

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.	1.5	8
2	Platforms and Pipelines for Proteomics Data Analysis and Management. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 203-215.	0.8	14
3	Mass Spectrometry-Based Protein Quantification. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 255-279.	0.8	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.	1.8	14
5	Proteome response of <i>Dunaliella parva</i> induced by nitrogen limitation. <i>Algal Research</i> , 2017, 23, 196-202.	2.4	37
6	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017, 355, .	6.0	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.	1.8	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.	1.6	9
9	Digging More Missing Proteins Using an Enrichment Approach with ProteoMiner. <i>Journal of Proteome Research</i> , 2017, 16, 4330-4339.	1.8	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.	1.7	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.	1.6	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.	1.6	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.	1.8	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.	1.8	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.	1.7	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.	1.8	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.	1.6	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.	1.7	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.	2.5	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.	4.8	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.	0.9	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.	1.5	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.	1.2	23
24	A proteomics of gills approach to understanding salinity adaptation of <i>Scylla paramamosain</i> . <i>Gene</i> , 2018, 677, 119-131.	1.0	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.	1.8	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.	1.6	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.	1.5	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.	1.1	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.	1.7	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.	1.2	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.	1.2	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.	0.5	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.	2.2	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.	0.2	17
35	Dataset supporting the proteomic characterization of human corneal epithelial cells with HSV-1 infection. <i>Data in Brief</i> , 2019, 27, 104579.	0.5	0
36	Identification of Genes/Proteins Related to Submergence Tolerance by Transcriptome and Proteome Analyses in Soybean. <i>Scientific Reports</i> , 2019, 9, 14688.	1.6	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.	1.3	29
38	Combined transcriptomics and proteomics forecast analysis for potential genes regulating the Columbian plumage color in chickens. <i>PLoS ONE</i> , 2019, 14, e0210850.	1.1	16
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.	2.9	68
40	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019, 47, 373-383.	2.7	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.	1.5	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.	1.8	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.	1.8	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.	1.0	13
46	Quantitative Proteomic Analysis of Castor (<i>Ricinus communis</i> L.) Seeds During Early Imbibition Provided Novel Insights into Cold Stress Response. <i>International Journal of Molecular Sciences</i> , 2019, 20, 355.	1.8	15
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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.	1.2	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.	1.1	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.	3.9	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.	0.4	0
54	Increased growth rate and amikacin resistance of <i>Salmonella enteritidis</i> after one-month spaceflight on China’s Shenzhou-11 spacecraft. <i>MicrobiologyOpen</i> , 2019, 8, e00833.	1.2	22

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57	An Integrated Transcriptome and Proteome Analysis Reveals Putative Regulators of Adventitious Root Formation in <i>Taxodium "Zhongshanshan"</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 1225.	1.8	32
58	Proteome Analysis Revealed Changes in Protein Expression Patterns Caused by Mutations in <i>Ehrlichia chaffeensis</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 58.	1.8	6
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.	0.6	4
60	Effects of magnetic nanoparticles plus microwave on the thawing of largemouth bass (<i>Micropterus</i>) Tj ETQq1 1 0.784314 rgBT /Overl	4.2	31
61	iTRAQ-based pharmacoproteomics reveals potential targets of berberine, a promising therapy for ulcerative colitis. <i>European Journal of Pharmacology</i> , 2019, 850, 167-179.	1.7	22
62	Global-warming-caused changes of temperature and oxygen alter the proteomic profile of sea cucumber <i>Apostichopus japonicus</i> . <i>Journal of Proteomics</i> , 2019, 193, 27-43.	1.2	37
63	Unraveling the molecular mechanism of the response to changing ambient phosphorus in the dinoflagellate <i>Alexandrium catenella</i> with quantitative proteomics. <i>Journal of Proteomics</i> , 2019, 196, 141-149.	1.2	14
64	iTRAQ-based comparative proteomic analysis of differentially expressed proteins in <i>Rhodococcus</i> sp. BAP-1 induced by fluoranthene. <i>Ecotoxicology and Environmental Safety</i> , 2019, 169, 282-291.	2.9	18
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69	A group of serum proteins as potential diagnostic biomarkers for Yin-deficiency-heat syndrome. <i>Anatomical Record</i> , 2020, 303, 2086-2094.	0.8	8
70	Plasma proteomic analysis of autoimmune hepatitis in an improved AIH mouse model. <i>Journal of Translational Medicine</i> , 2020, 18, 3.	1.8	15
71	Effects of terpinenol fumigation on protein levels of detoxification enzymes in <i>Tribolium confusum</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 103, e21653.	0.6	2
72	Combined transcriptomic and proteomic analysis of flubendiamide resistance in <i>Plutella xylostella</i> . <i>Entomological Research</i> , 2020, 50, 483-492.	0.6	6

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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.	1.3	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.	2.5	89
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79	Integrative Proteomic and MicroRNA Analysis: Insights Into Mechanisms of Eyestalk Ablation-Induced Ovarian Maturation in the Swimming Crab <i>Portunus trituberculatus</i> . <i>Frontiers in Endocrinology</i> , 2020, 11, 533.	1.5	13
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84	iTRAQ-based comparative proteomic analysis reveals high temperature accelerated leaf senescence of tobacco (<i>Nicotiana tabacum</i> L.) during flue-curing. <i>Genomics</i> , 2020, 112, 3075-3088.	1.3	15
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87	Robust expression of <i>p27Kip1</i> induced by viral infection is critical for antiviral innate immunity. <i>Cellular Microbiology</i> , 2020, 22, e13242.	1.1	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.	0.4	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.	3.9	10
90	Progress and pitfalls of using isobaric mass tags for proteome profiling. <i>Expert Review of Proteomics</i> , 2020, 17, 149-161.	1.3	22
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.	1.8	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, .	1.4	4
93	The metabolic pathways of polyhydroxyalkanoates and exopolysaccharides synthesized by <i>Haloferax mediterranei</i> in response to elevated salinity. <i>Journal of Proteomics</i> , 2021, 232, 104065.	1.2	21
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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.	1.5	5
97	Multi-Q 2 software facilitates isobaric labeling quantitation analysis with improved accuracy and coverage. <i>Scientific Reports</i> , 2021, 11, 2233.	1.6	3
98	Screening and identification of endometrial proteins as novel potential biomarkers for repeated implantation failure. <i>PeerJ</i> , 2021, 9, e11009.	0.9	8
99	Transcriptome and proteome analysis suggest enhanced photosynthesis in tetraploid <i>Liriodendron sino-americanum</i> . <i>Tree Physiology</i> , 2021, 41, 1953-1971.	1.4	14
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.	7.2	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, .	1.0	5
102	Proteomic analysis of <i>Laodelphax striatellus</i> in response to Rice stripe virus infection reveal a potential role of ZFP36L1 in restriction of viral proliferation. <i>Journal of Proteomics</i> , 2021, 239, 104184.	1.2	3
103	Proteomic Response of the Brain to Hypoxic Stress in Marine Medaka Fish (<i>Oryzias melastigma</i>). <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	1
104	Molecular mechanisms of mutualistic and antagonistic interactions in a plant-pollinator association. <i>Nature Ecology and Evolution</i> , 2021, 5, 974-986.	3.4	30
105	Screening of Key Proteins Affecting Floral Initiation of Saffron Under Cold Stress Using iTRAQ-Based Proteomics. <i>Frontiers in Plant Science</i> , 2021, 12, 644934.	1.7	10
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108	Quantitative Proteomics Reveals a Novel Role of the E3 Ubiquitin-Protein Ligase FANCL in the Activation of the Innate Immune Response through Regulation of TBK1 Phosphorylation during Peste des Petits Ruminants Virus Infection. <i>Journal of Proteome Research</i> , 2021, 20, 4113-4130.	1.8	7
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111	CD226 Is Required to Maintain Megakaryocytes/Platelets Homeostasis in the Treatment of Knee Osteoarthritis With Platelet-Rich Plasma in Mice. <i>Frontiers in Pharmacology</i> , 2021, 12, 732453.	1.6	3
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.	1.4	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.	1.1	6
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116	Mechanism of the growth and development of the posterior silk gland and silk secretion revealed by mutation of the fibroin light chain in silkworm. <i>International Journal of Biological Macromolecules</i> , 2021, 188, 375-384.	3.6	9
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.	1.7	19
118	Combined transcriptomic, proteomic and biochemical approaches to identify the cadmium hyper-tolerance mechanism of turnip seedling leaves. <i>Environmental Science and Pollution Research</i> , 2021, 28, 22458-22473.	2.7	11
120	MaxReport: An Enhanced Proteomic Result Reporting Tool for MaxQuant. <i>PLoS ONE</i> , 2016, 11, e0152067.	1.1	12
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126	Proteomic analysis of differentially expressed proteins in the serum of patients with acute renal allograft rejection using iTRAQ labelling technology. <i>Molecular Medicine Reports</i> , 2020, 22, 2329-2341.	1.1	7
127	Regulation of nitric oxide on lipoxygenase in peach fruit during cold storage. <i>Acta Horticulturae</i> , 2020, , 31-38.	0.1	2
128	FluxPRT: An Adaptable and Extensible Proteomics LIMS. <i>Lecture Notes in Computer Science</i> , 2021, , 125-130.	1.0	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.	1.7	6
130	Liver fibrosis alters the molecular structures of hepatic glycogen. <i>Carbohydrate Polymers</i> , 2022, 278, 118991.	5.1	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.	0.4	2

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132	Effects of DISC1 on Alzheimer's disease cell models assessed by iTRAQ proteomics analysis. <i>Bioscience Reports</i> , 2022, 42, .	1.1	5
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. <i>Frontiers in Genetics</i> , 2022, 13, 800178.	1.1	4
135	Proteomic Analysis of the Alterations in Follicular Fluid Proteins During Oocyte Maturation in Humans. <i>Frontiers in Endocrinology</i> , 2021, 12, 830691.	1.5	6
136	Quantitative Proteomics Based on iTRAQ Reveal that Nitidine Chloride Induces Apoptosis by Activating JNK/c-Jun Signaling in Hepatocellular Carcinoma Cells. <i>Planta Medica</i> , 2022, 88, 1233-1244.	0.7	4
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