

Finding one's way in proteomics: a protein species nom

Chemistry Central Journal

3, 11

DOI: 10.1186/1752-153x-3-11

Citation Report

#	ARTICLE	IF	CITATIONS
1	Relative protein quantitation with post translational modifications in mass spectrometry based proteomics. , 2010, , .		0
2	Integrated Multifunctional Microfluidics for Automated Proteome Analyses. Topics in Current Chemistry, 2011, 304, 261-294.	4.0	7
3	Mapping intact protein isoforms in discovery mode using top-down proteomics. Nature, 2011, 480, 254-258.	13.7	587
4	Analysis of Intact Protein Isoforms by Mass Spectrometry. Journal of Biological Chemistry, 2011, 286, 25451-25458.	1.6	88
5	Quantitative proteome analysis of the 20S proteasome of apoptotic Jurkat T cells. Amino Acids, 2011, 41, 351-361.	1.2	16
6	Proteome analysis of microtubule-associated proteins and their interacting partners from mammalian brain. Amino Acids, 2011, 41, 363-385.	1.2	16
7	Adaptation of proteomic techniques for the identification and characterization of protein species from murine heart. Amino Acids, 2011, 41, 401-414.	1.2	12
8	ADP-ribosylation of arginine. Amino Acids, 2011, 41, 257-269.	1.2	110
9	100% protein sequence coverage: a modern form of surrealism in proteomics. Amino Acids, 2011, 41, 291-310.	1.2	88
10	Tools for phospho- and glycoproteomics of plasma membranes. Amino Acids, 2011, 41, 223-233.	1.2	17
11	Towards the analysis of protein species: an overview about strategies and methods. Amino Acids, 2011, 41, 219-222.	1.2	18
12	Lights and shadows of proteomic technologies for the study of protein species including isoforms, splicing variants and protein post-translational modifications. Proteomics, 2011, 11, 590-603.	1.3	19
13	Proteomic analysis reveals a virtually complete set of proteins for translation and energy generation in elementary bodies of the amoeba symbiont <i>Protochlamydia amoebophila</i> . Proteomics, 2011, 11, 1868-1892.	1.3	12
14	Quantitative phosphoproteomics reveals link between <i>Helicobacter pylori</i> infection and RNA splicing modulation in host cells. Proteomics, 2011, 11, 2798-2811.	1.3	35
15	Analysis of Intact Monoclonal Antibody IgG1 by Electron Transfer Dissociation Orbitrap FTMS. Molecular and Cellular Proteomics, 2012, 11, 1758-1767.	2.5	137
16	Robust Analysis of the Yeast Proteome under 50 kDa by Molecular-Mass-Based Fractionation and Top-Down Mass Spectrometry. Analytical Chemistry, 2012, 84, 209-215.	3.2	62
17	Application of Metal-Coded Affinity Tags (MeCAT): Absolute Protein Quantification with Top-Down and Bottom-Up Workflows by Metal-Coded Tagging. Analytical Chemistry, 2012, 84, 5268-5275.	3.2	36
18	Comparison of displacement versus gradient mode for separation of a complex protein mixture by anion-exchange chromatography. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2012, 901, 34-40.	1.2	3

#	ARTICLE	IF	CITATIONS
19	Comparative proteome analysis of <i>Aspergillus oryzae</i> 3.042 and <i>A. oryzae</i> 100 strains: Towards the production of different soy sauce flavors. <i>Journal of Proteomics</i> , 2012, 75, 3914-3924.	1.2	30
20	Proteomic Profile of Human Aortic Stenosis: Insights into the Degenerative Process. <i>Journal of Proteome Research</i> , 2012, 11, 1537-1550.	1.8	57
21	An online nano-LC-ESI-FTICR-MS method for comprehensive characterization of endogenous fragments from amyloid I <sup>2</sup> and amyloid precursor protein in human and cat cerebrospinal fluid. <i>Journal of Mass Spectrometry</i> , 2012, 47, 591-603.	0.7	78
22	Cation exchange displacement batch chromatography of proteins guided by screening of protein purification parameters. <i>Journal of Separation Science</i> , 2012, 35, 3170-3176.	1.3	5
23	Restoration of full-length APC protein in SW480 colon cancer cells induces exosome-mediated secretion of DKK1. <i>Electrophoresis</i> , 2012, 33, 1873-1880.	1.3	34
24	Amino acids: Chemistry, functionality and selected non-enzymatic post-translational modifications. <i>Journal of Proteomics</i> , 2012, 75, 2275-2296.	1.2	131
25	Existing bioinformatics tools for the quantitation of post-translational modifications. <i>Amino Acids</i> , 2012, 42, 129-138.	1.2	13
26	Aberrant proteins in the saliva of patients with oral squamous cell carcinoma. <i>Electrophoresis</i> , 2013, 34, 2495-2502.	1.3	47
27	Proteomic Analysis of Leaves and Roots of Common Wheat ( <i>Triticum aestivum</i> L.) under Copper-Stress Conditions. <i>Journal of Proteome Research</i> , 2013, 12, 4846-4861.	1.8	67
28	Comparative proteomic analysis of the plant-virus interaction in resistant and susceptible ecotypes of maize infected with sugarcane mosaic virus. <i>Journal of Proteomics</i> , 2013, 89, 124-140.	1.2	88
29	2D difference gel electrophoresis reference map of a <i>Fusarium graminearum</i> nivalenol producing strain. <i>Electrophoresis</i> , 2013, 34, 505-509.	1.3	15
30	High Resolution Quantitative Proteomics of HeLa Cells Protein Species Using Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC), Two-Dimensional Gel Electrophoresis (2DE) and Nano-Liquid Chromatography Coupled to an LTQ-Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 529-538.	2.5	101
31	Quantitative and qualitative 2D electrophoretic analysis of differentially expressed mitochondrial proteins from five mouse organs. <i>Proteomics</i> , 2013, 13, 179-195.	1.3	7
32	A comparative proteomic analysis provides insights into pigment biosynthesis in brown color fiber. <i>Journal of Proteomics</i> , 2013, 78, 374-388.	1.2	37
33	Proteome Analysis of Hemolymph Changes during the Larval to Pupal Development Stages of Honeybee Workers ( <i>Apis mellifera ligustica</i> ). <i>Journal of Proteome Research</i> , 2013, 12, 5189-5198.	1.8	26
34	The response of <i>Mucor plumbeus</i> to pentachlorophenol: A toxicoproteomics study. <i>Journal of Proteomics</i> , 2013, 78, 159-171.	1.2	28
35	Characterization of the <i>Edwardsiella tarda</i> proteome in response to different environmental stresses. <i>Journal of Proteomics</i> , 2013, 80, 320-333.	1.2	16
36	Proteomic analysis on the leaves of TaBTF3 gene virus-induced silenced wheat plants may reveal its regulatory mechanism. <i>Journal of Proteomics</i> , 2013, 83, 130-143.	1.2	25

#	ARTICLE	IF	CITATIONS
37	Comparative studies focusing on transgenic through cp4EPSPS gene and non-transgenic soybean plants: An analysis of protein species and enzymes. <i>Journal of Proteomics</i> , 2013, 93, 107-116.	1.2	43
38	Proteoform: a single term describing protein complexity. <i>Nature Methods</i> , 2013, 10, 186-187.	9.0	1,180
39	Differential response of root proteome to drought stress in drought sensitive and tolerant sunflower inbred lines. <i>Functional Plant Biology</i> , 2013, 40, 609.	1.1	27
40	Application of two-dimensional gel-based mass spectrometry to functionally dissect resistance to targeted cancer therapy. <i>Proteomics - Clinical Applications</i> , 2013, 7, 813-824.	0.8	7
41	Functional and differential proteomic analyses to identify platelet derived factors affecting ex vivo expansion of mesenchymal stromal cells. <i>BMC Cell Biology</i> , 2013, 14, 48.	3.0	46
42	Mass spectrometric analysis of protein species of biologics. <i>Pharmaceutical Bioprocessing</i> , 2013, 1, 381-404.	0.8	5
43	Back to the future-The value of single protein species investigations. <i>Proteomics</i> , 2013, 13, 3103-3105.	1.3	8
44	Proteomic and redox-proteomic study on the role of glutathione reductase in human lung cancer cells. <i>Electrophoresis</i> , 2013, 34, 3305-3314.	1.3	8
45	Altered protein profiles in human umbilical cords with preterm and full-term delivery. <i>Electrophoresis</i> , 2013, 34, 493-500.	1.3	2
46	Differences in protein changes between stress-induced premature senescence and replicative senescence states. <i>Electrophoresis</i> , 2013, 34, 2209-2217.	1.3	25
47	Upregulation of Phosphorylated HSP27, PRDX2, GRP75, GRP78 and GRP94 in Acquired Middle Ear Cholesteatoma Growth. <i>International Journal of Molecular Sciences</i> , 2013, 14, 14439-14459.	1.8	13
48	Deep Imaging: How Much of the Proteome Does Current Top-Down Technology Already Resolve?. <i>PLoS ONE</i> , 2014, 9, e86058.	1.1	31
49	Proteome alterations of reverse photoperiod-sensitive genic male sterile rice ( <i>Oryza sativa</i> L.) at fertility transformation stage. <i>Genes and Genomics</i> , 2014, 36, 711-726.	0.5	5
50	Analysis of root proteome unravels differential molecular responses during compatible and incompatible interaction between chickpea ( <i>Cicer arietinum</i> L.) and <i>Fusarium oxysporum</i> f. sp. <i>ciceri</i> Race1 (Foc1). <i>BMC Genomics</i> , 2014, 15, 949.	1.2	39
51	Nuclear Proteomics with XRCC3 Knockdown to Reveal the Development of Doxorubicin-Resistant Uterine Cancer. <i>Toxicological Sciences</i> , 2014, 139, 396-406.	1.4	7
52	Biomarker discovery for neuroendocrine cervical cancer. <i>Electrophoresis</i> , 2014, 35, 2039-2045.	1.3	9
53	Alteration of protein profile in rat liver of animals exposed to subacute diazinon: A proteomic approach. <i>Electrophoresis</i> , 2014, 35, 1419-1427.	1.3	14
54	Aberrant proteins featured in the saliva of habitual betel quid chewers: An indication of early oral premalignancy?. <i>Electrophoresis</i> , 2014, 35, 3504-3511.	1.3	4

#	ARTICLE	IF	CITATIONS
55	Artifacts to avoid while taking advantage of top-down mass spectrometry based detection of protein S-thiolation. <i>Proteomics</i> , 2014, 14, 1152-1157.	1.3	20
56	Antigen 85 variation across lineages of <i>Mycobacterium tuberculosis</i> —Implications for vaccine and biomarker success. <i>Journal of Proteomics</i> , 2014, 97, 141-150.	1.2	19
57	Analysis of protein species differentiation among mycobacterial low-Mr-secreted proteins by narrow pH range Immobiline gel 2-DE-MALDI-MS. <i>Journal of Proteomics</i> , 2014, 97, 235-244.	1.2	31
58	Top-down proteomics: Enhancing 2D gel electrophoresis from tissue processing to high-sensitivity protein detection. <i>Proteomics</i> , 2014, 14, 872-889.	1.3	45
59	Growth inhibition and differences in protein profiles in azadirachtin-treated <i>Drosophila melanogaster</i> larvae. <i>Electrophoresis</i> , 2014, 35, 1122-1129.	1.3	15
60	5-Methoxytryptophan-dependent protection of cardiomyocytes from heart ischemia reperfusion injury. <i>Archives of Biochemistry and Biophysics</i> , 2014, 543, 15-22.	1.4	16
61	The proteomics quantification dilemma. <i>Journal of Proteomics</i> , 2014, 107, 98-102.	1.2	23
62	Characterization of protein species and weighted protein co-expression network regulation of <i>Escherichia coli</i> in response to serum killing using a 2-DE based proteomics approach. <i>Molecular BioSystems</i> , 2014, 10, 475-484.	2.9	7
63	Disclosure of Selective Advantages in the “modern” Sublineage of the <i>Mycobacterium tuberculosis</i> Beijing Genotype Family by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2632-2645.	2.5	28
64	Differential Responses of Three Grapevine Cultivars to <i>Botryosphaeria</i> Dieback. <i>Phytopathology</i> , 2014, 104, 1021-1035.	1.1	38
65	2DE-based approach for estimation of number of protein species in a cell. <i>Electrophoresis</i> , 2014, 35, 895-900.	1.3	19
66	Identification of up- and down-regulated proteins in doxorubicin-resistant uterine cancer cells: Reticulocalbin-1 plays a key role in the development of doxorubicin-associated resistance. <i>Pharmacological Research</i> , 2014, 90, 1-17.	3.1	10
67	Quantitative proteomics in cardiovascular research: Global and targeted strategies. <i>Proteomics - Clinical Applications</i> , 2014, 8, 488-505.	0.8	21
68	Comparative proteomics analysis of host cells infected with <i>Brucella abortus</i> A19. <i>Electrophoresis</i> , 2014, 35, 1130-1143.	1.3	6
69	Stress-related genes distinctly expressed in unfertilized wheat ovaries under both normal and water deficit conditions whereas differed in fertilized ovaries. <i>Journal of Proteomics</i> , 2014, 102, 11-27.	1.2	6
70	Deciphering the mode of action of a mutant <i>Allium sativum</i> Leaf Agglutinin (mASAL), a potent antifungal protein on <i>Rhizoctonia solani</i> . <i>BMC Microbiology</i> , 2015, 15, 237.	1.3	23
71	Tissue proteomics of splenic marginal zone lymphoma. <i>Electrophoresis</i> , 2015, 36, 1612-1621.	1.3	4
72	Distinct serum proteome profiles associated with collagen-induced arthritis and complete Freund's adjuvant-induced inflammation in CD38 <sup>+/+</sup> mice: The discriminative power of protein species or proteoforms. <i>Proteomics</i> , 2015, 15, 3382-3393.	1.3	6

#	ARTICLE	IF	CITATIONS
73	Proteome analysis of testis from infertile protein C inhibitor-deficient mice reveals novel changes in serpin processing and prostaglandin metabolism. <i>Electrophoresis</i> , 2015, 36, 2837-2840.	1.3	6
74	Top-down mass spectrometry of intact membrane protein complexes reveals oligomeric state and sequence information in a single experiment. <i>Protein Science</i> , 2015, 24, 1292-1300.	3.1	42
75	5-Methoxytryptophan-dependent inhibition of oral squamous cell carcinoma metastasis. <i>Electrophoresis</i> , 2015, 36, 2027-2034.	1.3	4
76	In vitro protein profiles in the early and late stages of Douglas fir xylogenesis. <i>Electrophoresis</i> , 2015, 36, 2035-2045.	1.3	2
77	Physiological, Ultrastructural and Proteomic Responses in the Leaf of Maize Seedlings to Polyethylene Glycol-Stimulated Severe Water Deficiency. <i>International Journal of Molecular Sciences</i> , 2015, 16, 21606-21625.	1.8	28
78	2-DE Mapping of the Blue Mussel Gill Proteome: The Usual Suspects Revisited. <i>Proteomes</i> , 2015, 3, 3-41.	1.7	15
79	Scientific standards and MIAPEs in plant proteomics research and publications. <i>Frontiers in Plant Science</i> , 2015, 6, 473.	1.7	7
80	Proteomic analysis of middle and late stages of bread wheat ( <i>Triticum aestivum</i> L.) grain development. <i>Frontiers in Plant Science</i> , 2015, 6, 735.	1.7	26
81	Quantification of biopharmaceuticals and biomarkers in complex biological matrices: a comparison of liquid chromatography coupled to tandem mass spectrometry and ligand binding assays. <i>Expert Review of Proteomics</i> , 2015, 12, 355-374.	1.3	32
82	Comparative proteomic analysis of <i>Populus trichocarpa</i> early stem from primary to secondary growth. <i>Journal of Proteomics</i> , 2015, 126, 94-108.	1.2	22
83	Exoproteome of <i>Aspergillus flavus</i> corneal isolates and saprophytes: Identification of proteoforms of an oversecreted alkaline protease. <i>Journal of Proteomics</i> , 2015, 115, 23-35.	1.2	35
84	Mitochondrial proteomics with siRNA knockdown to reveal ACAT1 and MDH2 in the development of doxorubicin-resistant uterine cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2015, 19, 744-759.	1.6	36
85	Proteome profiling of keratinocytes transforming to malignancy. <i>Electrophoresis</i> , 2015, 36, 564-576.	1.3	6
86	Succinylome Analysis Reveals the Involvement of Lysine Succinylation in Metabolism in Pathogenic <i>Mycobacterium tuberculosis</i> *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 796-811.	2.5	117
87	Western blotting revisited: Critical perusal of underappreciated technical issues. <i>Proteomics - Clinical Applications</i> , 2015, 9, 396-405.	0.8	54
88	Retinal proteins associated with redox regulation and protein folding play central roles in response to high glucose conditions. <i>Electrophoresis</i> , 2015, 36, 902-909.	1.3	1
89	Reconsidering Old Data: Non-canonical HspB1 Species and the Enigma of the Cytoskeletal Function of HspB1. <i>Heat Shock Proteins</i> , 2015, , 471-485.	0.2	1
90	Proteome changes during yeast-like and pseudohyphal growth in the biofilm-forming yeast <i>Pichia fermentans</i> . <i>Amino Acids</i> , 2015, 47, 1091-1106.	1.2	12

#	ARTICLE	IF	CITATIONS
91	Immunoproteomic technology offers an extraordinary diagnostic approach for <i>Toxoplasma gondii</i> infection. <i>Journal of Microbiological Methods</i> , 2015, 119, 18-30.	0.7	6
92	Transformative Impact of Proteomics on Cardiovascular Health and Disease. <i>Circulation</i> , 2015, 132, 852-872.	1.6	140
93	Fourteen years of plant proteomics reflected in <i>Proteomics</i> : Moving from model species and 2DE-based approaches to orphan species and gel-free platforms. <i>Proteomics</i> , 2015, 15, 1089-1112.	1.3	91
94	Concentration and pattern changes of porcine serum apolipoprotein A in four different infectious diseases. <i>Electrophoresis</i> , 2015, 36, 543-551.	1.3	7
95	p53 Proteoforms and Intrinsic Disorder: An Illustration of the Protein Structure-Function Continuum Concept. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1874.	1.8	131
96	Quantitative interactome reveals that porcine reproductive and respiratory syndrome virus nonstructural protein 2 forms a complex with viral nucleocapsid protein and cellular vimentin. <i>Journal of Proteomics</i> , 2016, 142, 70-81.	1.2	32
97	Identification of Winter-Responsive Proteins in Bread Wheat Using Proteomics Analysis and Virus-Induced Gene Silencing (VIGS). <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2954-2969.	2.5	32
98	The intricacy of biomarker complexity—the identification of a genuine proteomic biomarker is more complicated than believed. <i>Proteomics - Clinical Applications</i> , 2016, 10, 1073-1076.	0.8	6
99	Homogenization of tissues via picosecond-infrared laser (PIRL) ablation: Giving a closer view on the in-vivo composition of protein species as compared to mechanical homogenization. <i>Journal of Proteomics</i> , 2016, 134, 193-202.	1.2	33
100	Proteome analysis of <i>Bemisia tabaci</i> suggests specific targets for RNAi mediated control. <i>Journal of Proteomics</i> , 2016, 132, 93-102.	1.2	13
101	Towards deciphering proteomes via the proteoform, protein speciation, moonlighting and protein code concepts. <i>Journal of Proteomics</i> , 2016, 134, 1-4.	1.2	25
102	Analytical applications of partitioning in aqueous two-phase systems: Exploring protein structural changes and protein-partner interactions in vitro and in vivo by solvent interaction analysis method. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 622-644.	1.1	38
103	Protein species-specific characterization of conformational change induced by multisite phosphorylation. <i>Journal of Proteomics</i> , 2016, 134, 138-143.	1.2	13
104	Protein species as diagnostic markers. <i>Journal of Proteomics</i> , 2016, 134, 5-18.	1.2	24
105	Exoproteome analysis reveals higher abundance of proteins linked to alkaline stress in persistent <i>Listeria monocytogenes</i> strains. <i>International Journal of Food Microbiology</i> , 2016, 218, 17-26.	2.1	30
106	Genomic variability and protein species — Improving sequence coverage for proteogenomics. <i>Journal of Proteomics</i> , 2016, 134, 25-36.	1.2	10
107	Seroprototyping at the <i>Candida albicans</i> protein species level unveils an accurate molecular discriminator for candidemia. <i>Journal of Proteomics</i> , 2016, 134, 144-162.	1.2	33
108	Protein expression parallels thermal tolerance and ecologic changes in the diversification of a diving beetle species complex. <i>Heredity</i> , 2016, 116, 114-123.	1.2	6

#	ARTICLE	IF	CITATIONS
109	Comprehensive glycosylation profiling of IgG and IgG-fusion proteins by top-down MS with multiple fragmentation techniques. <i>Journal of Proteomics</i> , 2016, 134, 93-101.	1.2	36
110	Quantitative proteomics reveals the central changes of wheat in response to powdery mildew. <i>Journal of Proteomics</i> , 2016, 130, 108-119.	1.2	45
111	Protein species and moonlighting proteins: Very small changes in a protein's covalent structure can change its biochemical function. <i>Journal of Proteomics</i> , 2016, 134, 19-24.	1.2	59
112	Proteomic analysis of post translational modifications in cyanobacteria. <i>Journal of Proteomics</i> , 2016, 134, 57-64.	1.2	20
113	Proteolysis of chloroplast proteins is responsible for accumulation of free amino acids in dark-treated tea ( <i>Camellia sinensis</i> ) leaves. <i>Journal of Proteomics</i> , 2017, 157, 10-17.	1.2	105
114	Exo- and surface proteomes of the probiotic bacterium <i>Lactobacillus acidophilus</i> NCFM. <i>Proteomics</i> , 2017, 17, 1700019.	1.3	12
115	Proteomic analysis of erythropoietin-induced changes in neuron-like SH-SY5Y cells. <i>Turkish Journal of Biochemistry</i> , 2017, 42, 213-221.	0.3	0
116	Comparative proteomic analysis provides insight into 10-hydroxy-2-decenoic acid biosynthesis in honey bee workers. <i>Amino Acids</i> , 2017, 49, 1177-1192.	1.2	7
117	Identification of Alternative Splice Variants Using Unique Tryptic Peptide Sequences for Database Searches. <i>Journal of Proteome Research</i> , 2017, 16, 2571-2578.	1.8	6
118	Protein-species quantitative venomomics: looking through a crystal ball. <i>Journal of Venomous Animals and Toxins Including Tropical Diseases</i> , 2017, 23, 27.	0.8	26
119	Immunoproteomic identification and characterization of Ni <sup>2+</sup> -regulated proteins implicates Ni <sup>2+</sup> in the induction of monocyte cell death. <i>Cell Death and Disease</i> , 2017, 8, e2684-e2684.	2.7	13
120	Comparative proteomics of oxidative stress response of <i>Lactobacillus acidophilus</i> NCFM reveals effects on DNA repair and cysteine <i>de novo</i> synthesis. <i>Proteomics</i> , 2017, 17, 1600178.	1.3	35
121	Proteomic analysis of the compatible interaction of wheat and powdery mildew ( <i>Blumeria graminis</i> f.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.8	25
122	The roles of intrinsic disorder-based liquid-liquid phase transitions in the "Dr. Jekyll" behavior of proteins involved in amyotrophic lateral sclerosis and frontotemporal lobar degeneration. <i>Autophagy</i> , 2017, 13, 2115-2162.	4.3	48
123	Large-scale Proteomics Combined with Transgenic Experiments Demonstrates An Important Role of Jasmonic Acid in Potassium Deficiency Response in Wheat and Rice. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1889-1905.	2.5	62
124	Proteomic analysis of phytase transgenic and non-transgenic maize seeds. <i>Scientific Reports</i> , 2017, 7, 9246.	1.6	18
125	Proteomic analysis of developing wheat grains infected by powdery mildew ( <i>Blumeria graminis</i> f.sp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.6	8
126	Pattern recognition for predictive, preventive, and personalized medicine in cancer. <i>EPMA Journal</i> , 2017, 8, 51-60.	3.3	119



#	ARTICLE	IF	CITATIONS
127	MALDI mass spectrometry in medical research and diagnostic routine laboratories. <i>International Journal of Mass Spectrometry</i> , 2017, 416, 96-109.	0.7	12
128	Identification and Characterization of Human Proteoforms by Top-Down LC-21 Tesla FT-ICR Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 1087-1096.	1.8	81
129	Comparative Proteomic Analysis of Susceptible and Resistant Rice Plants during Early Infestation by Small Brown Planthopper. <i>Frontiers in Plant Science</i> , 2017, 8, 1744.	1.7	41
130	Variety and Dynamics of Proteoforms in the Human Proteome: Aspects of Markers for Hepatocellular Carcinoma. <i>Proteomes</i> , 2017, 5, 33.	1.7	10
131	Analysis of CA125 antigen in normal human seminal plasma highlightsthe molecular heterogeneity of underlying glycosylated species. <i>Turkish Journal of Biology</i> , 2017, 41, 543-551.	2.1	0
132	Looking at the recent advances in understanding $\hat{\pm}$ -synuclein and its aggregation through the proteoform prism. <i>F1000Research</i> , 2017, 6, 525.	0.8	43
133	A fully validated liquid chromatography-mass spectrometry method for the quantification of the soluble receptor of advanced glycation end-products (sRAGE) in serum using immunopurification in a 96-well plate format. <i>Talanta</i> , 2018, 182, 414-421.	2.9	25
134	A Targeted, Differential Top-Down Proteomic Methodology for Comparison of ApoA-I Proteoforms in Individuals with High and Low HDL Efflux Capacity. <i>Journal of Proteome Research</i> , 2018, 17, 2156-2164.	1.8	30
135	Proteomic analysis of the impacts of powdery mildew on wheat grain. <i>Food Chemistry</i> , 2018, 261, 30-35.	4.2	18
136	Physiological proteomics of heart failure. <i>Current Opinion in Physiology</i> , 2018, 1, 185-197.	0.9	1
137	Sex differences in murine myocardium are not exclusively regulated by gonadal hormones. <i>Journal of Proteomics</i> , 2018, 178, 43-56.	1.2	4
138	A quantitative LC-MS/MS method for insulin-like growth factor 1 in human plasma. <i>Clinical Chemistry and Laboratory Medicine</i> , 2018, 56, 1905-1912.	1.4	17
139	Small heat shock protein speciation: novel non-canonical 44ÅkDa HspB5-related protein species in rat and human tissues. <i>Cell Stress and Chaperones</i> , 2018, 23, 813-826.	1.2	1
140	Proteomics analysis of human breast milk to assess breast cancer risk. <i>Electrophoresis</i> , 2018, 39, 653-665.	1.3	27
141	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
142	Two-Dimensional Gel Electrophoresis as an Information Base for Human Proteome. , 2018, , .		0
143	Functions of short lifetime biological structures at large: the case of intrinsically disordered proteins. <i>Briefings in Functional Genomics</i> , 2020, 19, 60-68.	1.3	14
144	Fast and facile analysis of glycosylation and phosphorylation of fibrinogen from human plasmaâ€”correlation with liver cancer and liver cirrhosis. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 7965-7977.	1.9	12

#	ARTICLE	IF	CITATIONS
145	Quantification of the soluble Receptor of Advanced Glycation End-Products (sRAGE) by LC-MS after enrichment by strong cation exchange (SCX) solid-phase extraction (SPE) at the protein level. <i>Analytica Chimica Acta</i> , 2018, 1043, 45-51.	2.6	8
146	Proteomics analysis reveals that nitric oxide regulates photosynthesis of maize seedlings under water deficiency. <i>Nitric Oxide - Biology and Chemistry</i> , 2018, 81, 46-56.	1.2	7
147	Application of Proteomics Technologies in Oil Palm Research. <i>Protein Journal</i> , 2018, 37, 473-499.	0.7	7
148	Intrinsically Disordered Proteins: The Dark Horse of the Dark Proteome. <i>Proteomics</i> , 2018, 18, e1800061.	1.3	66
149	Further evidence for sustainable alternatives to replace threatened animal horn based on quantitative proteomic analysis. <i>Electrophoresis</i> , 2018, 39, 3185-3190.	1.3	3
150	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
151	Intrinsic Disorder and Posttranslational Modifications: The Darker Side of the Biological Dark Matter. <i>Frontiers in Genetics</i> , 2018, 9, 158.	1.1	190
152	Proteomics as a Tool to Study Molecular Changes During Plant Morphogenesis In Vitro. <i>Methods in Molecular Biology</i> , 2018, 1815, 339-349.	0.4	1
153	Variability of Some Milk-Associated Genes and Proteins in Several Breeds of Saudi Arabian Camels. <i>Protein Journal</i> , 2018, 37, 333-352.	0.7	4
154	Affimers as an Alternative to Antibodies in an Affinity LC-MS Assay for Quantification of the Soluble Receptor of Advanced Glycation End-Products (sRAGE) in Human Serum. <i>Journal of Proteome Research</i> , 2018, 17, 2892-2899.	1.8	20
155	Inventory of proteoforms as a current challenge of proteomics: Some technical aspects. <i>Journal of Proteomics</i> , 2019, 191, 22-28.	1.2	20
156	Multi-functionality of proteins involved in GPCR and G protein signaling: making sense of structure-function continuum with intrinsic disorder-based proteoforms. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 4461-4492.	2.4	47
157	Proteomics for cancer drug design. <i>Expert Review of Proteomics</i> , 2019, 16, 647-664.	1.3	9
158	Introduction to intrinsically disordered proteins and regions. , 2019, , 1-34.		17
159	Innovating the Concept and Practice of Two-Dimensional Gel Electrophoresis in the Analysis of Proteomes at the Proteoform Level. <i>Proteomes</i> , 2019, 7, 36.	1.7	53
160	Proteomics combined with BSMV-VIGS methods identified some N deficiency-responsive protein species and ABA role in wheat seedling. <i>Plant and Soil</i> , 2019, 444, 177-191.	1.8	12
161	Intrinsically Disordered Proteins and Their "Mysterious" (Meta)Physics. <i>Frontiers in Physics</i> , 2019, 7, .	1.0	352
162	Understanding anomalous mobility of proteins on SDS-PAGE with special reference to the highly acidic extracellular domains of human E-cadherins. <i>Electrophoresis</i> , 2019, 40, 1273-1281.	1.3	28

#	ARTICLE	IF	CITATIONS
163	Intact protein bioanalysis by liquid chromatography – High-resolution mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2019, 1110-1111, 155-167.	1.2	27
164	Investigation and development of maize fused network analysis with multi-omics. <i>Plant Physiology and Biochemistry</i> , 2019, 141, 380-387.	2.8	14
165	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
166	The Structural and Functional Diversity of Intrinsically Disordered Regions in Transmembrane Proteins. <i>Journal of Membrane Biology</i> , 2019, 252, 273-292.	1.0	14
167	Protein intrinsic disorder and structure-function continuum. <i>Progress in Molecular Biology and Translational Science</i> , 2019, 166, 1-17.	0.9	78
168	Comparative proteomic analysis of plasma of children with congenital heart disease. <i>Electrophoresis</i> , 2019, 40, 1848-1854.	1.3	4
169	Pathways and biomarkers of marbling and carcass fat deposition in bovine revealed by a combination of gel-based and gel-free proteomic analyses. <i>Meat Science</i> , 2019, 156, 146-155.	2.7	24
170	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	1.8	22
171	Quantification of surfactant protein D (SPD) in human serum by liquid chromatography-mass spectrometry (LC-MS). <i>Talanta</i> , 2019, 202, 507-513.	2.9	12
172	Netrin Family: Role for Protein Isoforms in Cancer. <i>Journal of Nucleic Acids</i> , 2019, 2019, 1-9.	0.8	19
174	Root Proteomics Reveals the Effects of Wood Vinegar on Wheat Growth and Subsequent Tolerance to Drought Stress. <i>International Journal of Molecular Sciences</i> , 2019, 20, 943.	1.8	36
175	Expanding the understanding of the heterogeneous nature of melanoma with bioinformatics and disorder-based proteomics. <i>International Journal of Biological Macromolecules</i> , 2020, 150, 1281-1293.	3.6	4
176	Mapping the Inorganic and Proteomic Differences among Different Types of Human Teeth: A Preliminary Compositional Insight. <i>Biomolecules</i> , 2020, 10, 1540.	1.8	12
177	Proteoforms: General Concepts and Methodological Process for Identification. , 0, , .		1
178	Zooming into the Dark Side of Human Annexin-S100 Complexes: Dynamic Alliance of Flexible Partners. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5879.	1.8	18
179	Introductory Chapter: Proteoforms. , 0, , .		0
180	Reply to Comments on Proteomic Investigations of Two Pakistani Naja Snake Venom Species Unravel the Venom Complexity, Posttranslational Modifications, and Presence of Extracellular Vesicles. <i>Toxins</i> 2020, 12, 669. <i>Toxins</i> , 2020, 12, 781.	1.5	0
181	A database for inventory of proteoform profiles: –pattern. <i>Electrophoresis</i> , 2020, 41, 1118-1124.	1.3	5

#	ARTICLE	IF	CITATIONS
182	Intrinsic disorder in protein sense-antisense recognition. <i>Journal of Molecular Recognition</i> , 2020, 33, e2868.	1.1	7
183	Developing a Robust Assay to Monitor and Quantify Key Players of Metabolic Pathways during Adipogenesis by Targeted Proteomics. <i>Proteomics</i> , 2020, 20, 1900141.	1.3	3
184	Proteomic Profiling of <i>Emiliana huxleyi</i> Using a Three-Dimensional Separation Method Combined with Tandem Mass Spectrometry. <i>Molecules</i> , 2020, 25, 3028.	1.7	5
185	Extended Snake Venomics by Top-Down In-Source Decay: Investigating the Newly Discovered Anatolian Meadow Viper Subspecies, <i>Vipera anatolica senliki</i> . <i>Journal of Proteome Research</i> , 2020, 19, 1731-1749.	1.8	15
186	Integrating Top-Down and Bottom-Up Mass Spectrometric Strategies for Proteomic Profiling of Iranian Saw-Scaled Viper, <i>Echis carinatus sochureki</i> , Venom. <i>Journal of Proteome Research</i> , 2021, 20, 895-908.	1.8	17
187	Mass spectrometry-based proteomics analyses of post-translational modifications and proteoforms in human pituitary adenomas. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140584.	1.1	13
188	Gel-based fluorescent proteomic tools for investigating cell redox signaling. A mini-review. <i>Electrophoresis</i> , 2021, 42, 1378-1387.	1.3	2
189	What's in a mass?. <i>Biochemical Society Transactions</i> , 2021, 49, 1027-1037.	1.6	3
190	New Interface for Faster Proteoform Analysis: Immunoprecipitation Coupled with SampleStream-Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1659-1670.	1.2	10
191	Complementing the pulp proteome via sampling with a picosecond infrared laser (PIRL). <i>Clinical Oral Investigations</i> , 2021, 25, 6757-6768.	1.4	0
192	Bull Sperm Capacitation Is Accompanied by Redox Modifications of Proteins. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7903.	1.8	10
193	Proteomes Are of Proteoforms: Embracing the Complexity. <i>Proteomes</i> , 2021, 9, 38.	1.7	46
194	<i>Per aspera ad chaos</i> : a personal journey to the wonderland of intrinsic disorder. <i>Biochemical Journal</i> , 2021, 478, 3015-3024.	1.7	7
195	Diving Deep into the Data: A Review of Deep Learning Approaches and Potential Applications in Foodomics. <i>Foods</i> , 2021, 10, 1803.	1.9	10
197	Comparative proteome analysis of human testis from newborn, young adult, and aged men identified spermatogenesis-associated proteins. <i>Electrophoresis</i> , 2015, , n/a-n/a.	1.3	7
198	Introduction to Proteomics Technologies. <i>Methods in Molecular Biology</i> , 2016, 1362, 3-27.	0.4	11
200	New technologies to analyse protein function: an intrinsic disorder perspective. <i>F1000Research</i> , 2020, 9, 101.	0.8	17
201	Mass spectrometry based approaches and strategies in bioanalysis for qualitative and quantitative analysis of pharmaceutically relevant molecules. <i>Drug Discovery Today: Technologies</i> , 2021, 40, 64-68.	4.0	1

#	ARTICLE	IF	CITATIONS
205	Gel electrophoresis for phosphorylated proteins: a brief introduction. <i>Journal of Electrophoresis</i> , 2020, 64, 13-17.	0.2	0
206	Adsorptive Microtiter Plates As Solid Supports in Affinity Purification Workflows. <i>Journal of Proteome Research</i> , 2021, 20, 5218-5221.	1.8	3
207	Preparing Proteoforms of Therapeutic Proteins for Top-Down Mass Spectrometry. , 0, , .		0
208	The Challenge of Human Spermatozoa Proteome: A Systematic Review. <i>Journal of Reproduction and Infertility</i> , 2017, 18, 267-279.	1.0	6
209	The comparison between 2DEâ€MS and bottomâ€up LCâ€MS demands highâ€end techniques for both technologies. <i>Electrophoresis</i> , 2022, 43, 1242-1245.	1.3	1
210	Eg95: A Vaccine against Cystic Echinococcosis. , 0, , .		0
211	Wool Keratin Nanoparticle-Based Micropatterns for Cellular Guidance Applications. <i>ACS Applied Nano Materials</i> , 2022, 5, 15272-15287.	2.4	5
212	Structure and disorder: protein functions depend on this new binary transforming lock-and-key into structure-function continuum. , 2023, , 127-148.		1
213	Role of plasticity and disorder in protein moonlighting: blurring of lines between biocatalysts and other biologically active proteins. , 2023, , 279-301.		2
214	Proteoforms expand the world of microproteins and short open reading frame-encoded peptides. <i>IScience</i> , 2023, 26, 106069.	1.9	10
215	A Practical and Analytical Comparative Study of Gel-Based Top-Down and Gel-Free Bottom-Up Proteomics Including Unbiased Proteoform Detection. <i>Cells</i> , 2023, 12, 747.	1.8	8
219	Growth hormone proteoformics atlas created to promote predictive, preventive, and personalized approach in overall management of pituitary neuroendocrine tumors. <i>EPMA Journal</i> , 2023, 14, 443-456.	3.3	1
226	Functional unfoldomics: Roles of intrinsic disorder in protein (multi)functionality. <i>Advances in Protein Chemistry and Structural Biology</i> , 2023, , .	1.0	0