

IQuant: An automated pipeline for quantitative proteom

Proteomics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A Combinational Strategy upon RNA Sequencing and Peptidomics Unravels a Set of Novel Toxin Peptides in Scorpion <i>Mesobuthus martensii</i> . <i>Toxins</i> , 2016, 8, 286.	3.4	8
2	Platforms and Pipelines for Proteomics Data Analysis and Management. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 203-215.	1.6	14
3	Mass Spectrometry-Based Protein Quantification. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 255-279.	1.6	11
4	Drug Resistance in Colorectal Cancer Cell Lines is Partially Associated with Aneuploidy Status in Light of Profiling Gene Expression. <i>Journal of Proteome Research</i> , 2016, 15, 4047-4059.	3.7	14
5	Proteome response of <i>Dunaliella parva</i> induced by nitrogen limitation. <i>Algal Research</i> , 2017, 23, 196-202.	4.6	37
6	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017, 355, .	12.6	163
7	iTRAQ and RNA-Seq Analyses Provide New Insights into Regulation Mechanism of Symbiotic Germination of <i>Dendrobium officinale</i> Seeds (Orchidaceae). <i>Journal of Proteome Research</i> , 2017, 16, 2174-2187.	3.7	55
8	Evidence for salicylic acid signalling and histological changes in the defence response of <i>Eucalyptus grandis</i> to <i>Chrysoporthe austroafricana</i> . <i>Scientific Reports</i> , 2017, 7, 45402.	3.3	9
9	Digging More Missing Proteins Using an Enrichment Approach with ProteoMiner. <i>Journal of Proteome Research</i> , 2017, 16, 4330-4339.	3.7	26
10	iTRAQ-based proteomic profiling of a <i>Microbacterium</i> sp. strain during benzo(a)pyrene removal under anaerobic conditions. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8365-8377.	3.6	4
11	The Combination of RNA and Protein Profiling Reveals the Response to Nitrogen Depletion in <i>Thalassiosira pseudonana</i> . <i>Scientific Reports</i> , 2017, 7, 8989.	3.3	23
12	Proteomic and microRNA Transcriptome Analysis revealed the microRNA-SmyD1 network regulation in Skeletal Muscle Fibers performance of Chinese perch. <i>Scientific Reports</i> , 2017, 7, 16498.	3.3	17
13	Quantitative Proteomics Reveals Potential Crosstalk between a Small RNA CoaR and a Two-Component Regulator Slr1037 in <i>Synechocystis</i> sp. PCC6803. <i>Journal of Proteome Research</i> , 2017, 16, 2954-2963.	3.7	15
14	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.	3.7	11
15	PLC-Mediated Signaling Pathway in Pollen Tubes Regulates the Gametophytic Self-incompatibility of <i>Pyrus</i> Species. <i>Frontiers in Plant Science</i> , 2017, 8, 1164.	3.6	29
16	An Adaptive Pipeline To Maximize Isobaric Tagging Data in Large-Scale MS-Based Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2165-2173.	3.7	11
17	Integrated transcriptomic and proteomic analyses reveal potential mechanisms linking thermal stress and depressed disease resistance in the turbot <i>Scophthalmus maximus</i> . <i>Scientific Reports</i> , 2018, 8, 1896.	3.3	17
18	New insight into ovary abortion during ovary development of hazelnut through a combined proteomic and transcriptomic analysis. <i>Scientia Horticulturae</i> , 2018, 234, 36-48.	3.6	8

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19	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.	3.8	33
20	Proteomic evaluation of human umbilical cord tissue exposed to polybrominated diphenyl ethers in an e-waste recycling area. <i>Environment International</i> , 2018, 111, 362-371.	10.0	36
21	The Chinese Medicinal Formulation Guzhi Zengsheng Zhitongwan Modulates Chondrocyte Structure, Dynamics, and Metabolism by Controlling Multiple Functional Proteins. <i>BioMed Research International</i> , 2018, 2018, 1-12.	1.9	4
22	<i>Lactobacillus gasseri</i> LA39 Activates the Oxidative Phosphorylation Pathway in Porcine Intestinal Epithelial Cells. <i>Frontiers in Microbiology</i> , 2018, 9, 3025.	3.5	12
23	Distinct sperm nucleus behaviors between genotypic and temperature-dependent sex determination males are associated with replication and expression-related pathways in a gynogenetic fish. <i>BMC Genomics</i> , 2018, 19, 437.	2.8	23
24	A proteomics of gills approach to understanding salinity adaptation of <i>Scylla paramamosain</i> . <i>Gene</i> , 2018, 677, 119-131.	2.2	27
25	iTRAQ-Based Proteomic Analysis Reveals Potential Regulation Networks of IBA-Induced Adventitious Root Formation in Apple. <i>International Journal of Molecular Sciences</i> , 2018, 19, 667.	4.1	41
26	Complementary iTRAQ-based proteomic and RNA sequencing-based transcriptomic analyses reveal a complex network regulating pomegranate (<i>Punica granatum</i> L.) fruit peel colour. <i>Scientific Reports</i> , 2018, 8, 12362.	3.3	31
27	Quantitative Proteomics Analysis of Membrane Proteins in <i>Enterococcus faecalis</i> With Low-Level Linezolid-Resistance. <i>Frontiers in Microbiology</i> , 2018, 9, 1698.	3.5	14
28	Integrated analysis of transcriptome and proteome changes related to the Ogura cytoplasmic male sterility in cabbage. <i>PLoS ONE</i> , 2018, 13, e0193462.	2.5	39
29	iTRAQ-based quantitative proteome revealed metabolic changes of <i>Sitophilus zeamais</i> in response to terpinen-4-ol fumigation. <i>Pest Management Science</i> , 2019, 75, 444-451.	3.4	26
30	Proteomic analysis of <i>Laodelphax striatellus</i> gonads reveals proteins that may manipulate host reproduction by <i>Wolbachia</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 113, 103211.	2.7	7
31	Decreased metabolism and increased tolerance to extreme environments in <i>Staphylococcus warneri</i> during long-term spaceflight. <i>MicrobiologyOpen</i> , 2019, 8, e917.	3.0	14
32	Studying the variations in differently expressed serum proteins of Hainan black goat during the breeding cycle using isobaric tags for relative and absolute quantitation (iTRAQ) technology. <i>Journal of Reproduction and Development</i> , 2019, 65, 413-421.	1.4	3
33	Quantitative Proteome Reveals Variation in the Condition Factor of Sea Urchin <i>Strongylocentrotus nudus</i> during the Fishing Season Using an iTRAQ-based Approach. <i>Marine Drugs</i> , 2019, 17, 397.	4.6	1
34	<i>Lactobacillus frumenti</i> improves antioxidant capacity via nitric oxide synthase 1 in intestinal epithelial cells. <i>FASEB Journal</i> , 2019, 33, 10705-10716.	0.5	17
35	Dataset supporting the proteomic characterization of human corneal epithelial cells with HSV-1 infection. <i>Data in Brief</i> , 2019, 27, 104579.	1.0	0
36	Identification of Genes/Proteins Related to Submergence Tolerance by Transcriptome and Proteome Analyses in Soybean. <i>Scientific Reports</i> , 2019, 9, 14688.	3.3	23

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37	Changes in Energy Metabolism Trigger Pupal Diapause Transition of <i>Bactrocera minax</i> After 20-Hydroxyecdysone Application. <i>Frontiers in Physiology</i> , 2019, 10, 1288.	2.8	29
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39	Integrated analysis of transcriptomic and proteomic data from tree peony (<i>P. ostii</i>) seeds reveals key developmental stages and candidate genes related to oil biosynthesis and fatty acid metabolism. <i>Horticulture Research</i> , 2019, 6, 111.	6.3	68
40	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019, 47, 373-383.	6.1	101
41	Proteomic Response to Rising Temperature in the Marine Cyanobacterium <i>Synechococcus</i> Grown in Different Nitrogen Sources. <i>Frontiers in Microbiology</i> , 2019, 10, 1976.	3.5	13
42	Comparative Analysis of Proteomics and Transcriptomics during Fertility Transition in a Two-Line Hybrid Rice Line Wuxiang S. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4542.	4.1	8
43	An Integrated Transcriptome and Proteome Analysis Reveals New Insights into Russetting of Bagging and Non-Bagging “Golden Delicious” Apple. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4462.	4.1	23
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45	Proteomic analysis of the effects of antler extract on chondrocyte proliferation, differentiation and apoptosis. <i>Molecular Biology Reports</i> , 2019, 46, 1635-1648.	2.3	13
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49	Quantitative proteomic analysis of human corneal epithelial cells infected with HSV-1. <i>Experimental Eye Research</i> , 2019, 185, 107664.	2.6	13
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51	High-throughput identification of heavy metal binding proteins from the byssus of chinese green mussel (<i>Perna viridis</i>) by combination of transcriptome and proteome sequencing. <i>PLoS ONE</i> , 2019, 14, e0216605.	2.5	7
52	Quantitative proteomics reveals the key molecular events occurring at different cell cycle phases of the in situ blooming dinoflagellate cells. <i>Science of the Total Environment</i> , 2019, 676, 62-71.	8.0	14
53	Peptide-to-Protein Summarization: An Important Step for Accurate Quantification in Label-Based Proteomics. <i>Methods in Molecular Biology</i> , 2019, 1977, 159-180.	0.9	0
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57	An Integrated Transcriptome and Proteome Analysis Reveals Putative Regulators of Adventitious Root Formation in <i>Taxodium â€Žhongshanshanâ€™™</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 1225.	4.1	32
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59	iTRAQ protein profiling reveals candidate proteins regulating ovary and ovule differentiation in pistillate inflorescences after pollination in hazel. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	1.6	4
60	Effects of magnetic nanoparticles plus microwave on the thawing of largemouth bass (<i>Micropterus</i>) Tj ETQq1 1 0.784314 rgBT /Overl	8.2	31
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68	Physiological and proteomic analyses of 1-MCP treatment on lignification in fresh common bean (<i>Phaseolus vulgaris</i> L) during storage. <i>Postharvest Biology and Technology</i> , 2020, 160, 111041.	6.0	16
69	A group of serum proteins as potential diagnostic biomarkers for Yinâ€™deficiencyâ€™heat syndrome. <i>Anatomical Record</i> , 2020, 303, 2086-2094.	1.4	8
70	Plasma proteomic analysis of autoimmune hepatitis in an improved AIH mouse model. <i>Journal of Translational Medicine</i> , 2020, 18, 3.	4.4	15
71	Effects of terpinenâ€™4â€™ol fumigation on protein levels of detoxification enzymes in <i>Tribolium confusum</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 103, e21653.	1.5	2
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74	Comparative proteomics analysis indicates that palmitine contributes to transepithelial migration by regulating cellular adhesion. <i>Pharmaceutical Biology</i> , 2020, 58, 646-654.	2.9	9
75	MSstatsTMT: Statistical Detection of Differentially Abundant Proteins in Experiments with Isobaric Labeling and Multiple Mixtures. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1706-1723.	3.8	89
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87	Robust expression of γ p27Kip1 induced by viral infection is critical for antiviral innate immunity. <i>Cellular Microbiology</i> , 2020, 22, e13242.	2.1	9
88	Identification and analysis of lipid droplet-related proteome in the adipose tissue of grass carp (<i>Ctenopharyngodon idella</i>) under fed and starved conditions. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 36, 100710.	1.0	4
89	A study on the degradation efficiency of fluoranthene and the transmembrane protein mechanism of <i>Rhodococcus</i> sp. BAP-1 based on iTRAQ. <i>Science of the Total Environment</i> , 2020, 737, 140208.	8.0	10
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91	Comparative Proteomic Analysis by iTRAQ Reveals that Plastid Pigment Metabolism Contributes to Leaf Color Changes in Tobacco (<i>Nicotiana tabacum</i>) during Curing. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2394.	4.1	25

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92	Integrated Transcriptome Sequencing (RNA-seq) and Proteomic Studies Reveal Resource Reallocation towards Energy Metabolism and Defense in <i>Skeletonema marinoi</i> in Response to CO ₂ Increase. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	4
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96	Quantitative proteomic analysis of chicken serum reveals key proteins affecting follicle development during reproductive phase transitions. <i>Poultry Science</i> , 2021, 100, 325-333.	3.4	5
97	Multi-Q 2 software facilitates isobaric labeling quantitation analysis with improved accuracy and coverage. <i>Scientific Reports</i> , 2021, 11, 2233.	3.3	3
98	Screening and identification of endometrial proteins as novel potential biomarkers for repeated implantation failure. <i>PeerJ</i> , 2021, 9, e11009.	2.0	8
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100	An isocaloric moderately high-fat diet extends lifespan in male rats and <i>Drosophila</i> . <i>Cell Metabolism</i> , 2021, 33, 581-597.e9.	16.2	24
101	Integrated transcriptome and proteome analysis reveals complex regulatory mechanism of cotton in response to salt stress. <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	5
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109	iTRAQ-based quantitative proteomic analysis of silkworm infected with <i>Beauveria bassiana</i> . <i>Molecular Immunology</i> , 2021, 135, 204-216.	2.2	1
110	Role of sericin 1 in the immune system of silkworms revealed by transcriptomic and proteomic analyses after gene knockout. <i>FEBS Open Bio</i> , 2021, 11, 2304-2318.	2.3	3

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112	Integrated transcriptome and proteome analysis of developing embryo reveals the mechanisms underlying the high levels of oil accumulation in <i>Carya cathayensis</i> Sarg.. <i>Tree Physiology</i> , 2022, 42, 684-702.	3.1	10
113	Comparative Analysis of <i>Botrytis cinerea</i> in Response to the Microbial Secondary Metabolite Benzothiazole Using iTRAQ-Based Quantitative Proteomics. <i>Phytopathology</i> , 2021, 111, 1313-1326.	2.2	6
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117	Insights into the molecular basis of biocontrol of <i>Botrytis cinerea</i> by <i>Clonostachys rosea</i> in tomato. <i>Scientia Horticulturae</i> , 2022, 291, 110547.	3.6	19
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120	MaxReport: An Enhanced Proteomic Result Reporting Tool for MaxQuant. <i>PLoS ONE</i> , 2016, 11, e0152067.	2.5	12
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128	FluxPRT: An Adaptable and Extensible Proteomics LIMS. <i>Lecture Notes in Computer Science</i> , 2021, , 125-130.	1.3	0
129	Transcriptomic and Proteomic Profiling Reveal the Key Role of AcMYB16 in the Response of <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> in Kiwifruit. <i>Frontiers in Plant Science</i> , 2021, 12, 756330.	3.6	6
130	Liver fibrosis alters the molecular structures of hepatic glycogen. <i>Carbohydrate Polymers</i> , 2022, 278, 118991.	10.2	3
131	Proteomics reveals the changes in energy metabolism associated with reproduction in the clam <i>Meretrix petechialis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 41, 100954.	1.0	2

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133	Integration of Transcriptome and Proteome in Lymph Nodes Reveal the Different Immune Responses to PRRSV Between PRRSV-Resistant Tongcheng Pigs and PRRSV-Susceptible Large White Pigs. Frontiers in Genetics, 2022, 13, 800178.	2.3	4
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