

# Marc R Wilkins

## List of Publications by Year in descending order

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153  
papers

9,573  
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61984

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40979

93  
g-index

160  
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160  
docs citations

160  
times ranked

12012  
citing authors

#	ARTICLE	IF	CITATIONS
1	Progress with Proteome Projects: Why all Proteins Expressed by a Genome Should be Identified and How To Do It. <i>Biotechnology and Genetic Engineering Reviews</i> , 1996, 13, 19-50.	6.2	981
2	Progress with geneâ€product mapping of the Mollicutes: <i>Mycoplasma genitalium</i> . <i>Electrophoresis</i> , 1995, 16, 1090-1094.	2.4	892
3	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	17.5	694
4	From Proteins to Proteomes: Large Scale Protein Identification by Two-Dimensional Electrophoresis and Amino Acid Analysis. <i>Nature Biotechnology</i> , 1996, 14, 61-65.	17.5	539
5	Detailed peptide characterization using PEPTIDEMASS - a World-Wide-Web-accessible tool. <i>Electrophoresis</i> , 1997, 18, 403-408.	2.4	334
6	Improved and simplified in-gel sample application using reswelling of dry immobilized pH gradients. <i>Electrophoresis</i> , 1997, 18, 324-327.	2.4	319
7	Guidelines for the next 10 years of proteomics. <i>Proteomics</i> , 2006, 6, 4-8.	2.2	314
8	Twoâ€dimensional gel electrophoresis for proteome projects: The effects of protein hydrophobicity and copy number. <i>Electrophoresis</i> , 1998, 19, 1501-1505.	2.4	196
9	Current challenges and future applications for protein maps and post-translational vector maps in proteome projects. <i>Electrophoresis</i> , 1996, 17, 830-838.	2.4	179
10	Adaptation and conservation insights from the koala genome. <i>Nature Genetics</i> , 2018, 50, 1102-1111.	21.4	163
11	Small <i>RNA</i> interactome of pathogenic <i>E.Âcoli</i> revealed through crosslinking of <i>RNA</i> ase E. <i>EMBO Journal</i> , 2017, 36, 374-387.	7.8	153
12	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	12.8	152
13	Translationally controlled tumor protein: A protein identified in several nontumoral cells including erythrocytes. <i>Electrophoresis</i> , 1997, 18, 150-155.	2.4	141
14	Unseen Proteome:Â Mining Below the Tip of the Iceberg To Find Low Abundance and Membrane Proteins. <i>Journal of Proteome Research</i> , 2003, 2, 303-311.	3.7	140
15	Renal cell carcinoma and normal kidney protein expression. <i>Electrophoresis</i> , 1997, 18, 599-604.	2.4	131
16	A Molecular Scanner To Automate Proteomic Research and To Display Proteome Images. <i>Analytical Chemistry</i> , 1999, 71, 4981-4988.	6.5	127
17	Cross-Species Protein Identification using Amino Acid Composition, Peptide Mass Fingerprinting, Isoelectric Point and Molecular Mass: A Theoretical Evaluation. <i>Journal of Theoretical Biology</i> , 1997, 186, 7-15.	1.7	126
18	Optimal Replication and the Importance of Experimental Design for Gel-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2005, 4, 809-819.	3.7	120

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19	Histone H3 Mutations: An Updated View of Their Role in Chromatin Deregulation and Cancer. <i>Cancers</i> , 2019, 11, 660.	3.7	105
20	Signatures within the esophageal microbiome are associated with host genetics, age, and disease. <i>Microbiome</i> , 2018, 6, 227.	11.1	101
21	Towards an automated approach for protein identification in proteome projects. <i>Electrophoresis</i> , 1998, 19, 1941-1949.	2.4	100
22	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. <i>Cell Reports</i> , 2017, 20, 572-585.	6.4	99
23	Protein identification with N and C-terminal sequence tags in proteome projects. <i>Journal of Molecular Biology</i> , 1998, 278, 599-608.	4.2	95
24	'98Escherichia coli SWISS-2DPAGE database update. <i>Electrophoresis</i> , 1998, 19, 1960-1971.	2.4	90
25	Automatic Poisson peak harvesting for high throughput protein identification. <i>Electrophoresis</i> , 2000, 21, 2243-2251.	2.4	90
26	Gene regulation by translational inhibition is determined by Dicer partnering proteins. <i>Nature Plants</i> , 2015, 1, 14027.	9.3	85
27	Identification of arginine- and lysine-methylation in the proteome of <i>Saccharomyces cerevisiae</i> and its functional implications. <i>BMC Genomics</i> , 2010, 11, 92.	2.8	78
28	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	17.5	75
29	The methylproteome and the intracellular methylation network. <i>Proteomics</i> , 2012, 12, 564-586.	2.2	73
30	Characterisation of proteins from two-dimensional electrophoresis gels by matrix-assisted laser desorption mass spectrometry and amino acid compositional analysis. <i>Electrophoresis</i> , 1996, 17, 580-587.	2.4	68
31	Large Scale Mass Spectrometry-based Identifications of Enzyme-mediated Protein Methylation Are Subject to High False Discovery Rates. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 989-1006.	3.8	65
32	Identification of differentiation-stage specific markers that define the ex vivo osteoblastic phenotype. <i>Bone</i> , 2014, 67, 23-32.	2.9	62
33	Proteomics data mining. <i>Expert Review of Proteomics</i> , 2009, 6, 599-603.	3.0	61
34	Multiple parameter cross-species protein identification using MultiIdent - a world-wide web accessible tool. <i>Electrophoresis</i> , 1998, 19, 3199-3206.	2.4	60
35	Draft genome assembly of the invasive cane toad, <i>Rhinella marina</i> . <i>GigaScience</i> , 2018, 7, .	6.4	60
36	Large-scale protein modelling and integration with the SWISS-PROT and SWISS-2DPAGE databases: The example of <i>Escherichia coli</i> . <i>Electrophoresis</i> , 1997, 18, 498-501.	2.4	59

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37	Methylation of translation-associated proteins in <i>Saccharomyces cerevisiae</i> : Identification of methylated lysines and their methyltransferases. <i>Proteomics</i> , 2012, 12, 960-972.	2.2	59
38	Novel N-terminal and Lysine Methyltransferases That Target Translation Elongation Factor 1A in Yeast and Human. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 164-176.	3.8	57
39	RNA-Seq analysis and comparison of corneal epithelium in keratoconus and myopia patients. <i>Scientific Reports</i> , 2018, 8, 389.	3.3	56
40	Respiratory viral co-infections among SARS-CoV-2 cases confirmed by virome capture sequencing. <i>Scientific Reports</i> , 2021, 11, 3934.	3.3	55
41	Synergy and antagonism between iron chelators and antifungal drugs in <i>Cryptococcus</i> . <i>International Journal of Antimicrobial Agents</i> , 2016, 48, 388-394.	2.5	54
42	Differential Ion Mobility-Mass Spectrometry for Detailed Analysis of the Proteome. <i>Trends in Biotechnology</i> , 2019, 37, 198-213.	9.3	54
43	Methylation of Elongation Factor 1A: Where, Who, and Why?. <i>Trends in Biochemical Sciences</i> , 2018, 43, 211-223.	7.5	52
44	A two-dimensional protein map of human amniotic fluid at 17 weeks' gestation. <i>Electrophoresis</i> , 1997, 18, 2816-2822.	2.4	49
45	Metabolite-based dietary supplementation in human type 1 diabetes is associated with microbiota and immune modulation. <i>Microbiome</i> , 2022, 10, 9.	11.1	46
46	A role for Edman degradation in proteome studies. <i>Electrophoresis</i> , 1997, 18, 1068-1072.	2.4	45
47	Protein arginine methylation in <i>Saccharomyces cerevisiae</i> . <i>FEBS Journal</i> , 2012, 279, 4423-4443.	4.7	45
48	Transcriptomic and Proteomic Analyses Reveal Key Innate Immune Signatures in the Host Response to the Gastrointestinal Pathogen <i>Campylobacter concisus</i> . <i>Infection and Immunity</i> , 2015, 83, 832-845.	2.2	45
49	A new link between transcriptional initiation and pre-mRNA splicing: The RNA binding histone variant H2A.B. <i>PLoS Genetics</i> , 2017, 13, e1006633.	3.5	42
50	Tools to Covisualize and Coanalyze Proteomic Data with Genomes and Transcriptomes: Validation of Genes and Alternative mRNA Splicing. <i>Journal of Proteome Research</i> , 2014, 13, 84-98.	3.7	40
51	454 pyrosequencing-based analysis of gene expression profiles in the amphipod <i>Melita plumulosa</i> : Transcriptome assembly and toxicant induced changes. <i>Aquatic Toxicology</i> , 2014, 153, 73-88.	4.0	38
52	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.	3.8	38
53	Interactive Three-Dimensional Visualization and Contextual Analysis of Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2008, 7, 104-112.	3.7	37
54	Higher abundance of enterovirus A species in the gut of children with islet autoimmunity. <i>Scientific Reports</i> , 2019, 9, 1749.	3.3	37

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55	Simultaneous analysis of cyclin and oncogene expression using multiple monoclonal antibody immunoblots. <i>Electrophoresis</i> , 1997, 18, 638-641.	2.4	35
56	Sticking together? Falling apart? Exploring the dynamics of the interactome. <i>Trends in Biochemical Sciences</i> , 2008, 33, 195-200.	7.5	35
57	Enhanced Methylarginine Characterization by Post-Translational Modification-Specific Targeted Data Acquisition and Electron-Transfer Dissociation Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1376-1389.	2.8	35
58	Characterisation of organellar proteomes: A guide to subcellular proteomic fractionation and analysis. <i>Proteomics</i> , 2006, 6, 5746-5757.	2.2	34
59	Immonium Ion Scanning for the Discovery of Post-Translational Modifications and Its Application to Histones. <i>Journal of Proteome Research</i> , 2008, 7, 2632-2641.	3.7	33
60	Interactions Affected by Arginine Methylation in the Yeast Proteinâ€“Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3184-3198.	3.8	33
61	Cardiac and skeletal muscles show molecularly distinct responses to cancer cachexia. <i>Physiological Genomics</i> , 2015, 47, 588-599.	2.3	33
62	Long-read genome sequence assembly provides insight into ongoing retroviral invasion of the koala germline. <i>Scientific Reports</i> , 2017, 7, 15838.	3.3	33
63	QuantSeq. 3â€“ Sequencing combined with Salmon provides a fast, reliable approach for high throughput RNA expression analysis. <i>Scientific Reports</i> , 2019, 9, 18895.	3.3	33
64	Distinct Gut Virome Profile of Pregnant Women With Type 1 Diabetes in the ENDIA Study. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz025.	0.9	32
65	Yeast proteins Gar1p, Nop1p, Npl3p, Nsr1p, and Rps2p are natively methylated and are substrates of the arginine methyltransferase Hmt1p. <i>Proteomics</i> , 2015, 15, 3209-3218.	2.2	31
66	Pyomelanin produced by <i>Vibrio cholerae</i> confers resistance to predation by <i>Acanthamoeba castellanii</i> . <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	31
67	Comparative Genome Analysis of <i>Lactobacillus rhamnosus</i> Clinical Isolates from Initial Stages of Dental Pulp Infection: Identification of a New Exopolysaccharide Cluster. <i>PLoS ONE</i> , 2014, 9, e90643.	2.5	30
68	The <i>Dictyostelium discoideum</i> proteome - the SWISS-2DPAGE database of the multicellular aggregate (slug). <i>Electrophoresis</i> , 1997, 18, 491-497.	2.4	29
69	A brief overview of the size and composition of the myrtle rust genome and its taxonomic status. <i>Mycology</i> , 2014, 5, 52-63.	4.4	29
70	Complete Chloroplast Genome of the Wollemi Pine ( <i>Wollemia nobilis</i> ): Structure and Evolution. <i>PLoS ONE</i> , 2015, 10, e0128126.	2.5	29
71	STAT3 regulates cytotoxicity of human CD57+ CD4+ T cells in blood and lymphoid follicles. <i>Scientific Reports</i> , 2018, 8, 3529.	3.3	29
72	Elevation of apolipoprotein E in the CSF of cattle affected by BSE. <i>FEBS Letters</i> , 1997, 416, 161-163.	2.8	27

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73	Analysis of the Proteome of <i>Saccharomyces cerevisiae</i> for Methylarginine. <i>Journal of Proteome Research</i> , 2013, 12, 3884-3899.	3.7	26
74	RNA Splicing Alterations Induce a Cellular Stress Response Associated with Poor Prognosis in Acute Myeloid Leukemia. <i>Clinical Cancer Research</i> , 2020, 26, 3597-3607.	7.0	26
75	Visualization and Analysis of the Complexome Network of <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2011, 10, 4744-4756.	3.7	25
76	Proteogenomic Discovery of a Small, Novel Protein in Yeast Reveals a Strategy for the Detection of Unannotated Short Open Reading Frames. <i>Journal of Proteome Research</i> , 2015, 14, 5038-5047.	3.7	25
77	<i>Campylobacter concisus</i> pathotypes induce distinct global responses in intestinal epithelial cells. <i>Scientific Reports</i> , 2016, 6, 34288.	3.3	23
78	Differentially expressed genes from RNA-Seq and functional enrichment results are affected by the choice of single-end versus paired-end reads and stranded versus non-stranded protocols. <i>BMC Genomics</i> , 2017, 18, 399.	2.8	23
79	MT-MAMS: Protein Methyltransferase Motif Analysis by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 3485-3491.	3.7	23
80	Stoichiometry of <i>Saccharomyces cerevisiae</i> Lysine Methylation: Insights into Non-histone Protein Lysine Methyltransferase Activity. <i>Journal of Proteome Research</i> , 2014, 13, 1744-1756.	3.7	22
81	MicroRNA Regulatory Mechanisms Play Different Roles in Arabidopsis. <i>Journal of Proteome Research</i> , 2015, 14, 4743-4751.	3.7	22
82	Crosstalk of Phosphorylation and Arginine Methylation in Disordered SRGG Repeats of <i>Saccharomyces cerevisiae</i> Fibrillar and Its Association with Nucleolar Localization. <i>Journal of Molecular Biology</i> , 2020, 432, 448-466.	4.2	22
83	Transcriptomic Analysis Shows Decreased Cortical Expression of NR4A1, NR4A2 and RXRB in Schizophrenia and Provides Evidence for Nuclear Receptor Dysregulation. <i>PLoS ONE</i> , 2016, 11, e0166944.	2.5	22
84	Characterization of Human Plasma Glycoproteins Separated by Two-Dimensional Gel Electrophoresis. <i>Nature Biotechnology</i> , 1996, 14, 66-70.	17.5	21
85	Methylation of a CGATA element inhibits binding and regulation by GATA-1. <i>Nature Communications</i> , 2020, 11, 2560.	12.8	21
86	RNA-Seq analysis of the toxicant-induced transcriptome of the marine diatom, <i>Ceratoneis closterium</i> . <i>Marine Genomics</i> , 2014, 16, 45-53.	1.1	20
87	Elongation factor methyltransferase 3 – A novel eukaryotic lysine methyltransferase. <i>Biochemical and Biophysical Research Communications</i> , 2014, 451, 229-234.	2.1	20
88	Plau and Tgfb3 are YAP-regulated genes that promote keratinocyte proliferation. <i>Cell Death and Disease</i> , 2018, 9, 1106.	6.3	20
89	Cross-linking Mass Spectrometry Analysis of the Yeast Nucleus Reveals Extensive Protein-Protein Interactions Not Detected by Systematic Two-Hybrid or Affinity Purification-Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 1874-1882.	6.5	20
90	Transcriptome and network analyses in <i>Saccharomyces cerevisiae</i> reveal that amphotericin B and lactoferrin synergy disrupt metal homeostasis and stress response. <i>Scientific Reports</i> , 2017, 7, 40232.	3.3	18

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91	Improved Quantitative Plant Proteomics via the Combination of Targeted and Untargeted Data Acquisition. <i>Frontiers in Plant Science</i> , 2017, 8, 1669.	3.6	18
92	Molecular interaction networks for the analysis of human disease: Utility, limitations, and considerations. <i>Proteomics</i> , 2013, 13, 3393-3405.	2.2	17
93	PTMOracle: A Cytoscape App for Covisualizing and Coanalyzing Post-Translational Modifications in Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2017, 16, 1988-2003.	3.7	17
94	Characterization of Protein Methyltransferases Rkm1, Rkm4, Efm4, Efm7, Set5 and Hmt1 Reveals Extensive Post-Translational Modification. <i>Journal of Molecular Biology</i> , 2018, 430, 102-118.	4.2	17
95	Characterization of the Interaction between Arginine Methyltransferase Hmt1 and Its Substrate Npl3: Use of Multiple Cross-Linkers, Mass Spectrometric Approaches, and Software Platforms. <i>Analytical Chemistry</i> , 2018, 90, 9101-9108.	6.5	17
96	Four-dimensional visualisation and analysis of protein-protein interaction networks. <i>Proteomics</i> , 2011, 11, 2672-2682.	2.2	16
97	A Web of Possibilities: Network-Based Discovery of Protein Interaction Codes. <i>Journal of Proteome Research</i> , 2014, 13, 5333-5338.	3.7	16
98	Systems-based approaches enable identification of gene targets which improve the flavour profile of low-ethanol wine yeast strains. <i>Metabolic Engineering</i> , 2018, 49, 178-191.	7.0	16
99	Combination efficacy of ruxolitinib with standard-of-care drugs in CRLF2-rearranged Ph-like acute lymphoblastic leukemia. <i>Leukemia</i> , 2021, 35, 3101-3112.	7.2	16
100	Novel genetic markers define a subgroup of pathogenic <i>Escherichia coli</i> strains belonging to the B2 phylogenetic group. <i>FEMS Microbiology Letters</i> , 2015, 362, fnv193.	1.8	15
101	RNase III-CLASH of multi-drug resistant <i>Staphylococcus aureus</i> reveals a regulatory mRNA 3'UTR required for intermediate vancomycin resistance. <i>Nature Communications</i> , 2022, 13, .	12.8	15
102	Hares and tortoises: The high-versus low-throughput proteomic race. <i>Electrophoresis</i> , 2009, 30, S150-5.	2.4	14
103	Analytical Guidelines for co-fractionation Mass Spectrometry Obtained through Global Profiling of Gold Standard <i>Saccharomyces cerevisiae</i> Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1876-1895.	3.8	14
104	A conditional two-hybrid (C2H) system for the detection of protein-protein interactions that are mediated by post-translational modification. <i>Proteomics</i> , 2013, 13, 1059-1064.	2.2	13
105	Proteomic Validation of Transcript Isoforms, Including Those Assembled from RNA-Seq Data. <i>Journal of Proteome Research</i> , 2015, 14, 3541-3554.	3.7	13
106	Lysine methylation modulates the protein-protein interactions of yeast cytochrome C Cyc1p. <i>Proteomics</i> , 2015, 15, 2166-2176.	2.2	13
107	RNA-Seq analysis of Gtf2ird1 knockout epidermal tissue provides potential insights into molecular mechanisms underpinning Williams-Beuren syndrome. <i>BMC Genomics</i> , 2016, 17, 450.	2.8	13
108	Australian black field crickets show changes in neural gene expression associated with socially-induced morphological, life-history, and behavioral plasticity. <i>BMC Genomics</i> , 2016, 17, 827.	2.8	13

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109	Ready, SET, Go: Post-translational regulation of the histone lysine methylation network in budding yeast. <i>Journal of Biological Chemistry</i> , 2021, 297, 100939.	3.4	13
110	Disturbed protein-protein interaction networks in metastatic melanoma are associated with worse prognosis and increased functional mutation burden. <i>Pigment Cell and Melanoma Research</i> , 2013, 26, 708-722.	3.3	12
111	MethylQuant: A Tool for Sensitive Validation of Enzyme-Mediated Protein Methylation Sites from Heavy-Methyl SILAC Data. <i>Journal of Proteome Research</i> , 2018, 17, 359-373.	3.7	11
112	Multi-omics of the esophageal microenvironment identifies signatures associated with progression of Barrett's esophagus. <i>Genome Medicine</i> , 2021, 13, 133.	8.2	11
113	Information management for proteomics: a perspective. <i>Expert Review of Proteomics</i> , 2008, 5, 663-678.	3.0	10
114	Visualization of the interactome: What are we looking at?. <i>Proteomics</i> , 2012, 12, 1669-1686.	2.2	10
115	Characterization of SNP and Structural Variations in the Mitochondrial Genomes of <i>Tilletia indica</i> and Its Closely Related Species Formed Basis for a Simple Diagnostic Assay. <i>PLoS ONE</i> , 2016, 11, e0166086.	2.5	10
116	Transcription factor ZNF25 is associated with osteoblast differentiation of human skeletal stem cells. <i>BMC Genomics</i> , 2016, 17, 872.	2.8	10
117	Separation of Isobaric Mono- and Dimethylated RGG-Repeat Peptides by Differential Ion Mobility-Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 11827-11833.	6.5	10
118	Higher frequency of vertebrate-infecting viruses in the gut of infants born to mothers with type 1 diabetes. <i>Pediatric Diabetes</i> , 2020, 21, 271-279.	2.9	10
119	Controlling the Controllers: Regulation of Histone Methylation by Phosphosignalling. <i>Trends in Biochemical Sciences</i> , 2020, 45, 1035-1048.	7.5	10
120	Transcriptomic insights into the zinc homeostasis of MCF-7 breast cancer cells via next-generation RNA sequencing. <i>Metallomics</i> , 2021, 13, .	2.4	10
121	Post-translational modification analysis of <i>Saccharomyces cerevisiae</i> histone methylation enzymes reveals phosphorylation sites of regulatory potential. <i>Journal of Biological Chemistry</i> , 2021, 296, 100192.	3.4	10
122	VAN: an R package for identifying biologically perturbed networks via differential variability analysis. <i>BMC Research Notes</i> , 2013, 6, 430.	1.4	9
123	Eukaryote-Conserved Methylarginine Is Absent in Diplomonads and Functionally Compensated in <i>Giardia</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 3525-3549.	8.9	9
124	Biogeochemical Mobility of Contaminants from a Replica Radioactive Waste Trench in Response to Rainfall-Induced Redox Oscillations. <i>Environmental Science &amp; Technology</i> , 2021, 55, 8793-8805.	10.0	9
125	The Interactorium: Visualising proteins, complexes and interaction networks in a virtual 3D cell. <i>Proteomics</i> , 2009, 9, 5309-5315.	2.2	8
126	Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays. <i>Proteomics</i> , 2016, 16, 465-476.	2.2	8



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127	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.	3.8	8
128	Fast <i>Short Read De-Novo</i> Assembly Using <i>Overlap-Layout-Consensus</i> Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 334-338.	3.0	8
129	Discovery of Arginine Methylation, Phosphorylation, and Their Co-occurrence in Condensate-Associated Proteins in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2021, 20, 2420-2434.	3.7	8
130	Monitoring cytoplasmic protein complexes with blue native gel electrophoresis and stable isotope labelling with amino acids in cell culture: Analysis of changes in the 20S proteasome. <i>Electrophoresis</i> , 2011, 32, 1819-1823.	2.4	7
131	Dynamic Hubs Show Competitive and Static Hubs Non-Competitive Regulation of Their Interaction Partners. <i>PLoS ONE</i> , 2012, 7, e48209.	2.5	7
132	Systematic investigation of PRMT6 substrate recognition reveals broad specificity with a preference for an RG motif or basic and bulky residues. <i>FEBS Journal</i> , 2021, 288, 5668-5691.	4.7	7
133	HGF/c-Met Inhibition as Adjuvant Therapy Improves Outcomes in an Orthotopic Mouse Model of Pancreatic Cancer. <i>Cancers</i> , 2021, 13, 2763.	3.7	7
134	Response of <i>Helicobacter hepaticus</i> to Bovine Bile. <i>Journal of Proteome Research</i> , 2010, 9, 1374-1384.	3.7	6
135	Serotype classification and characterisation of the rotavirus SA11 VP6 protein using mass spectrometry and two-dimensional gel electrophoresis. <i>Functional and Integrative Genomics</i> , 2000, 1, 12-24.	3.5	5
136	Micropreparative fractionation of the complexome by blue native continuous elution electrophoresis. <i>Proteomics</i> , 2009, 9, 2494-2502.	2.2	5
137	Using the clustered circular layout as an informative method for visualizing protein-protein interaction networks. <i>Proteomics</i> , 2010, 10, 2723-2727.	2.2	5
138	A Multidimensional Matrix for Systems Biology Research and Its Application to Interaction Networks. <i>Journal of Proteome Research</i> , 2012, 11, 5204-5220.	3.7	5
139	A Sydney proteome story. <i>Journal of Proteomics</i> , 2014, 107, 13-23.	2.4	5
140	The <i>Saccharomyces cerevisiae</i> poly(A)-binding protein is subject to multiple post-translational modifications, including the methylation of glutamic acid. <i>Biochemical and Biophysical Research Communications</i> , 2014, 443, 543-548.	2.1	5
141	The activity of a yeast Family 16 methyltransferase, Efm2, is affected by a conserved tryptophan and its N-terminal region. <i>FEBS Open Bio</i> , 2016, 6, 1320-1330.	2.3	5
142	Different Pathways Mediate Amphotericin-Lactoferrin Drug Synergy in <i>Cryptococcus</i> and <i>Saccharomyces</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2195.	3.5	5
143	Genomic Insights Into the Archaea Inhabiting an Australian Radioactive Legacy Site. <i>Frontiers in Microbiology</i> , 2021, 12, 732575.	3.5	5
144	Investigating the Network Basis of Negative Genetic Interactions in <i>Saccharomyces cerevisiae</i> with Integrated Biological Networks and Triplet Motif Analysis. <i>Journal of Proteome Research</i> , 2018, 17, 1014-1030.	3.7	4

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145	MS2â€Deisotoper: A Tool for Deisotoping Highâ€Resolution MS/MS Spectra in Normal and Heavy Isotopeâ€Labelled Samples. <i>Proteomics</i> , 2019, 19, 1800444.	2.2	4
146	Identification of Protein Isoforms Using Reference Databases Built from Long and Short Read RNA-Sequencing. <i>Journal of Proteome Research</i> , 2022, 21, 1628-1639.	3.7	4
147	Visualizing Postâ€Translational Modifications in Protein Interaction Networks Using PTMOracle. <i>Current Protocols in Bioinformatics</i> , 2019, 66, e71.	25.8	3
148	Intra-species variation within <i>Lactobacillus rhamnosus</i> correlates to beneficial or harmful outcomes: lessons from the oral cavity. <i>BMC Genomics</i> , 2020, 21, 661.	2.8	3
149	Site-specific Phosphorylation of Histone H3K36 Methyltransferase Set2p and Demethylase Jhd1p is Required for Stress Responses in <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2022, 434, 167500.	4.2	3
150	Raspberry ketone diet supplement reduces attraction of sterile male Queensland fruit fly to cuelure by altering expression of chemoreceptor genes. <i>Scientific Reports</i> , 2021, 11, 17632.	3.3	2
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153	Protein Post-Translational Modification Prediction. , 2019, , 15-27.		1