e7.	0.5	25
2099	The effects of improving low dietary protein utilization on the proteome of lamb tissues. <i>Journal of Proteomics</i> , 2020, 223, 103798.	1.2	7
2100	Blood plasma proteomic modulation induced by olanzapine and risperidone in schizophrenia patients. <i>Journal of Proteomics</i> , 2020, 224, 103813.	1.2	8
2101	N-glycosylation Site Analysis Reveals Sex-related Differences in Protein N-glycosylation in the Rice Brown Planthopper ( <i>Nilaparvata lugens</i> ). <i>Molecular and Cellular Proteomics</i> , 2020, 19, 529-539.	2.5	10
2102	Altered mitochondrial proteome and functional dynamics in patients with rheumatoid arthritis. <i>Mitochondrion</i> , 2020, 54, 8-14.	1.6	12
2103	Double the Fun, Double the Trouble: Paralogs and Homologs Functioning in the Endoplasmic Reticulum. <i>Annual Review of Biochemistry</i> , 2020, 89, 637-666.	5.0	10
2104	Interactome analysis reveals that lncRNA HULC promotes aerobic glycolysis through LDHA and PKM2. <i>Nature Communications</i> , 2020, 11, 3162.	5.8	114

#	ARTICLE	IF	CITATIONS
2105	Open Database Searching Enables the Identification and Comparison of Bacterial Glycoproteomes without Defining Glycan Compositions Prior to Searching. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1561-1574.	2.5	28
2106	An atlas of the catalytically active liver and spleen kinases in chicken identified by chemoproteomics. <i>Journal of Proteomics</i> , 2020, 225, 103850.	1.2	1
2107	Dynamic rewiring of the human interactome by interferon signaling. <i>Genome Biology</i> , 2020, 21, 140.	3.8	25
2108	Comparing serum protein levels can aid in differentiating HPV-negative and -positive oropharyngeal squamous cell carcinoma patients. <i>PLoS ONE</i> , 2020, 15, e0233974.	1.1	11
2109	Influence of Protein Glycosylation on <i>Campylobacter fetus</i> Physiology. <i>Frontiers in Microbiology</i> , 2020, 11, 1191.	1.5	7
2110	Seed Metabolism and Pathogen Resistance Enhancement in <i>Pisum sativum</i> During Colonization of Arbuscular Mycorrhizal Fungi: An Integrative Metabolomics-Proteomics Approach. <i>Frontiers in Plant Science</i> , 2020, 11, 872.	1.7	9
2111	The Leader Peptide peTrpL Forms Antibiotic-Containing Ribonucleoprotein Complexes for Posttranscriptional Regulation of Multiresistance Genes. <i>MBio</i> , 2020, 11, .	1.8	10
2112	Quantitative proteomics reveals specific metabolic features of acute myeloid leukemia stem cells. <i>Blood</i> , 2020, 136, 1507-1519.	0.6	57
2113	Mass Spectrometric Mapping of Glycoproteins Modified by Tn-Antigen Using Solid-Phase Capture and Enzymatic Release. <i>Analytical Chemistry</i> , 2020, 92, 9230-9238.	3.2	11
2114	Absence of miRNA-146a Differentially Alters Microglia Function and Proteome. <i>Frontiers in Immunology</i> , 2020, 11, 1110.	2.2	20
2115	Proteomics of saliva, plasma, and salivary gland tissue in Sjögren's syndrome and non-Sjögren patients identify novel biomarker candidates. <i>Journal of Proteomics</i> , 2020, 225, 103877.	1.2	24
2116	Response of <i>Pseudomonas putida</i> to Complex, Aromatic-Rich Fractions from Biomass. <i>ChemSusChem</i> , 2020, 13, 4455-4467.	3.6	23
2117	Few SINEs of life: Alu elements have little evidence for biological relevance despite elevated translation. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz023.	1.5	12
2118	SNAP29 mediates the assembly of histidine-induced CTP synthase filaments in proximity to the cytokeratin network. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	6
2119	Mass-spectrometry-based draft of the <i>Arabidopsis</i> proteome. <i>Nature</i> , 2020, 579, 409-414.	13.7	328
2120	Evidence for a novel overlapping coding sequence in POLG initiated at a CUG start codon. <i>BMC Genetics</i> , 2020, 21, 25.	2.7	30
2121	Mutagenesis of a Quintuple Mutant Impaired in Environmental Responses Reveals Roles for CHROMATIN REMODELING4 in the <i>Arabidopsis</i> Floral Transition. <i>Plant Cell</i> , 2020, 32, 1479-1500.	3.1	17
2122	Nucleolin Discriminates Drastically between Long-Loop and Short-Loop Quadruplexes. <i>Biochemistry</i> , 2020, 59, 1261-1272.	1.2	27

#	ARTICLE	IF	CITATIONS
2123	Proteome and Phosphoproteome Changes Associated with Prognosis in Acute Myeloid Leukemia. <i>Cancers</i> , 2020, 12, 709.	1.7	33
2124	Systems analysis of RhoGEF and RhoGAP regulatory proteins reveals spatially organized RAC1 signalling from integrin adhesions. <i>Nature Cell Biology</i> , 2020, 22, 498-511.	4.6	154
2125	Shifts in Ribosome Engagement Impact Key Gene Sets in Neurodevelopment and Ubiquitination in Rett Syndrome. <i>Cell Reports</i> , 2020, 30, 4179-4196.e11.	2.9	46
2126	Î²-Catenin/CBP inhibition alters epidermal growth factor receptor fucosylation status in oral squamous cell carcinoma. <i>Molecular Omics</i> , 2020, 16, 195-209.	1.4	14
2127	Synonymous Mutations in rpsT Lead to Ribosomal Assembly Defects That Can Be Compensated by Mutations in fis and rpoA. <i>Frontiers in Microbiology</i> , 2020, 11, 340.	1.5	3
2128	Mitochondrial peptide BRAWNIN is essential for vertebrate respiratory complex III assembly. <i>Nature Communications</i> , 2020, 11, 1312.	5.8	87
2129	Proteomic analysis of somatic embryo development in <i>Musa</i> spp. cv. Grand Naine (AAA). <i>Scientific Reports</i> , 2020, 10, 4501.	1.6	16
2130	Comprehensive cell surface proteomics defines markers of classical, intermediate and non-classical monocytes. <i>Scientific Reports</i> , 2020, 10, 4560.	1.6	28
2131	A Uniquely Complex Mitochondrial Proteome from <i>Euglena gracilis</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2173-2191.	3.5	22
2132	An array of 60,000 antibodies for proteome-scale antibody generation and target discovery. <i>Science Advances</i> , 2020, 6, eaax2271.	4.7	22
2133	Proteomic Investigation Uncovers Potential Targets and Target Sites of Pneumococcal Serine-Threonine Kinase StkP and Phosphatase PhpP. <i>Frontiers in Microbiology</i> , 2019, 10, 3101.	1.5	28
2134	Identification of signal peptide features for substrate specificity in human Sec62/Sec63â€dependent ER protein import. <i>FEBS Journal</i> , 2020, 287, 4612-4640.	2.2	40
2135	In-Depth Investigation of Low-Abundance Proteins in Matured and Filling Stages Seeds of <i>Glycine max</i> Employing a Combination of Protamine Sulfate Precipitation and TMT-Based Quantitative Proteomic Analysis. <i>Cells</i> , 2020, 9, 1517.	1.8	19
2136	Effectiveness of Resistive Vibration Exercise and Whey Protein Supplementation Plus Alkaline Salt on the Skeletal Muscle Proteome Following 21 Days of Bed Rest in Healthy Males. <i>Journal of Proteome Research</i> , 2020, 19, 3438-3451.	1.8	14
2137	Integrated Proteomics and Metabolomics Analysis Highlights Correlative Metabolite-Protein Networks in Soybean Seeds Subjected to Warm-Water Soaking. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 8057-8067.	2.4	15
2138	Proteomic profiling of sclerotic hippocampus revealed dysregulated packaging of vesicular neurotransmitters in temporal lobe epilepsy. <i>Epilepsy Research</i> , 2020, 166, 106412.	0.8	10
2139	Top down proteomic analysis of gingival crevicular fluid in deciduous, exfoliating and permanent teeth in children. <i>Journal of Proteomics</i> , 2020, 226, 103890.	1.2	10
2140	Orthogonal Proteomic Platforms and Their Implications for the Stable Classification of High-Grade Serous Ovarian Cancer Subtypes. <i>IScience</i> , 2020, 23, 101079.	1.9	23

#	ARTICLE	IF	CITATIONS
2141	Influence of subclinical mastitis and intramammary infection by coagulase-negative staphylococci on the cow milk peptidome. <i>Journal of Proteomics</i> , 2020, 226, 103885.	1.2	18
2142	Calcium-binding proteins are altered in the cerebellum in schizophrenia. <i>PLoS ONE</i> , 2020, 15, e0230400.	1.1	16
2143	ZapE/Afg1 interacts with Oxa1 and its depletion causes a multifaceted phenotype. <i>PLoS ONE</i> , 2020, 15, e0234918.	1.1	7
2144	Fast Quantitative Analysis of timsTOF PASEF Data with MSFragger and IonQuant. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1575-1585.	2.5	152
2145	Trichoderma Applications on Strawberry Plants Modulate the Physiological Processes Positively Affecting Fruit Production and Quality. <i>Frontiers in Microbiology</i> , 2020, 11, 1364.	1.5	49
2146	An Efficient Faiss-Based Search Method for Mass Spectral Library Searching. , 2020, , .		1
2147	Blood Contamination in CSF and Its Impact on Quantitative Analysis of Alpha-Synuclein. <i>Cells</i> , 2020, 9, 370.	1.8	30
2148	β2-Adrenergic Signalling Promotes Cell Migration by Upregulating Expression of the Metastasis-Associated Molecule LYPD3. <i>Biology</i> , 2020, 9, 39.	1.3	20
2149	Phosphoinositide-binding proteins mark, shape and functionally modulate highly-diverged endocytic compartments in the parasitic protist <i>Giardia lamblia</i> . <i>PLoS Pathogens</i> , 2020, 16, e1008317.	2.1	12
2150	Interactome and F-Actin Interaction Analysis of Dictyostelium discoideum Coronin A. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1469.	1.8	2
2151	CIP2A Constrains Th17 Differentiation by Modulating STAT3 Signaling. <i>IScience</i> , 2020, 23, 100947.	1.9	12
2152	Protein interactome of the Cancerous Inhibitor of protein phosphatase 2A (CIP2A) in Th17 cells. <i>Current Research in Immunology</i> , 2020, 1, 10-22.	1.2	6
2153	Using proteomics for an insight into the performance of activated sludge in a lab-scale WWTP. <i>International Biodeterioration and Biodegradation</i> , 2020, 149, 104934.	1.9	10
2154	Amino acids are key substrates to <i>Escherichia coli</i> BW25113 for achieving high specific growth rate. <i>Research in Microbiology</i> , 2020, 171, 185-193.	1.0	19
2155	Proteome Wide Profiling of N-μ-Lysine Acetylation Reveals a Novel Mechanism of Regulation of the Chitinase Activity in <i>Francisella novicida</i> . <i>Journal of Proteome Research</i> , 2020, 19, 1409-1422.	1.8	4
2156	Diversification of CORVET tethers facilitates transport complexity in <i>Tetrahymena thermophila</i> . <i>Journal of Cell Science</i> , 2020, 133, .	1.2	16
2157	Phenotypic Adaption of <i>Pseudomonas aeruginosa</i> by Hacking Siderophores Produced by Other Microorganisms. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 589-607.	2.5	40
2158	Blockade of Stat3 oncogene addiction induces cellular senescence and reveals a cell-nonautonomous activity suitable for cancer immunotherapy. <i>Oncimmunology</i> , 2020, 9, 1715767.	2.1	14



#	ARTICLE	IF	CITATIONS
2159	Changes in the proteome of sea urchin <i>Paracentrotus lividus</i> coelomocytes in response to LPS injection into the body cavity. <i>PLoS ONE</i> , 2020, 15, e0228893.	1.1	8
2160	Chaperone-Facilitated Aggregation of Thermo-Sensitive Proteins Shields Them from Degradation during Heat Stress. <i>Cell Reports</i> , 2020, 30, 2430-2443.e4.	2.9	33
2161	Structural insights into the main S-layer unit of <i>Deinococcus radiodurans</i> reveal a massive protein complex with porin-like features. <i>Journal of Biological Chemistry</i> , 2020, 295, 4224-4236.	1.6	21
2162	Active nuclear import of the deacetylase Sirtuin-2 is controlled by its C-terminus and importins. <i>Scientific Reports</i> , 2020, 10, 2034.	1.6	22
2163	Towards identification of novel putative biomarkers for infective endocarditis by serum proteomic analysis. <i>International Journal of Infectious Diseases</i> , 2020, 96, 73-81.	1.5	10
2164	Arginine in C9ORF72 Dipolypeptides Mediates Promiscuous Proteome Binding and Multiple Modes of Toxicity. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 640-654.	2.5	31
2165	Prolonged Heat Stress of <i>Lactobacillus paracasei</i> GCRL163 Improves Binding to Human Colorectal Adenocarcinoma HT-29 Cells and Modulates the Relative Abundance of Secreted and Cell Surface-Located Proteins. <i>Journal of Proteome Research</i> , 2020, 19, 1824-1846.	1.8	7
2166	Comprehensive Detection of Single Amino Acid Variants and Evaluation of Their Deleterious Potential in a PANC-1 Cell Line. <i>Journal of Proteome Research</i> , 2020, 19, 1635-1646.	1.8	11
2167	MAPDP: A Cloud-Based Computational Platform for Immuno-peptidomics Analyses. <i>Journal of Proteome Research</i> , 2020, 19, 1873-1881.	1.8	11
2168	Glycosaminoglycan Domain Mapping of Cellular Chondroitin/Dermatan Sulfates. <i>Scientific Reports</i> , 2020, 10, 3506.	1.6	16
2169	Extending Comet for Global Amino Acid Variant and Post-translational Modification Analysis Using the PSI Extended FASTA Format. <i>Proteomics</i> , 2020, 20, e1900362.	1.3	18
2170	Dataset on proteomic changes of whey protein after different heat treatment. <i>Data in Brief</i> , 2020, 29, 105227.	0.5	2
2171	Precise timing of transcription by c-di-GMP coordinates cell cycle and morphogenesis in <i>Caulobacter</i> . <i>Nature Communications</i> , 2020, 11, 816.	5.8	38
2172	TRAM1 protein may support ER protein import by modulating the phospholipid bilayer near the lateral gate of the Sec61-channel. <i>Channels</i> , 2020, 14, 28-44.	1.5	13
2173	Circadian rhythms in the absence of the clock gene <i>Bmal1</i> . <i>Science</i> , 2020, 367, 800-806.	6.0	156
2174	Proteomic analysis to identify differentially expressed proteins between subjects with metabolic healthy obesity and non-alcoholic fatty liver disease. <i>Journal of Proteomics</i> , 2020, 221, 103683.	1.2	19
2175	COPZ1 depletion in thyroid tumor cells triggers type I IFN response and immunogenic cell death. <i>Cancer Letters</i> , 2020, 476, 106-119.	3.2	7
2176	The LC3-conjugation machinery specifies the loading of RNA-binding proteins into extracellular vesicles. <i>Nature Cell Biology</i> , 2020, 22, 187-199.	4.6	300

#	ARTICLE	IF	CITATIONS
2177	A subcellular proteome atlas of the yeast <i>Komagataella phaffii</i> . FEMS Yeast Research, 2020, 20, .	1.1	16
2178	Hap2 <sup>Δ</sup> Ino80-facilitated transcription promotes de novo establishment of CENP-A chromatin. Genes and Development, 2020, 34, 226-238.	2.7	18
2179	LAX28 is required for stable assembly of the inner dynein arm f/11 and tether/tether head complex in <i>Leishmania</i> flagella. Journal of Cell Science, 2020, 133, .	1.2	3
2180	Developing front-end devices for improved sample preparation in MS-based proteome analysis. Journal of Mass Spectrometry, 2020, 55, e4494.	0.7	1
2181	Environmental arginine controls multinuclear giant cell metabolism and formation. Nature Communications, 2020, 11, 431.	5.8	37
2182	The most abundant maternal lncRNA Sirena1 acts post-transcriptionally and impacts mitochondrial distribution. Nucleic Acids Research, 2020, 48, 3211-3227.	6.5	25
2183	Biotin proximity tagging favours unfolded proteins and enables the study of intrinsically disordered regions. Communications Biology, 2020, 3, 38.	2.0	26
2184	Proteome Analyses Reveal <i>Macrophomina phaseolina</i> 's Survival Tools When Challenged by <i>Burkholderia contaminans</i> NZ. ACS Omega, 2020, 5, 1352-1362.	1.6	7
2185	ExtENDING Proteome Coverage with Legumain as a Highly Specific Digestion Protease. Analytical Chemistry, 2020, 92, 2961-2971.	3.2	17
2186	Delineating the venom toxin arsenal of Malabar pit viper ( <i>Trimeresurus malabaricus</i> ) from the Western Ghats of India and evaluating its immunological cross-reactivity and in vitro cytotoxicity. International Journal of Biological Macromolecules, 2020, 148, 1029-1045.	3.6	13
2187	Monosomes actively translate synaptic mRNAs in neuronal processes. Science, 2020, 367, .	6.0	166
2188	Proteomic Responses to Drought Vary Widely Among Eight Diverse Genotypes of Rice ( <i>Oryza sativa</i> ). International Journal of Molecular Sciences, 2020, 21, 363.	1.8	23
2189	Proteomic analysis reveals that calcium channel blockers affect radicle protrusion during rice seed germination. Plant Growth Regulation, 2020, 90, 393-407.	1.8	9
2190	Reconstructing kinase network topologies from phosphoproteomics data reveals cancer-associated rewiring. Nature Biotechnology, 2020, 38, 493-502.	9.4	72
2191	An integrated transcriptomic- and proteomic-based approach to evaluate the human skin sensitization potential of glyphosate and its commercial agrochemical formulations. Journal of Proteomics, 2020, 217, 103647.	1.2	12
2192	Interrogating the higher order structures of snake venom proteins using an integrated mass spectrometric approach. Journal of Proteomics, 2020, 216, 103680.	1.2	19
2193	Machine Learning Strategy That Leverages Large Data sets to Boost Statistical Power in Small-Scale Experiments. Journal of Proteome Research, 2020, 19, 1267-1274.	1.8	15
2194	A Novel D-Galacturonate Fermentation Pathway in <i>Lactobacillus suebicus</i> Links Initial Reactions of the Galacturonate-Isomerase Route With the Phosphoketolase Pathway. Frontiers in Microbiology, 2019, 10, 3027.	1.5	14

#	ARTICLE	IF	CITATIONS
2195	Longitudinal Transcriptomic, Proteomic, and Metabolomic Analysis of <i>Citrus limon</i> Response to Graft Inoculation by <i>Candidatus Liberibacter asiaticus</i> . <i>Journal of Proteome Research</i> , 2020, 19, 2247-2263.	1.8	25
2196	Glycomics and glycoproteomics of viruses: Mass spectrometry applications and insights toward structure–function relationships. <i>Mass Spectrometry Reviews</i> , 2020, 39, 371-409.	2.8	35
2197	A comprehensive analysis of sialolith proteins and the clinical implications. <i>Clinical Proteomics</i> , 2020, 17, 12.	1.1	7
2198	Impact of <i>Staphylococcus aureus</i> infection on the late lactation goat milk proteome: New perspectives for monitoring and understanding mastitis in dairy goats. <i>Journal of Proteomics</i> , 2020, 221, 103763.	1.2	14
2199	Proteomic fingerprints of damage in extracellular matrix assemblies. <i>Matrix Biology Plus</i> , 2020, 5, 100027.	1.9	19
2200	Quantitative Profiling of the Human Substantia Nigra Proteome from Laser-capture Microdissected FFPE Tissue. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 839-851.	2.5	39
2201	Large-scale Identification of N-linked Intact Glycopeptides in Human Serum using HILIC Enrichment and Spectral Library Search. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 672-689.	2.5	42
2202	The rRNA m <sup>6</sup> A methyltransferase METTL5 is involved in pluripotency and developmental programs. <i>Genes and Development</i> , 2020, 34, 715-729.	2.7	93
2203	Glycogen Metabolism Supports Photosynthesis Start through the Oxidative Pentose Phosphate Pathway in Cyanobacteria. <i>Plant Physiology</i> , 2020, 182, 507-517.	2.3	68
2204	Cell-type-resolved proteomic analysis of the human liver. <i>Liver International</i> , 2020, 40, 1770-1780.	1.9	31
2205	Multifunctional Acidocin 4356 Combats <i>Pseudomonas aeruginosa</i> through Membrane Perturbation and Virulence Attenuation: Experimental Results Confirm Molecular Dynamics Simulation. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	5
2206	Adaptive Evolution of <i>Geobacter sulfurreducens</i> in Coculture with <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2020, 11, .	1.8	5
2207	Leucine improves Î±-amylase secretion through the general secretory signaling pathway in pancreatic acinar cells of dairy calves. <i>American Journal of Physiology - Cell Physiology</i> , 2020, 318, C1284-C1293.	2.1	5
2208	Conditional deletion of Nedd4-2 in lung epithelial cells causes progressive pulmonary fibrosis in adult mice. <i>Nature Communications</i> , 2020, 11, 2012.	5.8	52
2209	Î±2,3 linkage of sialic acid to a GPI anchor and an unpredicted GPI attachment site in human prion protein. <i>Journal of Biological Chemistry</i> , 2020, 295, 7789-7798.	1.6	17
2210	SPD_1495 Contributes to Capsular Polysaccharide Synthesis and Virulence in <i>Streptococcus pneumoniae</i> . <i>MSystems</i> , 2020, 5, .	1.7	10
2211	Environmental Viscosity Modulates Interbacterial Killing during Habitat Transition. <i>MBio</i> , 2020, 11, .	1.8	34
2212	Proteomic Profiling of Fibroblasts Isolated from Chronic Wounds Identifies Disease-Relevant Signaling Pathways. <i>Journal of Investigative Dermatology</i> , 2020, 140, 2280-2290.e4.	0.3	14

#	ARTICLE	IF	CITATIONS
2213	Relative Retention Time Estimation Improves N-Glycopeptide Identifications by LC-MS/MS. <i>Journal of Proteome Research</i> , 2020, 19, 2113-2121.	1.8	27
2214	Human Hepatocyte Nuclear Factor 4 $\beta$ Encodes Isoforms with Distinct Transcriptional Functions. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 808-827.	2.5	31
2215	miR-181a regulates p62/SQSTM1, parkin, and protein DJ-1 promoting mitochondrial dynamics in skeletal muscle aging. <i>Aging Cell</i> , 2020, 19, e13140.	3.0	50
2216	Coimmunoprecipitation with MYR1 Identifies Three Additional Proteins within the <i>Toxoplasma gondii</i> Parasitophorous Vacuole Required for Translocation of Dense Granule Effectors into Host Cells. <i>MSphere</i> , 2020, 5, .	1.3	43
2217	Temporal Dynamics of High-Density Lipoprotein Proteome in Diet-Controlled Subjects with Type 2 Diabetes. <i>Biomolecules</i> , 2020, 10, 520.	1.8	13
2218	Combining Precursor and Fragment Information for Improved Detection of Differential Abundance in Data Independent Acquisition. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 421-430.	2.5	40
2219	Quantitative Proteomics of Human Heart Samples Collected In Vivo Reveal the Remodeled Protein Landscape of Dilated Left Atrium Without Atrial Fibrillation. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1132-1144.	2.5	24
2220	What is proteomics?. <i>Archives of Disease in Childhood: Education and Practice Edition</i> , 2021, 106, 178-181.	0.3	11
2221	Proper imputation of missing values in proteomics datasets for differential expression analysis. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	39
2222	MetaFS: Performance assessment of biomarker discovery in metaproteomics. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	71
2223	Mild Acid Elution and MHC Immunoaffinity Chromatography Reveal Similar Albeit Not Identical Profiles of the HLA Class I Immunoepitidome. <i>Journal of Proteome Research</i> , 2021, 20, 289-304.	1.8	32
2224	Reciprocal regulation of Aurora kinase A and ATIP3 in the control of metaphase spindle length. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 1765-1779.	2.4	9
2225	Personalized Metabolic Analysis of Diseases. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 1014-1025.	1.9	3
2226	Mutation-Specific and Common Phosphotyrosine Signatures of <i>KRAS</i> G12D and G13D Alleles. <i>Journal of Proteome Research</i> , 2021, 20, 670-683.	1.8	12
2227	Effect of cadmium in the microalga <i>Chlorella sorokiniana</i> : A proteomic study. <i>Ecotoxicology and Environmental Safety</i> , 2021, 207, 111301.	2.9	44
2228	Fractionation of DNA and protein from individual latent fingerprints for forensic analysis. <i>Forensic Science International: Genetics</i> , 2021, 50, 102405.	1.6	9
2229	Analysis of NIST Monoclonal Antibody Reference Material Glycosylation Using the LC-MS/MS-Based Glycoproteomic Approach. <i>Journal of Proteome Research</i> , 2021, 20, 818-830.	1.8	6
2230	LC-MS analysis reveals biological and metabolic processes essential for <i>Candida albicans</i> biofilm growth. <i>Microbial Pathogenesis</i> , 2021, 152, 104614.	1.3	8

#	ARTICLE	IF	CITATIONS
2231	Anti-A $\beta$ Antibody Aducanumab Regulates the Proteome of Senile Plaques and Closely Surrounding Tissue in a Transgenic Mouse Model of Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2021, 79, 249-265.	1.2	27
2232	Differential proteome analysis of the leaves of lead hyperaccumulator, <i>Rhoeo discolor</i> (L. Her.) Hance. <i>Journal of Mass Spectrometry</i> , 2021, 56, e4689.	0.7	5
2233	Chromoplast differentiation in bell pepper ( <i>Capsicum annuum</i> ) fruits. <i>Plant Journal</i> , 2021, 105, 1431-1442.	2.8	15
2235	Breath Biopsy and Discovery of Exclusive Volatile Organic Compounds for Diagnosis of Infectious Diseases. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 564194.	1.8	53
2236	Analysis of complement deposition and processing on <i>Chlamydia trachomatis</i> . <i>Medical Microbiology and Immunology</i> , 2021, 210, 13-32.	2.6	8
2237	Abundance of metalloprotease FtsH12 modulates chloroplast development in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 3455-3473.	2.4	19
2238	Overexpression and Inhibition of 3-Hydroxy-3-Methylglutaryl-CoA Synthase Affect Central Metabolic Pathways in Tobacco. <i>Plant and Cell Physiology</i> , 2021, 62, 205-218.	1.5	3
2239	What Are We Missing by Using Hydrophilic Enrichment? Improving Bacterial Glycoproteome Coverage Using Total Proteome and FAIMS Analyses. <i>Journal of Proteome Research</i> , 2021, 20, 599-612.	1.8	43
2240	Proteomic Characterization of the <i>Pseudomonas</i> sp. Strain phDV1 Response to Monocyclic Aromatic Compounds. <i>Proteomics</i> , 2021, 21, e2000003.	1.3	10
2241	A novel cucumisin-like serine protease from leaf of legume <i>Canavalia ensiformis</i> . <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 147-159.	0.9	3
2242	An apoplastic fluid extraction method for the characterization of grapevine leaves proteome and metabolome from a single sample. <i>Physiologia Plantarum</i> , 2021, 171, 343-357.	2.6	18
2243	A Review of Imputation Strategies for Isobaric Labeling-Based Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2021, 20, 1-13.	1.8	26
2244	Mining Protein Expression Databases Using Network. <i>Methods in Molecular Biology</i> , 2021, 2228, 419-431.	0.4	1
2245	Potential biomarkers of childhood brain tumor identified by proteomics of cerebrospinal fluid from extraventricular drainage (EVD). <i>Scientific Reports</i> , 2021, 11, 1818.	1.6	15
2246	Integrated analysis of label-free quantitative proteomics and bioinformatics reveal insights into signaling pathways in male breast cancer. <i>Genetics and Molecular Biology</i> , 2021, 44, e20190410.	0.6	2
2247	CSF SERPINA3 Levels Are Elevated in Patients With Progressive MS. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2021, 8, .	3.1	19
2248	Proteomic analysis reveals ginsenoside Rb1 attenuates myocardial ischemia/reperfusion injury through inhibiting ROS production from mitochondrial complex I. <i>Theranostics</i> , 2021, 11, 1703-1720.	4.6	92
2249	Acute environmental temperature variation affects brain protein expression, anxiety and explorative behaviour in adult zebrafish. <i>Scientific Reports</i> , 2021, 11, 2521.	1.6	28

#	ARTICLE	IF	CITATIONS
2250	HLA Class II Presentation Is Specifically Altered at Elevated Temperatures in the B-Lymphoblastic Cell Line JY. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100089.	2.5	6
2251	Bacterial symbiont subpopulations have different roles in a deep-sea symbiosis. <i>ELife</i> , 2021, 10, .	2.8	17
2252	The Expression of NTAL and Its Protein Interactors Is Associated With Clinical Outcomes in Acute Myeloid Leukemia. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100091.	2.5	1
2254	Proteomic Alterations in Multiple Myeloma: A Comprehensive Study Using Bone Marrow Interstitial Fluid and Serum Samples. <i>Frontiers in Oncology</i> , 2020, 10, 566804.	1.3	19
2255	The KLF14 Variant is Associated with Type 2 Diabetes and HbA1C Level. <i>Biochemical Genetics</i> , 2021, 59, 574-588.	0.8	5
2256	Hepatocyte size fractionation allows dissection of human liver zonation. <i>Journal of Cellular Physiology</i> , 2021, 236, 5885-5894.	2.0	7
2257	An acetate- $\gamma$ -yielding diet imprints an immune and anti- $\alpha$ -microbial programme against enteric infection. <i>Clinical and Translational Immunology</i> , 2021, 10, e1233.	1.7	23
2258	A glycoengineered antigen exploiting a conserved protein O-glycosylation pathway in the <i>Burkholderia</i> genus for detection of glanders infections. <i>Virulence</i> , 2021, 12, 493-506.	1.8	5
2259	In Well-Treated Celiac Patients Low-Level Mucosal Inflammation Predicts Response to 14-day Gluten Challenge. <i>Advanced Science</i> , 2021, 8, 2003526.	5.6	14
2260	Domain Mapping of Chondroitin/Dermatan Sulfate Glycosaminoglycans Enables Structural Characterization of Proteoglycans. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100074.	2.5	11
2261	The jPOST Repository as a Public Data Repository for Shotgun Proteomics. <i>Methods in Molecular Biology</i> , 2021, 2259, 309-322.	0.4	15
2262	Mitochondrial NAD <sup>+</sup> Controls Nuclear ARTD1-Induced ADP-Ribosylation. <i>Molecular Cell</i> , 2021, 81, 340-354.e5.	4.5	31
2264	The Effect of Interferons on Presentation of Defective Ribosomal Products as HLA Peptides. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100105.	2.5	10
2265	Autophagy activation, lipotoxicity and lysosomal membrane permeabilization synergize to promote pimozone- and loperamide-induced glioma cell death. <i>Autophagy</i> , 2021, 17, 3424-3443.	4.3	39
2266	An Integrated Transcriptomics and Proteomics Analysis Implicates lncRNA MALAT1 in the Regulation of Lipid Metabolism. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100141.	2.5	14
2267	Proximity-dependent Mapping of the Androgen Receptor Identifies Kruppel-like Factor 4 as a Functional Partner. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100064.	2.5	11
2268	ALK ligand ALKAL2 potentiates MYCN-driven neuroblastoma in the absence of <i>ALK</i> mutation. <i>EMBO Journal</i> , 2021, 40, e105784.	3.5	35
2270	SPA: A Quantitation Strategy for MS Data in Patient-derived Xenograft Models. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 522-533.	3.0	1

#	ARTICLE	IF	CITATIONS
2271	The Role of Pseudo-Orthocaspase (SyOC) of <i>Synechocystis</i> sp. PCC 6803 in Attenuating the Effect of Oxidative Stress. <i>Frontiers in Microbiology</i> , 2021, 12, 634366.	1.5	4
2272	mokapot: Fast and Flexible Semisupervised Learning for Peptide Detection. <i>Journal of Proteome Research</i> , 2021, 20, 1966-1971.	1.8	28
2273	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
2274	In silico identification of novel open reading frames in <i>Plasmodium falciparum</i> oocyte and salivary gland sporozoites using proteogenomics framework. <i>Malaria Journal</i> , 2021, 20, 71.	0.8	1
2275	Multiple Classes of Antimicrobial Peptides in <i>Amaranthus tricolor</i> Revealed by Prediction, Proteomics, and Mass Spectrometric Characterization. <i>Journal of Natural Products</i> , 2021, 84, 444-452.	1.5	10
2277	<i>Dinoroseobacter shibae</i> Outer Membrane Vesicles Are Enriched for the Chromosome Dimer Resolution Site <i>in vivo</i> . <i>MSystems</i> , 2021, 6, .	1.7	7
2278	Benchmarking accuracy and precision of intensity-based absolute quantification of protein abundances in <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2021, 21, e2000093.	1.3	13
2281	Reprogramming of sRNA target specificity by the leader peptide peTrpL in response to antibiotic exposure. <i>Nucleic Acids Research</i> , 2021, 49, 2894-2915.	6.5	9
2282	Arginine glycosylation enhances methylglyoxal detoxification. <i>Scientific Reports</i> , 2021, 11, 3834.	1.6	10
2283	Recent Advanced Technologies for the Characterization of Xenobiotic-Degrading Microorganisms and Microbial Communities. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 632059.	2.0	140
2284	Proteomic analyses identify major vault protein as a prognostic biomarker for fatal prostate cancer. <i>Carcinogenesis</i> , 2021, 42, 685-693.	1.3	10
2285	Proteomic Adaptation of <i>Clostridioides difficile</i> to Treatment with the Antimicrobial Peptide Nisin. <i>Cells</i> , 2021, 10, 372.	1.8	7
2286	Penalized partial least squares for pleiotropy. <i>BMC Bioinformatics</i> , 2021, 22, 86.	1.2	2
2287	New Provisional Function of OmpA from <i>Acinetobacter</i> sp. Strain SA01 Based on Environmental Challenges. <i>MSystems</i> , 2021, 6, .	1.7	11
2288	Dynamic proteome response of a marine <i>Vibrio</i> to a gradient of iron and ferrioxamine bioavailability. <i>Marine Chemistry</i> , 2021, 229, 103913.	0.9	5
2289	Myogenesis modelled by human pluripotent stem cells: a multi-omic study of Duchenne myopathy early onset. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021, 12, 209-232.	2.9	36
2290	Global Profiling of 2-hydroxyisobutyrylome in Common Wheat. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 688-701.	3.0	8
2291	ADAM10-Mediated Ectodomain Shedding Is an Essential Driver of Podocyte Damage. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1389-1408.	3.0	7

#	ARTICLE	IF	CITATIONS
2292	Dynamic Intracellular Metabolic Cell Signaling Profiles During Ag-Dependent B-Cell Differentiation. <i>Frontiers in Immunology</i> , 2021, 12, 637832.	2.2	4
2295	Alterations in the Global Proteome and Phosphoproteome in Third Generation EGFR TKI Resistance Reveal Drug Targets to Circumvent Resistance. <i>Cancer Research</i> , 2021, 81, 3051-3066.	0.4	38
2296	Coupled microbiome analyses highlights relative functional roles of bacteria in a bivalve hatchery. <i>Environmental Microbiomes</i> , 2021, 16, 7.	2.2	7
2297	Adaptation of <i>Dinoroseobacter shibae</i> to oxidative stress and the specific role of RirA. <i>PLoS ONE</i> , 2021, 16, e0248865.	1.1	2
2298	Redox sensor NPGPx restrains ZAP70 activity and modulates T cell homeostasis. <i>Free Radical Biology and Medicine</i> , 2021, 165, 368-384.	1.3	0
2299	Non-antibiotic pharmaceuticals promote the transmission of multidrug resistance plasmids through intra- and intergenera conjugation. <i>ISME Journal</i> , 2021, 15, 2493-2508.	4.4	76
2300	Focal adhesion kinase inhibition synergizes with nab-paclitaxel to target pancreatic ductal adenocarcinoma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021, 40, 91.	3.5	24
2302	Unbiased proteomic profiling of host cell extracellular vesicle composition and dynamics upon HIV-1 infection. <i>EMBO Journal</i> , 2021, 40, e105492.	3.5	36
2303	Multi-omic analyses in Abyssinian cats with primary renal amyloid deposits. <i>Scientific Reports</i> , 2021, 11, 8339.	1.6	6
2304	Proteomic Profiling of IgG1 Producing CHO Cells Using LC/LC-SPS-MS3: The Effects of Bioprocessing Conditions on Productivity and Product Quality. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 569045.	2.0	8
2305	Parallel G-quadruplexes recruit the HSV-1 transcription factor ICP4 to promote viral transcription in herpes virus-infected human cells. <i>Communications Biology</i> , 2021, 4, 510.	2.0	23
2307	Knock out of specific maternal vitellogenins in zebrafish ( <i>Danio rerio</i> ) evokes vital changes in egg proteomic profiles that resemble the phenotype of poor quality eggs. <i>BMC Genomics</i> , 2021, 22, 308.	1.2	14
2308	Daytime Restricted Feeding Affects Day-Night Variations in Mouse Cerebellar Proteome. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 613161.	1.4	1
2309	Factors affecting the rapid changes of protein under short-term heat stress. <i>BMC Genomics</i> , 2021, 22, 263.	1.2	6
2310	Exploring the dermatotoxicity of the mycotoxin deoxynivalenol: combined morphologic and proteomic profiling of human epidermal cells reveals alteration of lipid biosynthesis machinery and membrane structural integrity relevant for skin barrier function. <i>Archives of Toxicology</i> , 2021, 95, 2201-2221.	1.9	11
2311	Proteomic Studies of Primary Acute Myeloid Leukemia Cells Derived from Patients Before and during Disease-Stabilizing Treatment Based on All-Trans Retinoic Acid and Valproic Acid. <i>Cancers</i> , 2021, 13, 2143.	1.7	6
2312	USP7 limits CDK1 activity throughout the cell cycle. <i>EMBO Journal</i> , 2021, 40, e99692.	3.5	23
2313	An Integrated Genomic, Proteomic, and Immunopeptidomic Approach to Discover Treatment-Induced Neoantigens. <i>Frontiers in Immunology</i> , 2021, 12, 662443.	2.2	22



#	ARTICLE	IF	CITATIONS
2314	Glycan-Induced Protein Dynamics in Human Norovirus P Dimers Depend on Virus Strain and Deamidation Status. <i>Molecules</i> , 2021, 26, 2125.	1.7	13
2316	Bacterial Hsp90 Facilitates the Degradation of Aggregation-Prone Hsp70â€“Hsp40 Substrates. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 653073.	1.6	18
2317	Comprehensive Profiling of Secretome Formulations from Fetal- and Perinatal Human Amniotic Fluid Stem Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3713.	1.8	14
2318	Divergent Proteomic Responses Offer Insights into Resistant Physiological Responses of a Reef-Foraminifera to Climate Change Scenarios. <i>Oceans</i> , 2021, 2, 281-314.	0.6	16
2319	Erosion of human X chromosome inactivation causes major remodeling of the iPSC proteome. <i>Cell Reports</i> , 2021, 35, 109032.	2.9	23
2320	Proteomic response of <i>Escherichia coli</i> to a membrane lytic and iron chelating truncated <i>Amaranthus tricolor</i> defensin. <i>BMC Microbiology</i> , 2021, 21, 110.	1.3	9
2322	Atypical acute myeloid leukemia-specific transcripts generate shared and immunogenic MHC class-I-associated epitopes. <i>Immunity</i> , 2021, 54, 737-752.e10.	6.6	58
2324	An intercrypt subpopulation of goblet cells is essential for colonic mucus barrier function. <i>Science</i> , 2021, 372, .	6.0	144
2325	Salivary Proteomic Profiling Identifies Role of Neutrophil Extracellular Traps Formation in Pregnancy Gingivitis. <i>Immunological Investigations</i> , 2022, 51, 103-119.	1.0	3
2326	Online biophysical predictions for SARS-CoV-2 proteins. <i>BMC Molecular and Cell Biology</i> , 2021, 22, 23.	1.0	1
2328	Proteome constraints reveal targets for improving microbial fitness in nutrientâ€“rich environments. <i>Molecular Systems Biology</i> , 2021, 17, e10093.	3.2	46
2330	Molecular insights into plant desiccation tolerance: transcriptomics, proteomics and targeted metabolite profiling in <i>Cratogeomys plantagineum</i> . <i>Plant Journal</i> , 2021, 107, 377-398.	2.8	40
2331	Quantitative proteomics analysis identifies salivary biomarkers for early detection of pregnancy loss in a Singaporean cohortâ€“A pilot study. <i>Proteomics - Clinical Applications</i> , 2021, 15, 2000068.	0.8	3
2332	Identification of novel inner membrane complex and apical annuli proteins of the malaria parasite <i>Plasmodium falciparum</i> . <i>Cellular Microbiology</i> , 2021, 23, e13341.	1.1	19
2333	Retinal Proteomics of a Mouse Model of Dystroglycanopathies Reveals Molecular Alterations in Photoreceptors. <i>Journal of Proteome Research</i> , 2021, 20, 3268-3277.	1.8	5
2336	Detection and quantitation of host cell proteins in monoclonal antibody drug products using automated sample preparation and data-independent acquisition LC-MS/MS. <i>Journal of Pharmaceutical Analysis</i> , 2021, 11, 726-731.	2.4	12
2337	Proteomics-Based Data Integration of Wheat Cultivars Facing <i>Fusarium graminearum</i> Strains Revealed a Core-Responsive Pattern Controlling <i>Fusarium</i> Head Blight. <i>Frontiers in Plant Science</i> , 2021, 12, 644810.	1.7	8
2339	Design, Synthesis, and Evaluation of WD-Repeat-Containing Protein 5 (WDR5) Degradable. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 10682-10710.	2.9	38

#	ARTICLE	IF	CITATIONS
2340	Bacterial Microcompartment-Dependent 1,2-Propanediol Utilization of <i>Propionibacterium freudenreichii</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 679827.	1.5	9
2341	Lipopolysaccharide-regulated secretion of soluble and vesicle-based proteins from a panel of colorectal cancer cell lines. <i>Proteomics - Clinical Applications</i> , 2021, 15, 1900119.	0.8	2
2342	Liver proteomics analysis reveals abnormal metabolism of bile acid and arachidonic acid in Chinese hamsters with type 2 diabetes mellitus. <i>Journal of Proteomics</i> , 2021, 239, 104186.	1.2	10
2343	Molecular Pathobiology of the Cerebrovasculature in Aging and in Alzheimers Disease Cases With Cerebral Amyloid Angiopathy. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 658605.	1.7	11
2344	The chemical compound Heatin™ stimulates hypocotyl elongation and interferes with the Arabidopsis NIT1-subfamily of nitrilases. <i>Plant Journal</i> , 2021, 106, 1523-1540.	2.8	7
2345	Targeting public neoantigens for cancer immunotherapy. <i>Nature Cancer</i> , 2021, 2, 487-497.	5.7	79
2346	Genomic and proteomic profiles of biofilms on microplastics are decoupled from artificial surface properties. <i>Environmental Microbiology</i> , 2021, 23, 3099-3115.	1.8	43
2347	Identification of an Altered Matrix Signature in Kidney Aging and Disease. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1713-1732.	3.0	45
2348	Transfer learning for small molecule retention predictions. <i>Journal of Chromatography A</i> , 2021, 1644, 462119.	1.8	9
2349	A native conjugative plasmid confers potential selective advantages to plant growth-promoting <i>Bacillus velezensis</i> strain GH1-13. <i>Communications Biology</i> , 2021, 4, 582.	2.0	3
2350	A Small RNA Is Linking CRISPR-Cas and Zinc Transport. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 640440.	1.6	4
2351	DIaproteomics: A Multifunctional Data Analysis Pipeline for Data-Independent Acquisition Proteomics and Peptidomics. <i>Journal of Proteome Research</i> , 2021, 20, 3758-3766.	1.8	17
2352	A Universal and High-Throughput Proteomics Sample Preparation Platform. <i>Analytical Chemistry</i> , 2021, 93, 8423-8431.	3.2	24
2354	Global proteomic response of unicellular cyanobacterium <i>Synechocystis</i> sp. PCC 6803 to fluctuating light upon CO <sub>2</sub> step-down. <i>Physiologia Plantarum</i> , 2021, 173, 305-320.	2.6	2
2355	Gene Replacement in Arabidopsis Reveals Manganese Transport as an Ancient Feature of Human, Plant and Cyanobacterial UPF0016 Proteins. <i>Frontiers in Plant Science</i> , 2021, 12, 697848.	1.7	5
2356	ATP Drives Efficient Terpene Biosynthesis in Marine Thraustochytrids. <i>MBio</i> , 2021, 12, e0088121.	1.8	11
2357	BAG3 is a negative regulator of ciliogenesis in glioblastoma and triple-negative breast cancer cells. <i>Journal of Cellular Biochemistry</i> , 2022, 123, 77-90.	1.2	8
2358	The AGE receptor, OST48 drives podocyte foot process effacement and basement membrane expansion (alters structural composition). <i>Endocrinology, Diabetes and Metabolism</i> , 2021, 4, e00278.	1.0	4

#	ARTICLE	IF	CITATIONS
2359	TNF- $\alpha$ induces endothelial-mesenchymal transition promoting stromal development of pancreatic adenocarcinoma. <i>Cell Death and Disease</i> , 2021, 12, 649.	2.7	31
2360	RNA pull-down confocal nanoscopy (RP-CONA) detects quercetin as pri-miR-7/HuR interaction inhibitor that decreases $\beta$ -synuclein levels. <i>Nucleic Acids Research</i> , 2021, 49, 6456-6473.	6.5	7
2362	A hub-and-spoke nuclear lamina architecture in trypanosomes. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	4
2363	Comparative Proteomic Analysis Reveals Varying Impact on Immune Responses in Phorbol 12-Myristate-13-Acetate-Mediated THP-1 Monocyte-to-Macrophage Differentiation. <i>Frontiers in Immunology</i> , 2021, 12, 679458.	2.2	22
2364	The highly conserved FOXJ1 target CFAP161 is dispensable for motile ciliary function in mouse and <i>Xenopus</i> . <i>Scientific Reports</i> , 2021, 11, 13333.	1.6	3
2365	Tripartite Separation of Glomerular Cell Types and Proteomes from Reporter-Free Mice. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 2175-2193.	3.0	16
2366	Methane-dependent selenate reduction by a bacterial consortium. <i>ISME Journal</i> , 2021, 15, 3683-3692.	4.4	17
2368	Quantitative Proteomics and Differential Protein Abundance Analysis after Depletion of Putative mRNA Receptors in the ER Membrane of Human Cells Identifies Novel Aspects of mRNA Targeting to the ER. <i>Molecules</i> , 2021, 26, 3591.	1.7	14
2369	Identification of amyloidogenic proteins in the microbiomes of a rat Parkinson's disease model and wild-type rats. <i>Protein Science</i> , 2021, 30, 1854-1870.	3.1	5
2370	Hepatic stellate cells suppress NK cell-sustained breast cancer dormancy. <i>Nature</i> , 2021, 594, 566-571.	13.7	139
2371	Propionate Production from Carbon Monoxide by Synthetic Cocultures of <i>Acetobacterium wieringae</i> and Propionigenic Bacteria. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0283920.	1.4	17
2372	Maturation of the preterm gastrointestinal tract can be defined by host and microbial markers for digestion and barrier defense. <i>Scientific Reports</i> , 2021, 11, 12808.	1.6	15
2373	Proteomics reveals commitment to germination in barley seeds is marked by loss of stress response proteins and mobilisation of nutrient reservoirs. <i>Journal of Proteomics</i> , 2021, 242, 104221.	1.2	18
2374	ALKBH3 partner ASCC3 mediates P-body formation and selective clearance of MMS-induced 1-methyladenosine and 3-methylcytosine from mRNA. <i>Journal of Translational Medicine</i> , 2021, 19, 287.	1.8	13
2375	GIP_HUMAN[22-51] is a new proatherogenic peptide identified by native plasma peptidomics. <i>Scientific Reports</i> , 2021, 11, 14470.	1.6	5
2376	Metabolic responses of two pioneer wood decay fungi to diurnally cycling temperature. <i>Journal of Ecology</i> , 2022, 110, 68-79.	1.9	4
2377	Integrated Quantitative Phosphoproteomics and Cell-Based Functional Screening Reveals Specific Pathological Cardiac Hypertrophy-Related Phosphorylation Sites. <i>Molecules and Cells</i> , 2021, 44, 500-516.	1.0	4
2378	The Arabidopsis Root Tip (Phospho)Proteomes at Growth-Promoting versus Growth-Repressing Conditions Reveal Novel Root Growth Regulators. <i>Cells</i> , 2021, 10, 1665.	1.8	8

#	ARTICLE	IF	CITATIONS
2379	Redirected nuclear glutamate dehydrogenase supplies Tet3 with $\hat{\iota}$ -ketoglutarate in neurons. <i>Nature Communications</i> , 2021, 12, 4100.	5.8	7
2381	DIAMeter: matching peptides to data-independent acquisition mass spectrometry data. <i>Bioinformatics</i> , 2021, 37, i434-i442.	1.8	9
2382	A serum proteome signature to predict mortality in severe COVID-19 patients. <i>Life Science Alliance</i> , 2021, 4, e202101099.	1.3	62
2383	The non-canonical target PARP16 contributes to polypharmacology of the PARP inhibitor talazoparib and its synergy with WEE1 inhibitors. <i>Cell Chemical Biology</i> , 2022, 29, 202-214.e7.	2.5	19
2384	HLA-B and cysteinylated ligands distinguish the antigen presentation landscape of extracellular vesicles. <i>Communications Biology</i> , 2021, 4, 825.	2.0	9
2385	Microbial metabolism and adaptations in <i>Atribacteria</i> -dominated methane hydrate sediments. <i>Environmental Microbiology</i> , 2021, 23, 4646-4660.	1.8	20
2386	Characterization of RNA-binding proteins in the cell nucleus and cytoplasm. <i>Analytica Chimica Acta</i> , 2021, 1168, 338609.	2.6	5
2387	The RNA-binding protein Nab2 regulates the proteome of the developing <i>Drosophila</i> brain. <i>Journal of Biological Chemistry</i> , 2021, 297, 100877.	1.6	4
2388	APOE genotype dependent molecular abnormalities in the cerebrovasculature of Alzheimer's disease and age-matched non-demented brains. <i>Molecular Brain</i> , 2021, 14, 110.	1.3	14
2389	An atlas of protein-protein interactions across mouse tissues. <i>Cell</i> , 2021, 184, 4073-4089.e17.	13.5	59
2390	The distinctive flagellar proteome of <i>Euglena gracilis</i> illuminates the complexities of protistan flagella adaptation. <i>New Phytologist</i> , 2021, 232, 1323-1336.	3.5	14
2391	Comparative analysis of stalked and acorn barnacle adhesive proteomes. <i>Open Biology</i> , 2021, 11, 210142.	1.5	13
2392	Sodium valproate increases activity of the sirtuin pathway resulting in beneficial effects for spinocerebellar ataxia-3 in vivo. <i>Molecular Brain</i> , 2021, 14, 128.	1.3	12
2393	Stress response of lettuce ( <i>Lactuca sativa</i> ) to environmental contamination with selected pharmaceuticals: A proteomic study. <i>Journal of Proteomics</i> , 2021, 245, 104291.	1.2	8
2394	Modern <i>Acinetobacter baumannii</i> clinical isolates replicate inside spacious vacuoles and egress from macrophages. <i>PLoS Pathogens</i> , 2021, 17, e1009802.	2.1	21
2395	CdrS Is a Global Transcriptional Regulator Influencing Cell Division in <i>Haloferax volcanii</i> . <i>MBio</i> , 2021, 12, e0141621.	1.8	14
2398	Activation of the Type VI Secretion System in the Squid Symbiont <i>Vibrio fischeri</i> Requires the Transcriptional Regulator TasR and the Structural Proteins TssM and TssA. <i>Journal of Bacteriology</i> , 2021, 203, e0039921.	1.0	11
2399	Data-Independent-Acquisition-Based Proteomic Approach towards Understanding the Acclimation Strategy of Oleaginous Microalga <i>Microchloropsis gaditana</i> CCMP526 in Hypersaline Conditions. <i>ACS Omega</i> , 2021, 6, 22151-22164.	1.6	2

#	ARTICLE	IF	CITATIONS
2400	The effect of exercise on the protein profile of rat knee joint intra- and extra-articular ligaments. <i>Scandinavian Journal of Medicine and Science in Sports</i> , 2021, 31, 2033-2043.	1.3	2
2401	Chronic binge alcohol and ovariectomy dysregulate omental adipose tissue metabolome in simian immunodeficiency virus-infected female macaques. <i>Physiological Genomics</i> , 2021, 53, 358-371.	1.0	3
2402	The tumor suppressor folliculin inhibits lactate dehydrogenase A and regulates the Warburg effect. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 662-670.	3.6	19
2403	Too Hot to Handle: Antibacterial Peptides Identified in Ghost Pepper. <i>Journal of Natural Products</i> , 2021, 84, 2200-2208.	1.5	6
2404	Tight Adherence (Tad) Pilus Genes Indicate Putative Niche Differentiation in Phytoplankton Bloom Associated Rhodobacterales. <i>Frontiers in Microbiology</i> , 2021, 12, 718297.	1.5	16
2405	Proteome Dynamics during Antibiotic Persistence and Resuscitation. <i>MSystems</i> , 2021, 6, e0054921.	1.7	4
2406	Isotopically Dimethyl Labeling-Based Quantitative Proteomic Analysis of Phosphoproteomes of Soybean Cultivars. <i>Biomolecules</i> , 2021, 11, 1218.	1.8	5
2407	Triple extraction method enables high quality mass spectrometry-based proteomics and phosphoproteomics for eventual multi-omics integration studies. <i>Proteomics</i> , 2021, 21, 2000303.	1.3	2
2409	Expression Dysregulation as a Mediator of Fitness Costs in Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0050421.	1.4	5
2410	Allotype-Specific Glycosylation and Cellular Localization of Human Leukocyte Antigen Class I Proteins. <i>Journal of Proteome Research</i> , 2021, 20, 4518-4528.	1.8	9
2411	Ketogenesis impact on liver metabolism revealed by proteomics of lysine $\epsilon^2$ -hydroxybutyrylation. <i>Cell Reports</i> , 2021, 36, 109487.	2.9	56
2412	Activation of Endogenous H <sub>2</sub> S Biosynthesis or Supplementation with Exogenous H <sub>2</sub> S Enhances Adipose Tissue Adipogenesis and Preserves Adipocyte Physiology in Humans. <i>Antioxidants and Redox Signaling</i> , 2021, 35, 319-340.	2.5	18
2413	Accessory enzymes of hypercellulolytic <i>Penicillium funiculosum</i> facilitate complete saccharification of sugarcane bagasse. <i>Biotechnology for Biofuels</i> , 2021, 14, 171.	6.2	14
2414	A Linkage-specific Sialic Acid Labeling Strategy Reveals Different Site-specific Glycosylation Patterns in SARS-CoV-2 Spike Protein Produced in CHO and HEK Cell Substrates. <i>Frontiers in Chemistry</i> , 2021, 9, 735558.	1.8	12
2415	Triangulation of microbial fingerprinting in anaerobic digestion reveals consistent fingerprinting profiles. <i>Water Research</i> , 2021, 202, 117422.	5.3	12
2416	Na <sup>+</sup> -Coupled Respiration and Reshaping of Extracellular Polysaccharide Layer Counteract Monensin-Induced Cation Permeability in <i>Prevotella bryantii</i> B14. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10202.	1.8	2
2417	A phosphatase-centric mechanism drives stress signaling response. <i>EMBO Reports</i> , 2021, 22, e52476.	2.0	9
2418	The Cell Wall Proteome of <i>Craterostigma plantagineum</i> Cell Cultures Habituated to Dichlobenil and Isoxaben. <i>Cells</i> , 2021, 10, 2295.	1.8	4

#	ARTICLE	IF	CITATIONS
2419	Disturbed mitochondrial acetylation in accordance with the availability of acetyl groups in hepatocellular carcinoma. <i>Mitochondrion</i> , 2021, 60, 150-159.	1.6	4
2420	Inositol polyphosphates and target of rapamycin kinase signalling govern photosystem II protein phosphorylation and photosynthetic function under light stress in <i>Chlamydomonas</i> . <i>New Phytologist</i> , 2021, 232, 2011-2025.	3.5	10
2421	A Shotgun Proteomic Platform for a Global Mapping of Lymphoblastoid Cells to Gain Insight into Nasu-Hakola Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9959.	1.8	2
2422	Interactome screening of <i>C9orf72</i> dipeptide repeats reveals VCP sequestration and functional impairment by polyGA. <i>Brain</i> , 2022, 145, 684-699.	3.7	15
2423	Discovery of a small protein-encoding cis-regulatory overlapping gene of the tumor suppressor gene <i>Scribble</i> in humans. <i>Communications Biology</i> , 2021, 4, 1098.	2.0	4
2424	High-throughput microfluidic 3D biomimetic model enabling quantitative description of the human breast tumor microenvironment. <i>Acta Biomaterialia</i> , 2021, 132, 473-488.	4.1	20
2425	Elamipretide (SS-31) treatment attenuates age-associated post-translational modifications of heart proteins. <i>GeroScience</i> , 2021, 43, 2395-2412.	2.1	17
2426	<i>Burkholderia</i> PglL enzymes are Serine preferring oligosaccharyltransferases which target conserved proteins across the <i>Burkholderia</i> genus. <i>Communications Biology</i> , 2021, 4, 1045.	2.0	4
2427	Defining Proximity Proteome of Histone Modifications by Antibody-mediated Protein A-APEX2 Labeling. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 87-100.	3.0	7
2428	Systematic analysis of chemical-protein interactions from zebrafish embryo by proteome-wide thermal shift assay, bridging the gap between molecular interactions and toxicity pathways. <i>Journal of Proteomics</i> , 2021, 249, 104382.	1.2	6
2429	Limited light intensity and low temperature: Can plants survive freezing in light conditions that more accurately replicate the cold season in temperate regions?. <i>Environmental and Experimental Botany</i> , 2021, 190, 104581.	2.0	10
2430	Atypical activation of signaling downstream of inactivated Bcr-Abl mediates chemoresistance in chronic myeloid leukemia. <i>Journal of Cell Communication and Signaling</i> , 2022, 16, 207-222.	1.8	2
2431	PRIMUS: Comprehensive proteomics of mouse intervertebral discs that inform novel biology and relevance to human disease modelling. <i>Matrix Biology Plus</i> , 2021, 12, 100082.	1.9	13
2432	Chromatin phosphoproteomics unravels a function for AT-hook motif nuclear localized protein AHL13 in PAMP-triggered immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	25
2433	Unraveling the MAX2 Protein Network in <i>Arabidopsis thaliana</i> : Identification of the Protein Phosphatase PAPP5 as a Novel MAX2 Interactor. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100040.	2.5	11
2434	Benchtop micro-mashing: high-throughput, robust, experimental beer brewing. <i>Scientific Reports</i> , 2021, 11, 1480.	1.6	7
2435	Octenidine-based hydrogel shows anti-inflammatory and protease-inhibitory capacities in wounded human skin. <i>Scientific Reports</i> , 2021, 11, 32.	1.6	20
2436	Combination of to Functionally Characterize Dark Proteins in Human Olfactory Neuroepithelial Cells. <i>Methods in Molecular Biology</i> , 2021, 2344, 227-238.	0.4	1

#	ARTICLE	IF	CITATIONS
2437	Another layer of complexity in <i>Staphylococcus aureus</i> methionine biosynthesis control: unusual RNase III-driven T-box riboswitch cleavage determines <i>met</i> operon mRNA stability and decay. <i>Nucleic Acids Research</i> , 2021, 49, 2192-2212.	6.5	7
2438	Network Analysis Combining Proteomics and Metabolomics Reveals New Insights Into Early Responses of <i>Eucalyptus grandis</i> During Rust Infection. <i>Frontiers in Plant Science</i> , 2020, 11, 604849.	1.7	12
2439	Rab7-harboring vesicles are carriers of the transferrin receptor through the biosynthetic secretory pathway. <i>Science Advances</i> , 2021, 7, .	4.7	11
2440	Quantitative proteome profiles help reveal efficient xylose utilization mechanisms in solventogenic <i>Clostridium</i> sp. strain BOH3. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1959-1969.	1.7	5
2441	Mitochondrial Complexome Profiling. <i>Methods in Molecular Biology</i> , 2021, 2192, 269-285.	0.4	8
2442	Creation of Reusable Bioinformatics Workflows for Reproducible Analysis of LC-MS Proteomics Data. <i>Neuroinformatics</i> , 2017, , 305-324.	0.2	2
2443	Targeted Proteomics as a Tool for Quantifying Urine-Based Biomarkers. <i>Methods in Molecular Biology</i> , 2020, 2051, 277-295.	0.4	3
2444	Validation of Chimeric Fusion Peptides Using Proteomics Data. <i>Methods in Molecular Biology</i> , 2020, 2079, 117-124.	0.4	1
2445	Mass Spectra Interpretation and the Interest of SpecFit for Identifying Uncommon Modifications. <i>Lecture Notes in Computer Science</i> , 2020, , 80-89.	1.0	1
2446	On the Mechanism and Origin of Isoleucyl-tRNA Synthetase Editing against Norvaline. <i>Journal of Molecular Biology</i> , 2019, 431, 1284-1297.	2.0	20
2447	Quantitative Performance Evaluator for Proteomics (QPEP): Web-based Application for Reproducible Evaluation of Proteomics Preprocessing Methods. <i>Journal of Proteome Research</i> , 2017, 16, 2359-2369.	1.8	5
2448	Dedicated surveillance mechanism controls G-quadruplex forming non-coding RNAs in human mitochondria. <i>Nature Communications</i> , 2018, 9, 2558.	5.8	67
2449	Small-RNA-mediated transgenerational silencing of histone genes impairs fertility in piRNA mutants. <i>Nature Cell Biology</i> , 2020, 22, 235-245.	4.6	64
2450	The phosphatase PAC1 acts as a T cell suppressor and attenuates host antitumor immunity. <i>Nature Immunology</i> , 2020, 21, 287-297.	7.0	73
2451	A tissue-based draft map of the murine MHC class I immunopeptidome. <i>Scientific Data</i> , 2018, 5, 180157.	2.4	45
2452	Generation of a zebrafish SWATH-MS spectral library to quantify 10,000 proteins. <i>Scientific Data</i> , 2019, 6, 190011.	2.4	37
2453	Phosphoproteomics reveals that the hVPS34 regulated SGK3 kinase specifically phosphorylates endosomal proteins including Syntaxin-7, Syntaxin-12, RFP4 and WDR44. <i>Biochemical Journal</i> , 2019, 476, 3081-3107.	1.7	14
2454	Ubiquitome analysis reveals the involvement of lysine ubiquitination in the spermatogenesis process of adult buffalo ( <i>Bubalus bubalis</i> ) testis. <i>Bioscience Reports</i> , 2020, 40, .	1.1	6

#	ARTICLE	IF	CITATIONS
2455	Upregulation of polycistronic microRNA-143 and microRNA-145 in colonocytes suppresses colitis and inflammation-associated colon cancer. <i>Epigenetics</i> , 2021, 16, 1317-1334.	1.3	10
2456	Reactive oxygen species triggers unconventional secretion of antioxidants and Acb1. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	19
2457	Intersection of TKS5 and FGD1/CDC42 signaling cascades directs the formation of invadopodia. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	23
2458	Replacing fish oil and astaxanthin by microalgal sources produced different metabolic responses in juvenile rainbow trout fed 2 types of practical diets. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	4
2459	ADAPT identifies an ESCRT complex composition that discriminates VCaP from LNCaP prostate cancer cell exosomes. <i>Nucleic Acids Research</i> , 2020, 48, 4013-4027.	6.5	15
2460	Cooperation of the NEIL3 and Fanconi anemia/BRCA pathways in interstrand crosslink repair. <i>Nucleic Acids Research</i> , 2020, 48, 3014-3028.	6.5	53
2461	GlycoPOST realizes FAIR principles for glycomics mass spectrometry data. <i>Nucleic Acids Research</i> , 2021, 49, D1523-D1528.	6.5	78
2462	Insertion sequences drive the emergence of a highly adapted human pathogen. <i>Microbial Genomics</i> , 2020, 6, .	1.0	19
2527	Multiplex quantitative SILAC for analysis of archaeal proteomes: a case study of oxidative stress responses. <i>Environmental Microbiology</i> , 2018, 20, 385-401.	1.8	21
2528	The modulation of the burn wound environment by negative pressure wound therapy: Insights from the proteome. <i>Wound Repair and Regeneration</i> , 2021, 29, 288-297.	1.5	10
2529	Towards Co-Evolution of Data-Centric Ecosystems. , 2020, , .		5
2530	Systematic Analysis of Intronic miRNAs Reveals Cooperativity within the Multicomponent <i>FTX</i> Locus to Promote Colon Cancer Development. <i>Cancer Research</i> , 2021, 81, 1308-1320.	0.4	14
2531	Glomerular filtrate proteins in acute cardiorenal syndrome. <i>JCI Insight</i> , 2019, 4, .	2.3	10
2532	Microdissected pancreatic cancer proteomes reveal tumor heterogeneity and therapeutic targets. <i>JCI Insight</i> , 2020, 5, .	2.3	36
2533	Erythrocyte-derived microvesicles induce arterial spasms in JAK2V617F myeloproliferative neoplasm. <i>Journal of Clinical Investigation</i> , 2020, 130, 2630-2643.	3.9	42
2534	Reticulocyte and red blood cell deformation triggers specific phosphorylation events. <i>Blood Advances</i> , 2019, 3, 2653-2663.	2.5	13
2535	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	0.8	13
2536	Loss of the Greatwall Kinase Weakens the Spindle Assembly Checkpoint. <i>PLoS Genetics</i> , 2016, 12, e1006310.	1.5	32



#	ARTICLE	IF	CITATIONS
2537	The <i>Legionella pneumophila</i> genome evolved to accommodate multiple regulatory mechanisms controlled by the CsrA-system. <i>PLoS Genetics</i> , 2017, 13, e1006629.	1.5	83
2538	A systematic genomic screen implicates nucleocytoplasmic transport and membrane growth in nuclear size control. <i>PLoS Genetics</i> , 2017, 13, e1006767.	1.5	52
2539	The PHD finger protein Spp1 has distinct functions in the Set1 and the meiotic DSB formation complexes. <i>PLoS Genetics</i> , 2018, 14, e1007223.	1.5	41
2540	Identification of RNA Binding Proteins Associated with Dengue Virus RNA in Infected Cells Reveals Temporally Distinct Host Factor Requirements. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004921.	1.3	56
2541	Nanonets Collect Cancer Secretome from Pericellular Space. <i>PLoS ONE</i> , 2016, 11, e0154126.	1.1	11
2542	Proteomic Insight into the Response of Arabidopsis Chloroplasts to Darkness. <i>PLoS ONE</i> , 2016, 11, e0154235.	1.1	20
2543	Quantitative Proteome Analysis of <i>Leishmania donovani</i> under Spermidine Starvation. <i>PLoS ONE</i> , 2016, 11, e0154262.	1.1	10
2544	Enhanced snoMEN Vectors Facilitate Establishment of GFP <sup>HIF-1</sup> Protein Replacement Human Cell Lines. <i>PLoS ONE</i> , 2016, 11, e0154759.	1.1	2
2545	Variations of Phosphorous Accessibility Causing Changes in Microbiome Functions in the Gastrointestinal Tract of Chickens. <i>PLoS ONE</i> , 2016, 11, e0164735.	1.1	37
2546	Quantitative Proteomics Reveals Ecophysiological Effects of Light and Silver Stress on the Mixotrophic Protist <i>Poteroiochromonas malhamensis</i> . <i>PLoS ONE</i> , 2017, 12, e0168183.	1.1	8
2547	Proteomic Analysis of Kveim Reagent Identifies Targets of Cellular Immunity in Sarcoidosis. <i>PLoS ONE</i> , 2017, 12, e0170285.	1.1	41
2548	PGRMC1 Is a Novel Potential Tumor Biomarker of Human Renal Cell Carcinoma Based on Quantitative Proteomic and Integrative Biological Assessments. <i>PLoS ONE</i> , 2017, 12, e0170453.	1.1	23
2549	Exposure to atheroma-relevant 7-oxysterols causes proteomic alterations in cell death, cellular longevity, and lipid metabolism in THP-1 macrophages. <i>PLoS ONE</i> , 2017, 12, e0174475.	1.1	17
2550	Intravitreal injection of $\beta$ -crystallin B2 improves retinal ganglion cell survival in an experimental animal model of glaucoma. <i>PLoS ONE</i> , 2017, 12, e0175451.	1.1	28
2551	Salt stress induces changes in the proteomic profile of micropropagated sugarcane shoots. <i>PLoS ONE</i> , 2017, 12, e0176076.	1.1	47
2552	Proteome-wide profiling of protein lysine acetylation in <i>Aspergillus flavus</i> . <i>PLoS ONE</i> , 2017, 12, e0178603.	1.1	27
2553	Contrasting effects of copper limitation on the photosynthetic apparatus in two strains of the open ocean diatom <i>Thalassiosira oceanica</i> . <i>PLoS ONE</i> , 2017, 12, e0181753.	1.1	24
2554	Time-course global proteome analyses reveal an inverse correlation between A $\beta$ burden and immunoglobulin M levels in the APPNL-F mouse model of Alzheimer disease. <i>PLoS ONE</i> , 2017, 12, e0182844.	1.1	6

#	ARTICLE	IF	CITATIONS
2555	Vitamin C alters the amount of specific endoplasmic reticulum associated proteins involved in lipid metabolism in the liver of mice synthesizing a nonfunctional Werner syndrome (Wrn) mutant protein. PLoS ONE, 2018, 13, e0193170.	1.1	9
2556	Quantitative N-glycoproteomics reveals altered glycosylation levels of various plasma proteins in bloodstream infected patients. PLoS ONE, 2018, 13, e0195006.	1.1	19
2557	Community-intrinsic properties enhance keratin degradation from bacterial consortia. PLoS ONE, 2020, 15, e0228108.	1.1	16
2558	An Interactome-Centered Protein Discovery Approach Reveals Novel Components Involved in Mitosome Function and Homeostasis in Giardia lamblia. PLoS Pathogens, 2016, 12, e1006036.	2.1	22
2559	Disrupting assembly of the inner membrane complex blocks Plasmodium falciparum sexual stage development. PLoS Pathogens, 2017, 13, e1006659.	2.1	69
2560	Protective effect of <i>Vigna unguiculata</i> extract against aging and neurodegeneration. Aging, 2020, 12, 19785-19808.	1.4	9
2561	Biological characteristics of aging in human acute myeloid leukemia cells: the possible importance of aldehyde dehydrogenase, the cytoskeleton and altered transcriptional regulation. Aging, 2020, 12, 24734-24777.	1.4	13
2562	Proteomic analysis uncovers common effects of IFN- $\beta$ and IL-27 on the HLA class I antigen presentation machinery in human cancer cells. Oncotarget, 2016, 7, 72518-72536.	0.8	20
2563	Nitration of tyrosines in complement factor H domains alters its immunological activity and mediates a pathogenic role in age related macular degeneration. Oncotarget, 2017, 8, 49016-49032.	0.8	16
2564	A systematic approach for peptide characterization of B-cell receptor in chronic lymphocytic leukemia cells. Oncotarget, 2017, 8, 42836-42846.	0.8	7
2565	Proteome profiling of clear cell renal cell carcinoma in von Hippel-Lindau patients highlights upregulation of Xaa-Pro aminopeptidase-1, an anti-proliferative and anti-migratory exoprotease. Oncotarget, 2017, 8, 100066-100078.	0.8	13
2566	Integrated analysis of fine-needle-aspiration cystic fluid proteome, cancer cell secretome, and public transcriptome datasets for papillary thyroid cancer biomarker discovery. Oncotarget, 2018, 9, 12079-12100.	0.8	23
2567	Quantitative mass spectrometry analysis reveals a panel of nine proteins as diagnostic markers for colon adenocarcinomas. Oncotarget, 2018, 9, 13530-13544.	0.8	23
2568	Proteomic alterations in early stage cervical cancer. Oncotarget, 2018, 9, 18128-18147.	0.8	20
2569	GSTM3 and GSTP1: novel players driving tumor progression in cervical cancer. Oncotarget, 2018, 9, 21696-21714.	0.8	34
2570	Delineating the HMGB1 and HMGB2 interactome in prostate and ovary epithelial cells and its relationship with cancer. Oncotarget, 2018, 9, 19050-19064.	0.8	9
2571	PAF1 complex interactions with SETDB1 mediate promoter H3K9 methylation and transcriptional repression of <i>Hoxa9</i> and <i>Meis1</i> in acute myeloid leukemia. Oncotarget, 2018, 9, 22123-22136.	0.8	22
2572	Two hits - one stone - increased efficacy of cisplatin-based therapies by targeting PCNA's role in both DNA repair and cellular signaling. Oncotarget, 2018, 9, 32448-32465.	0.8	35

#	ARTICLE	IF	CITATIONS
2573	Targeting the non-canonical roles of PCNA modifies and increases the response to targeted anti-cancer therapy. <i>Oncotarget</i> , 2019, 10, 7185-7197.	0.8	14
2574	An Atlas of Protein-Protein Interactions Across Mammalian Tissues. <i>SSRN Electronic Journal</i> , 0, , .	0.4	8
2575	Alterations of RNA Metabolism by Proteomic Analysis of Breast Cancer Cells Exposed to Marycin: A New Optically Active Porphyrin. <i>Current Molecular Pharmacology</i> , 2019, 12, 147-159.	0.7	1
2576	Proteomics and <i>C9orf72</i> neuropathology identify ribosomes as poly-GR/PR interactors driving toxicity. <i>Life Science Alliance</i> , 2018, 1, e201800070.	1.3	88
2577	Transformation-induced stress at telomeres is counteracted through changes in the telomeric proteome including SAMHD1. <i>Life Science Alliance</i> , 2018, 1, e201800121.	1.3	18
2578	Peptide-based quorum sensing systems in <i>Paenibacillus polymyxa</i> . <i>Life Science Alliance</i> , 2020, 3, e202000847.	1.3	11
2579	Collapsin Response Mediator Proteins: Novel Targets for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2020, 77, 949-960.	1.2	9
2580	Cathepsins Drive Anti-Inflammatory Activity by Regulating Autophagy and Mitochondrial Dynamics in Macrophage Foam Cells. <i>Cellular Physiology and Biochemistry</i> , 2019, 53, 550-572.	1.1	20
2581	Proteomics and functional study reveal marginal zone B and B1 cell specific protein as a candidate marker of multiple myeloma. <i>International Journal of Oncology</i> , 2020, 57, 325-337.	1.4	10
2582	Protein microarray technology: Assisting personalized medicine in oncology (Review). <i>World Academy of Sciences Journal</i> , 0, , .	0.4	11
2583	Extensive cargo identification reveals distinct biological roles of the 12 importin pathways. <i>ELife</i> , 2017, 6, .	2.8	77
2584	Control of immune ligands by members of a cytomegalovirus gene expansion suppresses natural killer cell activation. <i>ELife</i> , 2017, 6, .	2.8	67
2585	The genomic landscape of human cellular circadian variation points to a novel role for the signalosome. <i>ELife</i> , 2017, 6, .	2.8	9
2586	Ubiquilin1 promotes antigen-receptor mediated proliferation by eliminating mislocalized mitochondrial proteins. <i>ELife</i> , 2017, 6, .	2.8	37
2587	A druggable secretory protein maturase of <i>Toxoplasma</i> essential for invasion and egress. <i>ELife</i> , 2017, 6, .	2.8	89
2588	Dynamics of venom composition across a complex life cycle. <i>ELife</i> , 2018, 7, .	2.8	83
2589	Structural plasticity of actin-spectrin membrane skeleton and functional role of actin and spectrin in axon degeneration. <i>ELife</i> , 2019, 8, .	2.8	47
2590	New insights into the cellular temporal response to proteostatic stress. <i>ELife</i> , 2018, 7, .	2.8	47

#	ARTICLE	IF	CITATIONS
2591	Combined transcriptome and proteome profiling reveals specific molecular brain signatures for sex, maturation and circalunar clock phase. <i>ELife</i> , 2019, 8, .	2.8	51
2592	Quantitative insights into the cyanobacterial cell economy. <i>ELife</i> , 2019, 8, .	2.8	82
2593	A de novo evolved gene in the house mouse regulates female pregnancy cycles. <i>ELife</i> , 2019, 8, .	2.8	37
2594	HDX-MS reveals nucleotide-dependent, anti-correlated opening and closure of SecA and SecY channels of the bacterial translocon. <i>ELife</i> , 2019, 8, .	2.8	20
2595	Human cytomegalovirus interactome analysis identifies degradation hubs, domain associations and viral protein functions. <i>ELife</i> , 2019, 8, .	2.8	84
2596	Proteome profile of peripheral myelin in healthy mice and in a neuropathy model. <i>ELife</i> , 2020, 9, .	2.8	63
2597	Peroxiredoxin promotes longevity and H <sub>2</sub> O <sub>2</sub> -resistance in yeast through redox-modulation of protein kinase A. <i>ELife</i> , 2020, 9, .	2.8	20
2598	Differential impact of BTK active site inhibitors on the conformational state of full-length BTK. <i>ELife</i> , 2020, 9, .	2.8	25
2599	Association of potential salivary biomarkers with diabetic retinopathy and its severity in type-2 diabetes mellitus: a proteomic analysis by mass spectrometry. <i>PeerJ</i> , 2016, 4, e2022.	0.9	24
2600	Metaproteomics of saliva identifies human protein markers specific for individuals with periodontitis and dental caries compared to orally healthy controls. <i>PeerJ</i> , 2016, 4, e2433.	0.9	56
2601	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. <i>PeerJ</i> , 2016, 4, e2687.	0.9	124
2602	Comparative proteomics of <i>Rhizopus delemar</i> ATCC 20344 unravels the role of amino acid catabolism in fumarate accumulation. <i>PeerJ</i> , 2017, 5, e3133.	0.9	14
2603	Phosphoproteomic insights into processes influenced by the kinase-like protein DIA1/C3orf58. <i>PeerJ</i> , 2018, 6, e4599.	0.9	7
2604	Proteomics (SWATH-MS) informed by transcriptomics approach of tropical herb <i>Persicaria minor</i> leaves upon methyl jasmonate elicitation. <i>PeerJ</i> , 2018, 6, e5525.	0.9	13
2605	Dynamic proteomic changes in soft wheat seeds during accelerated ageing. <i>PeerJ</i> , 2018, 6, e5874.	0.9	9
2606	iTRAQ-based quantitative proteome analysis reveals metabolic changes between a cleistogamous wheat mutant and its wild-type wheat counterpart. <i>PeerJ</i> , 2019, 7, e7104.	0.9	4
2607	The IsoGenie database: an interdisciplinary data management solution for ecosystems biology and environmental research. <i>PeerJ</i> , 0, 8, e9467.	0.9	5
2608	Quantitative model suggests both intrinsic and contextual features contribute to the transcript coding ability determination in cells. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	0

#	ARTICLE	IF	CITATIONS
2609	PLK1-dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBV-infected mice. <i>EMBO Reports</i> , 2021, 22, e53007.	2.0	5
2610	Analysis of Brain Protein Stability Changes in Mouse Models of Normal Aging and $\pm$ -Synucleinopathy Reveals Age- and Disease-Related Differences. <i>Journal of Proteome Research</i> , 2021, 20, 5156-5168.	1.8	4
2611	Characterization of the Human Eccrine Sweat Proteome—A Focus on the Biological Variability of Individual Sweat Protein Profiles. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10871.	1.8	8
2612	Delineating the Switch between Senescence and Apoptosis in Cervical Cancer Cells under Ciclopirox Treatment. <i>Cancers</i> , 2021, 13, 4995.	1.7	5
2613	Microtubules tune mechanosensitive cell responses. <i>Nature Materials</i> , 2022, 21, 366-377.	13.3	77
2614	Lactococcus lactis Mutants Obtained From Laboratory Evolution Showed Elevated Vitamin K2 Content and Enhanced Resistance to Oxidative Stress. <i>Frontiers in Microbiology</i> , 2021, 12, 746770.	1.5	9
2615	Proteomic analysis of the lake trout ( <i>Salvelinus namaycush</i> ) heart and blood: The beginning of a comprehensive lake trout protein database. <i>Proteomics</i> , 2022, 22, e2100146.	1.3	2
2616	Increased abundance of Cbl E3 ligases alters PDGFR signaling in recessive dystrophic epidermolysis bullosa. <i>Matrix Biology</i> , 2021, 103-104, 58-73.	1.5	1
2617	Investigation of the blood proteome in response to spinal cord injury in rodent models. <i>Spinal Cord</i> , 2022, 60, 320-325.	0.9	2
2618	Multiomic profiling of the liver across diets and age in a diverse mouse population. <i>Cell Systems</i> , 2022, 13, 43-57.e6.	2.9	24
2619	Identification of Biochemical and Molecular Markers of Early Aging in Childhood Cancer Survivors. <i>Cancers</i> , 2021, 13, 5214.	1.7	5
2620	Combined serum anti-SSA/Ro and salivary TRIM29 reveals promising high diagnostic accuracy in patients with primary Sjögren's syndrome. <i>PLoS ONE</i> , 2021, 16, e0258428.	1.1	4
2621	Defining NASH from a Multi-Omics Systems Biology Perspective. <i>Journal of Clinical Medicine</i> , 2021, 10, 4673.	1.0	9
2623	In vivo Profiling of the Alk Proximitome in the Developing Drosophila Brain. <i>Journal of Molecular Biology</i> , 2021, 433, 167282.	2.0	15
2624	Conditions for maintenance of hepatocyte differentiation and function in 3D cultures. <i>IScience</i> , 2021, 24, 103235.	1.9	8
2625	Chapter 16. Proteomics Informed by Transcriptomics. <i>New Developments in Mass Spectrometry</i> , 2016, , 385-405.	0.2	0
2650	Multi-Omics Insights into Functional Alterations of the Liver in Insulin-Deficient Diabetes Mellitus. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2651	A system-wide approach to monitor responses to synergistic BRAF and EGFR inhibition in colorectal cancer cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
2698	Identification of Human Blood Plasma Proteins Using Spike-In Peptides in Shotgun Proteomics. <i>Biomedical Chemistry Research and Methods</i> , 2019, 2, e00093.	0.1	0
2699	Model Building: Part Two. , 2019, , 55-62.		0
2700	Shifts in Ribosome Engagement Impact Key Gene Sets in Neurodevelopment and Ubiquitination in Rett Syndrome. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2726	Blind normalization of public high-throughput databases. <i>PeerJ Computer Science</i> , 2019, 5, e231.	2.7	1
2729	Challenges, Current Trends, and Future Directions. , 2020, , 235-266.		0
2741	Extracellular vesicles in patients in the acute phase of psychosis and after clinical improvement: an explorative study. <i>PeerJ</i> , 2020, 8, e9714.	0.9	6
2742	Evaluation of RNA <i>later</i> as a Field-Compatible Preservation Method for Metaproteomic Analyses of Bacterium-Animal Symbioses. <i>Microbiology Spectrum</i> , 2021, 9, e0142921.	1.2	4
2744	New mixture models for decoy-free false discovery rate estimation in mass spectrometry proteomics. <i>Bioinformatics</i> , 2020, 36, i745-i753.	1.8	8
2746	Registered report protocol: Quantitative analysis of septin Cdc10-associated proteome in <i>Cryptococcus neoformans</i> . <i>PLoS ONE</i> , 2020, 15, e0242381.	1.1	1
2749	Bioinformatics Tools for SRM-MS. , 2020, , 115-144.		0
2759	Hepatocyte-specific perturbation of NAD <sup>+</sup> biosynthetic pathways in mice induces reversible nonalcoholic steatohepatitis-like phenotypes. <i>Journal of Biological Chemistry</i> , 2021, 297, 101388.	1.6	20
2760	Host Plant Adaptation Drives Changes in <i>Diaphorina citri</i> Proteome Regulation, Proteoform Expression, and Transmission of <i>Candidatus Liberibacter asiaticus</i> <sup>TM</sup> , the Citrus Greening Pathogen. <i>Phytopathology</i> , 2022, 112, 101-115.	1.1	6
2761	The Two-Component System RstA/RstB Regulates Expression of Multiple Efflux Pumps and Influences Anaerobic Nitrate Respiration in <i>Pseudomonas fluorescens</i> . <i>MSystems</i> , 2021, 6, e0091121.	1.7	6
2763	Targeting of parvulin interactors by diazirine mediated cross-linking discloses a cellular role of human Par14/17 in actin polymerization. <i>Biological Chemistry</i> , 2020, 401, 955-968.	1.2	1
2768	The interactome of multifunctional HAX1 protein suggests its role in the regulation of energy metabolism, de-aggregation, cytoskeleton organization and RNA-processing. <i>Bioscience Reports</i> , 2020, 40, .	1.1	10
2769	Comprehensive characterization of the adult ND4 Swiss Webster mouse retina: Using discovery-based mass spectrometry to decipher the total proteome and phosphoproteome. <i>Molecular Vision</i> , 2018, 24, 875-889.	1.1	14
2770	Inositol 1,4,5-trisphosphate receptor type 3 (ITPR3) is overexpressed in cholangiocarcinoma and its expression correlates with S100 calcium-binding protein A4 (S100A4). <i>Biomedicine and Pharmacotherapy</i> , 2022, 145, 112403.	2.5	4
2771	MAGED2 controls vasopressin-induced aquaporin-2 expression in collecting duct cells. <i>Journal of Proteomics</i> , 2022, 252, 104424.	1.2	1

#	ARTICLE	IF	CITATIONS
2773	Defactinib inhibits PYK2 phosphorylation of IRF5 and reduces intestinal inflammation. <i>Nature Communications</i> , 2021, 12, 6702.	5.8	13
2774	Identification of proximal SUMO-dependent interactors using SUMO-ID. <i>Nature Communications</i> , 2021, 12, 6671.	5.8	27
2775	Proteomic Analysis of a Syntrophic Coculture of Syntrophobacter fumaroxidans MPOBT and Geobacter sulfurreducens PCAT. <i>Frontiers in Microbiology</i> , 2021, 12, 708911.	1.5	3
2776	Statins affect cancer cell plasticity with distinct consequences for tumor progression and metastasis. <i>Cell Reports</i> , 2021, 37, 110056.	2.9	24
2777	Computational cancer neoantigen prediction: current status and recent advances. <i>Immuno-Oncology Technology</i> , 2021, 12, 100052.	0.2	14
2779	ATR inhibition enables complete tumour regression in ALK-driven NB mouse models. <i>Nature Communications</i> , 2021, 12, 6813.	5.8	21
2780	Effect of actinorhizal root exudates on the proteomes of <i>Frankia soli</i> NRRL B-16219, a strain colonizing the root tissues of its actinorhizal host via intercellular pathway. <i>Research in Microbiology</i> , 2022, 173, 103900.	1.0	5
2781	Mass Spectrometric Identification of Antimicrobial Peptides from Medicinal Seeds. <i>Molecules</i> , 2021, 26, 7304.	1.7	3
2782	Quantitative Proteomics and Differential Protein Abundance Analysis after the Depletion of PEX3 from Human Cells Identifies Additional Aspects of Protein Targeting to the ER. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13028.	1.8	7
2784	Follistatin-related protein 1 interacting partner of Syndecan-1 promotes an aggressive phenotype on Oral Squamous cell carcinoma (OSCC) models. <i>Journal of Proteomics</i> , 2022, 254, 104474.	1.2	1
2785	Recent advances in plastic degradation – From microbial consortia-based methods to data sciences and computational biology driven approaches. <i>Journal of Hazardous Materials</i> , 2022, 426, 128086.	6.5	46
2786	<i>Amaranthus hypochondriacus</i> seeds as a rich source of cysteine rich bioactive peptides. <i>Food Chemistry</i> , 2022, 377, 131959.	4.2	5
2787	Sequestration of eIF4A by angiomin: A novel mechanism to restrict global protein synthesis in trophoblast cells. <i>Stem Cells</i> , 2021, 39, 210-226.	1.4	8
2788	Proteome Profiling of <i>Mycobacterium tuberculosis</i> Cells Exposed to Nitrosative Stress. <i>ACS Omega</i> , 2022, 7, 3470-3482.	1.6	7
2789	Activity-Based Protein Profiling for the Identification of Novel Carbohydrate-Active Enzymes Involved in Xylan Degradation in the Hyperthermophilic Euryarchaeon <i>Thermococcus</i> sp. Strain 2319x1E. <i>Frontiers in Microbiology</i> , 2021, 12, 734039.	1.5	6
2790	Comparative genomics and proteomics of <i>Eubacterium maltosivorans</i> : functional identification of trimethylamine methyltransferases and bacterial microcompartments in a human intestinal bacterium with a versatile lifestyle. <i>Environmental Microbiology</i> , 2022, 24, 517-534.	1.8	8
2791	Antigen Discovery in Circulating Extracellular Vesicles From <i>Plasmodium vivax</i> Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 811390.	1.8	9
2792	Proteomic Characterization of Dry Blood Spots of Healthy Women During Simulation the Microgravity Effects Using Dry Immersion. <i>Frontiers in Physiology</i> , 2021, 12, 753291.	1.3	3

#	ARTICLE	IF	CITATIONS
2793	Effect of dietary incorporation of <i>Chlorella vulgaris</i> and CAZyme supplementation on the hepatic proteome of finishing pigs. <i>Journal of Proteomics</i> , 2022, 256, 104504.	1.2	5
2794	Proteomic analysis in primary T cells reveals IL-7 alters T cell receptor thresholding via CYTIP/cytohesin/LFA-1 localisation and activation. <i>Biochemical Journal</i> , 2022, 479, 225-243.	1.7	0
2795	Shotgun Proteomics as a Powerful Tool for the Study of the Proteomes of Plants, Their Pathogens, and Plant-Pathogen Interactions. <i>Proteomes</i> , 2022, 10, 5.	1.7	18
2796	High Throughput Screening of a Prescription Drug Library for Inhibitors of Organic Cation Transporter 3, OCT3. <i>Pharmaceutical Research</i> , 2022, 39, 1599-1613.	1.7	13
2797	The <i>H. pylori</i> CagA Oncoprotein Induces DNA Double Strand Breaks through Fanconi Anemia Pathway Downregulation and Replication Fork Collapse. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1661.	1.8	6
2798	Tau interactome maps synaptic and mitochondrial processes associated with neurodegeneration. <i>Cell</i> , 2022, 185, 712-728.e14.	13.5	114
2800	Proteomic analysis of metabolic pathways supports chloroplast-mitochondria cross-talk in a Cu-limited diatom. <i>Plant Direct</i> , 2022, 6, e376.	0.8	6
2801	Rv1258c acts as a drug efflux pump and growth controlling factor in <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2022, 133, 102172.	0.8	4
2802	Making Biomedical Sciences publications more accessible for machines. <i>Medicine, Health Care and Philosophy</i> , 2022, , 1.	0.9	2
2803	Vps501, a novel vacuolar SNX protein cooperates with the SEA complex to regulate TORC1 signaling. <i>Traffic</i> , 2022, , .	1.3	3
2804	Exploring Human Milk Dynamics: Interindividual Variation in Milk Proteome, Peptidome, and Metabolome. <i>Journal of Proteome Research</i> , 2022, 21, 1002-1016.	1.8	7
2805	Label-free proteome data of susceptible and resistant rice cultivars in response to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> inoculation. <i>Data in Brief</i> , 2022, 41, 107890.	0.5	3
2806	Venomomics and antivenomics of Indian spectacled cobra ( <i>Naja naja</i> ) from the Western Ghats. <i>Acta Tropica</i> , 2022, 228, 106324.	0.9	4
2808	Phosphoproteome of signaling by ErbB2 in ovarian cancer cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2022, 1870, 140768.	1.1	3
2810	Receptor-interacting protein kinase 2 (RIPK2) stabilizes c-Myc and is a therapeutic target in prostate cancer metastasis. <i>Nature Communications</i> , 2022, 13, 669.	5.8	19
2812	A novel strategy to uncover specific GO terms/phosphorylation pathways in phosphoproteomic data in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2021, 21, 592.	1.6	1
2813	Evaluation of Sample Preservation and Storage Methods for Metaproteomics Analysis of Intestinal Microbiomes. <i>Microbiology Spectrum</i> , 2021, 9, e0187721.	1.2	8
2814	Macrophages secrete murinoglobulin-1 and galectin-3 to regulate neutrophil degranulation after myocardial infarction. <i>Molecular Omics</i> , 2022, 18, 186-195.	1.4	9



#	ARTICLE	IF	CITATIONS
2815	Review of Liquid Chromatography-Mass Spectrometry-Based Proteomic Analyses of Body Fluids to Diagnose Infectious Diseases. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2187.	1.8	6
2817	PCBP2 maintains antiviral signaling homeostasis by regulating cGAS enzymatic activity via antagonizing its condensation. <i>Nature Communications</i> , 2022, 13, 1564.	5.8	15
2818	Phosphoproteome Profiling Using an Isobaric Carrier without the Need for Phosphoenrichment. <i>Analytical Chemistry</i> , 2022, 94, 4192-4200.	3.2	8
2819	LC-MS/MS-Based Serum Protein Profiling for Identification of Candidate Biomarkers in Pakistani Rheumatoid Arthritis Patients. <i>Life</i> , 2022, 12, 464.	1.1	1
2821	SWATH-MS identification of CXCL7, LBP, TGF $\beta$ 1 and PDGFR $\beta$ as novel biomarkers in human systemic mastocytosis. <i>Scientific Reports</i> , 2022, 12, 5087.	1.6	4
2822	Proteomic profiling of metformin effects in 3T3L1 adipocytes by SILAC-based quantification. <i>Proteomics</i> , 2022, , 2100196.	1.3	1
2823	Posttranslational modification of the RHO of plants protein RACB by phosphorylation and cross-kingdom conserved ubiquitination. <i>PLoS ONE</i> , 2022, 17, e0258924.	1.1	4
2824	The life history of <i>Drosophila</i> sperm involves molecular continuity between male and female reproductive tracts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2119899119.	3.3	24
2825	A Wide-Proteome Analysis to Identify Molecular Pathways Involved in Kidney Response to High-Fat Diet in Mice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3809.	1.8	1
2826	Vertebrate lonesome kinase modulates the hepatocyte secretome to prevent perivascular liver fibrosis and inflammation. <i>Journal of Cell Science</i> , 2022, , .	1.2	2
2827	Hyperphosphorylated Human Tau Accumulates at the Synapse, Localizing on Synaptic Mitochondrial Outer Membranes and Disrupting Respiration in a Mouse Model of Tauopathy. <i>Frontiers in Molecular Neuroscience</i> , 2022, 15, 852368.	1.4	10
2828	Effects of Fe and Mn Deficiencies on the Root Protein Profiles of Tomato ( <i>Solanum lycopersicum</i> ) Using Two-Dimensional Electrophoresis and Label-Free Shotgun Analyses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3719.	1.8	5
2830	Physiological Roles of Short-Chain and Long-Chain Menaquinones (Vitamin K2) in <i>Lactococcus cremoris</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 823623.	1.5	5
2831	KAT7-mediated CANX (calnexin) crotonylation regulates leucine-stimulated MTORC1 activity. <i>Autophagy</i> , 2022, 18, 2799-2816.	4.3	5
2832	<i>Pseudomonas aeruginosa</i> posttranslational responses to elevated cAMP levels. <i>Molecular Microbiology</i> , 2022, 117, 1213-1226.	1.2	6
2833	A Monoclonal Anti-HMGB1 Antibody Attenuates Neurodegeneration in an Experimental Animal Model of Glaucoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4107.	1.8	10
2834	Characterization of Glycoproteoforms of Integrins $\beta$ 2 and $\beta$ 1 in Megakaryocytes in the Occurrence of JAK2V617F Mutation-Induced Primary Myelofibrosis. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100213.	2.5	1
2835	A Census of Hsp70-Mediated Proteome Solubility Changes upon Recovery from Heat Stress. <i>Journal of Proteome Research</i> , 2022, 21, 1251-1261.	1.8	2

#	ARTICLE	IF	CITATIONS
2836	Transcriptome, metabolome and suppressor analysis reveal an essential role for the ubiquitin-proteasome system in seedling chloroplast development. <i>BMC Plant Biology</i> , 2022, 22, 183.	1.6	1
2837	Identification and characterisation of sPEPs in <i>Cryptococcus neoformans</i> . <i>Fungal Genetics and Biology</i> , 2022, 160, 103688.	0.9	0
2838	BoxCar and shotgun proteomic analyses reveal molecular networks regulated by UBR5 in prostate cancer. <i>Proteomics</i> , 2022, 22, e2100172.	1.3	2
2839	Proteogenomics analysis of CUG codon translation in the human pathogen <i>Candida albicans</i> . <i>BMC Biology</i> , 2021, 19, 258.	1.7	2
2840	How the Presence of Hemin Affects the Expression of the Different Iron Uptake Pathways in <i>Pseudomonas aeruginosa</i> Cells. <i>ACS Infectious Diseases</i> , 2022, 8, 183-196.	1.8	4
2841	Moving translational mass spectrometry imaging towards transparent and reproducible data analyses: a case study of an urothelial cancer cohort analyzed in the Galaxy framework. <i>Clinical Proteomics</i> , 2022, 19, 8.	1.1	8
2842	Migration of <i>Acanthamoeba</i> through <i>Legionella</i> biofilms is regulated by the bacterial $\sigma^{LqsA}$ network, effector proteins and the flagellum. <i>Environmental Microbiology</i> , 2022, .	1.8	4
2843	Effect of Sample Transportation on the Proteome of Human Circulating Blood Extracellular Vesicles. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4515.	1.8	11
2844	Cas1 and Fen1 Display Equivalent Functions During Archaeal DNA Repair. <i>Frontiers in Microbiology</i> , 2022, 13, 822304.	1.5	3
2846	PP2ARts1 antagonizes Rck2-mediated hyperosmotic stress signaling in yeast. <i>Microbiological Research</i> , 2022, 260, 127031.	2.5	1
3243	The Phenylacetic Acid Catabolic Pathway Regulates Antibiotic and Oxidative Stress Responses in <i>Acinetobacter</i> . <i>MBio</i> , 2022, 13, e0186321.	1.8	18
3244	Sculpting the Bacterial $\sigma^O$ -Glycoproteome: Functional Analyses of Orthologous Oligosaccharyltransferases with Diverse Targeting Specificities. <i>MBio</i> , 2022, 13, e0379721.	1.8	2
3245	Quantitative Isotope-Labeled Cross-Linker Proteomics Reveals Developmental Variation in Protein Interactions and Post-Translational Modifications in <i>Diaphorina citri</i> , the Citrus Greening Insect Vector. <i>ACS Agricultural Science and Technology</i> , 2022, 2, 486-500.	1.0	3
3246	Global, distinctive, and personal changes in molecular and microbial profiles by specific fibers in humans. <i>Cell Host and Microbe</i> , 2022, 30, 848-862.e7.	5.1	48
3247	Uptake Mechanisms and Regulatory Responses to MECAM- and DOTAM-Based Artificial Siderophores and Their Antibiotic Conjugates in <i>Pseudomonas aeruginosa</i> . <i>ACS Infectious Diseases</i> , 2022, 8, 1134-1146.	1.8	10
3248	Application of two-dimensional difference gel electrophoresis to identify protein changes between center, margin, and adjacent non-tumor tissues obtained from non-small-cell lung cancer with adenocarcinoma or squamous cell carcinoma subtype. <i>PLoS ONE</i> , 2022, 17, e0268073.	1.1	4
3250	Ethanolamine phosphate on the second mannose is a preferential bridge for some GPI-anchored proteins. <i>EMBO Reports</i> , 2022, 23, .	2.0	7
3251	Patterning of the Autotrophic, Mixotrophic, and Heterotrophic Proteomes of Oxygen-Evolving Cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	5

#	ARTICLE	IF	CITATIONS
3253	InlV, an Invasin-Like Adhesin, Is a Type II Secretion System Substrate Required for <i>Acinetobacter baumannii</i> Uropathogenesis. <i>MBio</i> , 2022, 13, .	1.8	11
3254	Manganese Modulates Metabolic Activity and Redox Homeostasis in Translationally Blocked <i>Lactococcus cremoris</i> , Impacting Metabolic Persistence, Cell Culturability, and Flavor Formation. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	1
3255	Molecular response of <i>Sargassum vulgare</i> to acidification at volcanic $\text{CO}_2$ vents: Insights from proteomic and metabolite analyses. <i>Molecular Ecology</i> , 2022, 31, 3844-3858.	2.0	4
3256	Ethylene augments root hypoxia tolerance via growth cessation and reactive oxygen species amelioration. <i>Plant Physiology</i> , 2022, 190, 1365-1383.	2.3	30
3257	Brain Proteome and Behavioural Analysis in Wild Type, BDNF <sup>+/+</sup> and BDNF <sup>-/-</sup> Adult Zebrafish ( <i>Danio rerio</i> ). <i>Frontiers in Molecular and Cellular Neuroscience</i> , 2022, 16, 960616.	1.8	4
3258	Persister state-directed transitioning and vulnerability in melanoma. <i>Nature Communications</i> , 2022, 13, .	5.8	20
3259	Uncovering cryptic pockets in the SARS-CoV-2 spike glycoprotein. <i>Structure</i> , 2022, 30, 1062-1074.e4.	1.6	21
3261	Proteomic and functional analyses of the periodic membrane skeleton in neurons. <i>Nature Communications</i> , 2022, 13, .	5.8	15
3262	Light Quality Modulates Plant Cold Response and Freezing Tolerance. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	6
3263	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. <i>Nature Ecology and Evolution</i> , 2022, 6, 1007-1023.	3.4	26
3264	iTRAQ-based quantitative proteomics reveals biomarkers/pathways in psoriasis that can predict the efficacy of methotrexate. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2022, 36, 1784-1795.	1.3	6
3265	In-depth Profiling and Quantification of the Lysine Acetylome in Hepatocellular Carcinoma with a Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100255.	2.5	7
3266	Protein Markers for the Identification of Cork Oak Plants Infected with <i>Phytophthora cinnamomi</i> by Applying an (L <sub>1</sub> , L <sub>2</sub> )-k-Feature Set Approach. <i>Forests</i> , 2022, 13, 940.	0.9	0
3267	Selective modulation of cell surface proteins during vaccinia infection: A resource for identifying viral immune evasion strategies. <i>PLoS Pathogens</i> , 2022, 18, e1010612.	2.1	6
3268	Stimulating Effect of <i>Trichococcus flocculiformis</i> on a Coculture of <i>Syntrophomonas wolfei</i> and <i>Methanospirillum hungatei</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, .	1.4	7
3269	A Dual-Acting Nitric Oxide Donor and Phosphodiesterase 5 Inhibitor Activates Autophagy in Primary Skin Fibroblasts. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6860.	1.8	0
3271	Reconstruction of a catalogue of genome-scale metabolic models with enzymatic constraints using GECKO 2.0. <i>Nature Communications</i> , 2022, 13, .	5.8	39
3272	Crizotinib Shows Antibacterial Activity against Gram-Positive Bacteria by Reducing ATP Production and Targeting the CTP Synthase PyrG. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5

#	ARTICLE	IF	CITATIONS
3273	Characterization of a flexible AAV-DTR/DT mouse model of acute epithelial lung injury. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2022, 323, L206-L218.	1.3	1
3274	Melanoma RBPome identification reveals PDIA6 as an unconventional RNA-binding protein involved in metastasis. <i>Nucleic Acids Research</i> , 2022, 50, 8207-8225.	6.5	9
3275	Identification of growth hormone receptor as a relevant target for precision medicine in low-EGFR expressing glioblastoma. <i>Clinical and Translational Medicine</i> , 2022, 12, .	1.7	4
3276	Lagovirus Non-structural Protein p23: A Putative Viroporin That Interacts With Heat Shock Proteins and Uses a Disulfide Bond for Dimerization. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
3278	Urine Proteomics Reveals Sex-Specific Response to Total Pancreatectomy With Islet Autotransplantation. <i>Pancreas</i> , 2022, 51, 435-444.	0.5	2
3279	Comprehensive and systematic characterization of multi-functionalized cisplatin nano-conjugate: from the chemistry and proteomic biocompatibility to the animal model. <i>Journal of Nanobiotechnology</i> , 2022, 20, .	4.2	5
3280	Proteomics Evidence of a Systemic Response to Desiccation in the Resurrection Plant <i>Haberlea rhodopensis</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 8520.	1.8	7
3281	Local burn wound environment versus systemic response: Comparison of proteins and metabolites. <i>Wound Repair and Regeneration</i> , 2022, 30, 560-572.	1.5	3
3282	Characterization of protein complexes in extracellular vesicles by intact extracellular vesicle crosslinking mass spectrometry (iEVXL). <i>Journal of Extracellular Vesicles</i> , 2022, 11, .	5.5	5
3283	Metagenomics combined with activity-based proteomics point to gut bacterial enzymes that reactivate mycophenolate. <i>Gut Microbes</i> , 2022, 14, .	4.3	10
3284	Targeting of microvillus protein Eps8 by the NleH effector kinases from enteropathogenic <i>E. coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	4
3286	Quantitative bile and serum proteomics for the screening and differential diagnosis of primary sclerosing cholangitis. <i>PLoS ONE</i> , 2022, 17, e0272810.	1.1	4
3287	Ezrin deficiency triggers glial fibrillary acidic protein upregulation and a distinct reactive astrocyte phenotype. <i>Glia</i> , 2022, 70, 2309-2329.	2.5	12
3288	The <i>Plasmodium falciparum</i> Nuclear Protein Phosphatase NIF4 Is Required for Efficient Merozoite Invasion and Regulates Artemisinin Sensitivity. <i>MBio</i> , 2022, 13, .	1.8	1
3289	Dataset from a proteomics analysis of tumor antigens shared between an allogenic tumor cell lysate vaccine and pancreatic tumor tissue.. <i>Data in Brief</i> , 2022, 44, 108490.	0.5	2
3290	Microplastics as potential carriers of viruses could prolong virus survival and infectivity. <i>Water Research</i> , 2022, 225, 119115.	5.3	14
3291	A molecular study of Italian ryegrass grown on Martian regolith simulant. <i>Science of the Total Environment</i> , 2023, 854, 158774.	3.9	1
3292	Quantitative Mass Spectrometry by SILAC in <i>Haloferax volcanii</i> . <i>Methods in Molecular Biology</i> , 2022, , 255-266.	0.4	0

#	ARTICLE	IF	CITATIONS
3293	Proteomic changes associated with racial background and sepsis survival outcomes. <i>Molecular Omics</i> , 0, .	1.4	4
3294	Proteomic Analysis of Ginseng ( <i>Panax ginseng</i> C. A. Meyer) Fluid Proteins under Salt Stress. <i>Agronomy</i> , 2022, 12, 2048.	1.3	4
3296	Erythropoietin-driven dynamic proteome adaptations during erythropoiesis prevent iron overload in the developing embryo. <i>Cell Reports</i> , 2022, 40, 111360.	2.9	3
3298	ABP1â€™TMK auxin perception for global phosphorylation and auxin canalization. <i>Nature</i> , 2022, 609, 575-581.	13.7	79
3299	PFKFB4 interacts with FBXO28 to promote HIF-1Î± signaling in glioblastoma. <i>Oncogenesis</i> , 2022, 11, .	2.1	5
3300	An Unprecedented Tolerance to Deletion of the Periplasmic Chaperones SurA, Skp, and DegP in the Nosocomial Pathogen <i>Acinetobacter baumannii</i> . <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	0
3301	Ku proteins promote DNA binding and condensation of cyclic GMP-AMP synthase. <i>Cell Reports</i> , 2022, 40, 111310.	2.9	15
3302	<i>Methylocystis</i> sp. Strain SC2 Acclimatizes to Increasing NH <sub>4</sub> <sup>+</sup> Levels by a Precise Rebalancing of Enzymes and Osmolyte Composition. <i>MSystems</i> , 2022, 7, .	1.7	3
3303	Global landscape of 2-hydroxyisobutyrylation in human pancreatic cancer. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	3
3304	A multi-adenylate cyclase regulator at the flagellar tip controls African trypanosome transmission. <i>Nature Communications</i> , 2022, 13, .	5.8	19
3305	Prognostic value of Talin-1 in renal cell carcinoma and its association with B7-H3. <i>Cancer Biomarkers</i> , 2022, 35, 269-292.	0.8	3
3306	Potential Role of Lysine Acetylation in Antibiotic Resistance of <i>Escherichia coli</i> . <i>MSystems</i> , 2022, 7, .	1.7	4
3307	The human milk proteome and allergy of mother and child: Exploring associations with protein abundances and protein network connectivity. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	2
3308	Blood plasma protein profiles of neuropsychiatric symptoms and related cognitive decline in older people. <i>Journal of Neurochemistry</i> , 2023, 164, 242-254.	2.1	5
3310	Triclosan Promotes Conjugative Transfer of Antibiotic Resistance Genes to Opportunistic Pathogens in Environmental Microbiome. <i>Environmental Science &amp; Technology</i> , 2022, 56, 15108-15119.	4.6	12
3311	Metabolic engineering enables <i>Bacillus licheniformis</i> to grow on the marine polysaccharide ulvan. <i>Microbial Cell Factories</i> , 2022, 21, .	1.9	2
3312	Transcriptome and proteome associated analysis of flavonoid metabolism in haploid <i>Ginkgo biloba</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 224, 306-318.	3.6	7
3313	Human genetic defects in SRP19 and SRPRA cause severe congenital neutropenia with distinctive proteome changes. <i>Blood</i> , 2023, 141, 645-658.	0.6	10

#	ARTICLE	IF	CITATIONS
3314	Mapping Proteome and Lipidome Changes in Early-Onset Non-Alcoholic Fatty Liver Disease Using Hepatic 3D Spheroids. <i>Cells</i> , 2022, 11, 3216.	1.8	3
3315	Hydrodynamic conditions affect the proteomic profile of marine biofilms formed by filamentous cyanobacterium. <i>Npj Biofilms and Microbiomes</i> , 2022, 8, .	2.9	3
3316	Integrated Omics analysis of pig muscle metabolism under the effects of dietary <i>Chlorella vulgaris</i> and exogenous enzymes. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
3317	A comprehensive set of ER protein disulfide isomerase family members supports the biogenesis of proinflammatory interleukin 12 family cytokines. <i>Journal of Biological Chemistry</i> , 2022, 298, 102677.	1.6	2
3318	Mapping prohormone processing by proteases in human enteroendocrine cells using genetically engineered organoid models. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	5
3319	Dynamin-like Protein 1 (DNML1) as a Molecular Target for Antibody-Based Immunotherapy to Treat Glaucoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13618.	1.8	4
3320	Proteomics of Aqueous Humor as a Source of Disease Biomarkers in Retinoblastoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13458.	1.8	7
3321	Identification of fungal lignocellulose-degrading biocatalysts secreted by <i>Phanerochaete chrysosporium</i> via activity-based protein profiling. <i>Communications Biology</i> , 2022, 5, .	2.0	2
3323	MS-proteomics provides insight into the host responses towards alginate microspheres. <i>Materials Today Bio</i> , 2022, 17, 100490.	2.6	1
3324	Expanded Proteomic Survey of the Human Parasite <i>Leishmania major</i> Focusing on Changes in Null Mutants of the Golgi GDP-Mannose/Fucose/Arabinopyranose Transporter <i>LPG2</i> and of the Mitochondrial Fucosyltransferase <i>FUT1</i>. <i>Microbiology Spectrum</i> , 0, , .	1.2	0
3325	Differential requirements of IQUB for the assembly of radial spoke 1 and the motility of mouse cilia and flagella. <i>Cell Reports</i> , 2022, 41, 111683.	2.9	10
3327	<i>Aedes aegypti</i> Malpighian tubules are immunologically activated following systemic Toll activation. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	7
3328	Normalization of organ-on-a-Chip samples for mass spectrometry based proteomics and metabolomics via Dansylation-based assay. <i>Toxicology in Vitro</i> , 2023, 88, 105540.	1.1	1
3329	Unique and Shared Proteome Responses of Rice Plants ( <i>Oryza sativa</i> ) to Individual Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15552.	1.8	2
3330	Leucine-973 is a crucial residue differentiating insulin and IGF-1 receptor signaling. <i>Journal of Clinical Investigation</i> , 2023, 133, .	3.9	6
3331	Disentangling the lipid divide: Identification of key enzymes for the biosynthesis of membrane-spanning and ether lipids in Bacteria. <i>Science Advances</i> , 2022, 8, .	4.7	6
3333	Environmental impacts on barley grain composition and longevity. <i>Journal of Experimental Botany</i> , 2023, 74, 1609-1628.	2.4	4
3334	The role of auxiliary domains in modulating CHD4 activity suggests mechanistic commonality between enzyme families. <i>Nature Communications</i> , 2022, 13, .	5.8	4

#	ARTICLE	IF	CITATIONS
3335	Liver RBFOX2 regulates cholesterol homeostasis via Scarb1 alternative splicing in mice. <i>Nature Metabolism</i> , 2022, 4, 1812-1829.	5.1	12
3336	PCNA regulates primary metabolism by scaffolding metabolic enzymes. <i>Oncogene</i> , 2023, 42, 613-624.	2.6	4
3337	Intraglandular mesenchymal stem cell treatment induces changes in the salivary proteome of irradiated patients. <i>Communications Medicine</i> , 2022, 2, .	1.9	3
3338	Comparative proteomic analysis of seminal plasma exosomes in buffalo with high and low sperm motility. <i>BMC Genomics</i> , 2023, 24, .	1.2	2
3339	Both age and social environment shape the phenotype of ant workers. <i>Scientific Reports</i> , 2023, 13, .	1.6	1
3340	The Cellular Abundance of Chemoreceptors, Chemosensory Signaling Proteins, Sensor Histidine Kinases, and Solute Binding Proteins of <i>Pseudomonas aeruginosa</i> Provides Insight into Sensory Preferences and Signaling Mechanisms. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1363.	1.8	1
3341	The adaptive response to alternative carbon sources in the pathogen <i>Candida albicans</i> involves a remodeling of thiol- and glutathione-dependent redox status. <i>Biochemical Journal</i> , 0, , .	1.7	0
3342	Whole lung proteome of an acute epithelial injury mouse model in comparison to spatially resolved proteomes. <i>Proteomics</i> , 2023, 23, .	1.3	1
3343	Biodegradation of poly(ethylene terephthalate): Mechanistic insights, advances, and future innovative strategies. <i>Chemical Engineering Journal</i> , 2023, 457, 141230.	6.6	25
3344	Response to microplastic exposure: An exploration into the sea urchin immune cell proteome. <i>Environmental Pollution</i> , 2023, 320, 121062.	3.7	10
3345	Mesothelioma-associated fibroblasts enhance proliferation and migration of pleural mesothelioma cells via c-Met/PI3K and WNT signaling but do not protect against cisplatin. <i>Journal of Experimental and Clinical Cancer Research</i> , 2023, 42, .	3.5	7
3346	Loss of dyskerin facilitates the acquisition of metastatic traits by altering the mevalonate pathway. <i>Life Science Alliance</i> , 2023, 6, e202201692.	1.3	1
3347	Isolation of lymph shows dysregulation of <i>STAT3</i> and <i>CREB</i> pathways in the spleen and liver during leukemia development in a rat model. <i>Microcirculation</i> , 2023, 30, .	1.0	1
3348	mRNA-Based Therapeutics in Cancer Treatment. <i>Pharmaceutics</i> , 2023, 15, 622.	2.0	11
3349	The remarkably enzyme-rich venom of the Big Bend Scorpion ( <i>Diplocentrus whitei</i> ). <i>Toxicon</i> , 2023, 226, 107080.	0.8	2
3350	Characterizing the origin of blood plasma proteins from organ tissues in rainbow trout ( <i>Oncorhynchus mykiss</i> ) using a comparative non-targeted proteomics approach. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 46, 101070.	0.4	0
3351	Organ Protection by Caloric Restriction Depends on Activation of the De Novo NAD <sup>+</sup> Synthesis Pathway. <i>Journal of the American Society of Nephrology: JASN</i> , 2023, 34, 772-792.	3.0	4
3352	The deficiency of poly- $\beta$ -1,6-N-acetyl-glucosamine deacetylase trigger <i>A. baumannii</i> to convert to biofilm-independent colistin-tolerant cells. <i>Scientific Reports</i> , 2023, 13, .	1.6	1

#	ARTICLE	IF	CITATIONS
3354	The alphavirus nonstructural protein 2 NTPase induces a host translational shut-off through phosphorylation of eEF2 via cAMP-PKA-eEF2K signaling. <i>PLoS Pathogens</i> , 2023, 19, e1011179.	2.1	4
3355	Nanoporous Quercetin-Loaded Silicon-Stabilized Hybrid Lipid Nanoparticles Alleviate Salt Stress in Tomato Plants. <i>ACS Applied Nano Materials</i> , 2023, 6, 3647-3660.	2.4	7
3357	ProlInfer: An interpretable protein inference tool leveraging on biological networks. <i>PLoS Computational Biology</i> , 2023, 19, e1010961.	1.5	0
3358	Spatial Proteome Reorganization of a Photosynthetic Model Cyanobacterium in Response to Abiotic Stresses. <i>Journal of Proteome Research</i> , 2023, 22, 1255-1269.	1.8	1
3359	LncRNA HCP5-Encoded Protein Regulates Ferroptosis to Promote the Progression of Triple-Negative Breast Cancer. <i>Cancers</i> , 2023, 15, 1880.	1.7	7
3360	Systemic LRG1 Expression in Melanoma is Associated with Disease Progression and Recurrence. <i>Cancer Research Communications</i> , 2023, 3, 672-683.	0.7	4
3361	Proteome Dynamics of Persulfidation in Leaf Tissue under Light/Dark Conditions and Carbon Deprivation. <i>Antioxidants</i> , 2023, 12, 789.	2.2	3
3362	The root pathogen <i>Aphanomyces euteiches</i> secretes modular proteases in pea apoplast during host infection. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
3363	Thermodynamic and Kinetic Modeling Directs Pathway Optimization for Isopropanol Production in a Gas-Fermenting Bacterium. <i>MSystems</i> , 0, , .	1.7	0
3366	Signalling inhibition by ponatinib disrupts productive alternative lengthening of telomeres (ALT). <i>Nature Communications</i> , 2023, 14, .	5.8	3
3367	Comprehensive Characterization of Protein Turnover by Comparative SILAC Labeling Analysis in 3T3-L1. <i>Journal of Proteome Research</i> , 0, , .	1.8	0
3368	Meta-analysis of published cerebrospinal fluid proteomics data identifies and validates metabolic enzyme panel as Alzheimer's disease biomarkers. <i>Cell Reports Medicine</i> , 2023, 4, 101005.	3.3	3
3370	Spatial and temporal dynamics of ATP synthase from mitochondria toward the cell surface. <i>Communications Biology</i> , 2023, 6, .	2.0	5
3371	l-tyrosine modulates biofilm formation of <i>Bacillus cereus</i> ATCC 14579. <i>Research in Microbiology</i> , 2023, 174, 104072.	1.0	2
3372	DeepFLR facilitates false localization rate control in phosphoproteomics. <i>Nature Communications</i> , 2023, 14, .	5.8	4
3377	New Developments in Techniques Like Metagenomics and Metaproteomics for Isolation, Identification, and Characterization of Microbes from Varied Environment. <i>Rhizosphere Biology</i> , 2023, , 487-496.	0.4	0
3419	Multi-Omics Databases. , 2024, , 151-166.		0
3420	Cardinal v.3: a versatile open-source software for mass spectrometry imaging analysis. <i>Nature Methods</i> , 2023, 20, 1883-1886.	9.0	2



#	ARTICLE	IF	CITATIONS
---	---------	----	-----------