

Marc R Wilkins

List of Publications by Year in descending order

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153
papers

9,573
citations

61984

43
h-index

40979

93
g-index

160
all docs

160
docs citations

160
times ranked

12012
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	RNA sequencing identifies genes reliant upon Ser26 in early growth response-1 in vascular endothelial cells exposed to fibroblast growth factor-2. <i>Vascular Pharmacology</i> , 2022, , 106952.	2.1	2
3	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
4	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
5	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
6	Respiratory viral co-infections among SARS-CoV-2 cases confirmed by virome capture sequencing. <i>Scientific Reports</i> , 2021, 11, 3934.	3.3	55
7	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
8	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
9	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
10	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
11	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
12	Biogeochemical Mobility of Contaminants from a Replica Radioactive Waste Trench in Response to Rainfall-Induced Redox Oscillations. <i>Environmental Science & Technology</i> , 2021, 55, 8793-8805.	10.0	9
13	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	17.5	75
14	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
15	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
16	Raspberry ketone diet supplement reduces attraction of sterile male Queensland fruit fly to cue lure by altering expression of chemoreceptor genes. <i>Scientific Reports</i> , 2021, 11, 17632.	3.3	2
17	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
18	Genomic Insights Into the Archaea Inhabiting an Australian Radioactive Legacy Site. <i>Frontiers in Microbiology</i> , 2021, 12, 732575.	3.5	5

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19	Fast <i>Short Read De-Novo</i> Assembly Using <i>Overlap-Layout-Consensus</i> Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 334-338.	3.0	8
20	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. Analytical Chemistry, 2020, 92, 1874-1882.	6.5	20
21	Crosstalk of Phosphorylation and Arginine Methylation in Disordered SRGG Repeats of <i>Saccharomyces cerevisiae</i> Fibrillar and Its Association with Nucleolar Localization. Journal of Molecular Biology, 2020, 432, 448-466.	4.2	22
22	Higher frequency of vertebrate-infecting viruses in the gut of infants born to mothers with type 1 diabetes. Pediatric Diabetes, 2020, 21, 271-279.	2.9	10
23	Intra-species variation within <i>Lactobacillus rhamnosus</i> correlates to beneficial or harmful outcomes: lessons from the oral cavity. BMC Genomics, 2020, 21, 661.	2.8	3
24	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	12.8	152
25	Analytical Guidelines for co-fractionation Mass Spectrometry Obtained through Global Profiling of Gold Standard <i>Saccharomyces cerevisiae</i> Protein Complexes. Molecular and Cellular Proteomics, 2020, 19, 1876-1895.	3.8	14
26	Eukaryote-Conserved Methylarginine Is Absent in Diplomonads and Functionally Compensated in <i>Giardia</i> . Molecular Biology and Evolution, 2020, 37, 3525-3549.	8.9	9
27	Controlling the Controllers: Regulation of Histone Methylation by Phosphosignalling. Trends in Biochemical Sciences, 2020, 45, 1035-1048.	7.5	10
28	RNA Splicing Alterations Induce a Cellular Stress Response Associated with Poor Prognosis in Acute Myeloid Leukemia. Clinical Cancer Research, 2020, 26, 3597-3607.	7.0	26
29	Methylation of a CGATA element inhibits binding and regulation by GATA-1. Nature Communications, 2020, 11, 2560.	12.8	21
30	Protein Post-Translational Modification Prediction. , 2019, , 15-27.		1
31	Separation of Isobaric Mono- and Dimethylated RGG-Repeat Peptides by Differential Ion Mobility-Mass Spectrometry. Analytical Chemistry, 2019, 91, 11827-11833.	6.5	10
32	MS2-Deisotoper: A Tool for Deisotoping High-Resolution MS/MS Spectra in Normal and Heavy Isotope-Labelled Samples. Proteomics, 2019, 19, 1800444.	2.2	4
33	Different Pathways Mediate Amphotericin-Lactoferrin Drug Synergy in <i>Cryptococcus</i> and <i>Saccharomyces</i> . Frontiers in Microbiology, 2019, 10, 2195.	3.5	5
34	Histone H3 Mutations: An Updated View of Their Role in Chromatin Deregulation and Cancer. Cancers, 2019, 11, 660.	3.7	105
35	Distinct Gut Virome Profile of Pregnant Women With Type 1 Diabetes in the ENDIA Study. Open Forum Infectious Diseases, 2019, 6, ofz025.	0.9	32
36	Higher abundance of enterovirus A species in the gut of children with islet autoimmunity. Scientific Reports, 2019, 9, 1749.	3.3	37

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37	QuantSeq. 3â€² 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
38	Differential Ion Mobilityâ€“Mass Spectrometry for Detailed Analysis of the Proteome. <i>Trends in Biotechnology</i> , 2019, 37, 198-213.	9.3	54
39	Visualizing Postâ€“Translational Modifications in Protein Interaction Networks Using PTMOracle. <i>Current Protocols in Bioinformatics</i> , 2019, 66, e71.	25.8	3
40	STAT3 regulates cytotoxicity of human CD57+ CD4+ T cells in blood and lymphoid follicles. <i>Scientific Reports</i> , 2018, 8, 3529.	3.3	29
41	Methylation of Elongation Factor 1A: Where, Who, and Why?. <i>Trends in Biochemical Sciences</i> , 2018, 43, 211-223.	7.5	52
42	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
43	RNA-Seq analysis and comparison of corneal epithelium in keratoconus and myopia patients. <i>Scientific Reports</i> , 2018, 8, 389.	3.3	56
44	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
45	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
46	Signatures within the esophageal microbiome are associated with host genetics, age, and disease. <i>Microbiome</i> , 2018, 6, 227.	11.1	101
47	Plau and Tgfbr3 are YAP-regulated genes that promote keratinocyte proliferation. <i>Cell Death and Disease</i> , 2018, 9, 1106.	6.3	20
48	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
49	MT-MAMS: Protein Methyltransferase Motif Analysis by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 3485-3491.	3.7	23
50	Adaptation and conservation insights from the koala genome. <i>Nature Genetics</i> , 2018, 50, 1102-1111.	21.4	163
51	Draft genome assembly of the invasive cane toad, <i>Rhinella marina</i> . <i>GigaScience</i> , 2018, 7, .	6.4	60
52	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
53	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
54	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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55	Small <sc>RNA</sc> interactome of pathogenic <i>E.Âcoli</i> revealed through crosslinking of <sc>RN</sc>ase E. EMBO Journal, 2017, 36, 374-387.	7.8	153
56	PTMOracle: A Cytoscape App for Covisualizing and Coanalyzing Post-Translational Modifications in Protein Interaction Networks. Journal of Proteome Research, 2017, 16, 1988-2003.	3.7	17
57	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. Cell Reports, 2017, 20, 572-585.	6.4	99
58	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. BMC Genomics, 2017, 18, 399.	2.8	23
59	METTL21B Is a Novel Human Lysine Methyltransferase of Translation Elongation Factor 1A: Discovery by CRISPR/Cas9 Knockout. Molecular and Cellular Proteomics, 2017, 16, 2229-2242.	3.8	38
60	Improved Quantitative Plant Proteomics via the Combination of Targeted and Untargeted Data Acquisition. Frontiers in Plant Science, 2017, 8, 1669.	3.6	18
61	A new link between transcriptional initiation and pre-mRNA splicing: The RNA binding histone variant H2A.B. PLoS Genetics, 2017, 13, e1006633.	3.5	42
62	Long-read genome sequence assembly provides insight into ongoing retroviral invasion of the koala germline. Scientific Reports, 2017, 7, 15838.	3.3	33
63	Pyomelanin produced by <i>Vibrio cholerae</i> confers resistance to predation by <i>Acanthamoeba castellanii</i> . FEMS Microbiology Ecology, 2017, 93, .	2.7	31
64	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. PLoS ONE, 2016, 11, e0166086.	2.5	10
65	Transcription factor ZNF25 is associated with osteoblast differentiation of human skeletal stem cells. BMC Genomics, 2016, 17, 872.	2.8	10
66	Synergy and antagonism between iron chelators and antifungal drugs in <i>Cryptococcus</i> . International Journal of Antimicrobial Agents, 2016, 48, 388-394.	2.5	54
67	RNA-Seq analysis of <i>Gtf2ird1</i> knockout epidermal tissue provides potential insights into molecular mechanisms underpinning Williams-Beuren syndrome. BMC Genomics, 2016, 17, 450.	2.8	13
68	Australian black field crickets show changes in neural gene expression associated with socially-induced morphological, life-history, and behavioral plasticity. BMC Genomics, 2016, 17, 827.	2.8	13
69	<i>Campylobacter concisus</i> pathotypes induce distinct global responses in intestinal epithelial cells. Scientific Reports, 2016, 6, 34288.	3.3	23
70	The activity of a yeast Family 16 methyltransferase, Efm2, is affected by a conserved tryptophan and its Nâ€terminal region. FEBS Open Bio, 2016, 6, 1320-1330.	2.3	5
71	Protein substrates of the arginine methyltransferase Hmt1 identified by proteome arrays. Proteomics, 2016, 16, 465-476.	2.2	8
72	Large Scale Mass Spectrometry-based Identifications of Enzyme-mediated Protein Methylation Are Subject to High False Discovery Rates. Molecular and Cellular Proteomics, 2016, 15, 989-1006.	3.8	65

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73	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
74	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
75	Gene regulation by translational inhibition is determined by Dicer partnering proteins. <i>Nature Plants</i> , 2015, 1, 14027.	9.3	85
76	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
77	Complete Chloroplast Genome of the Wollemi Pine (<i>Wollemia nobilis</i>): Structure and Evolution. <i>PLoS ONE</i> , 2015, 10, e0128126.	2.5	29
78	Cardiac and skeletal muscles show molecularly distinct responses to cancer cachexia. <i>Physiological Genomics</i> , 2015, 47, 588-599.	2.3	33
79	Molecular characterisation of stromal populations derived from human embryonic stem cells: Similarities to immortalised bone marrow derived stromal stem cells. <i>Bone Reports</i> , 2015, 3, 32-39.	0.4	1
80	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
81	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
82	Lysine methylation modulates the protein-protein interactions of yeast cytochrome C Cyc1p. <i>Proteomics</i> , 2015, 15, 2166-2176.	2.2	13
83	MicroRNA Regulatory Mechanisms Play Different Roles in Arabidopsis. <i>Journal of Proteome Research</i> , 2015, 14, 4743-4751.	3.7	22
84	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
85	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, fmv193.	1.8	15
86	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
87	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
88	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
89	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
90	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

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91	A Web of Possibilities: Network-Based Discovery of Protein Interaction Codes. <i>Journal of Proteome Research</i> , 2014, 13, 5333-5338.	3.7	16
92	Identification of differentiation-stage specific markers that define the ex vivo osteoblastic phenotype. <i>Bone</i> , 2014, 67, 23-32.	2.9	62
93	Elongation factor methyltransferase 3 – A novel eukaryotic lysine methyltransferase. <i>Biochemical and Biophysical Research Communications</i> , 2014, 451, 229-234.	2.1	20
94	A Sydney proteome story. <i>Journal of Proteomics</i> , 2014, 107, 13-23.	2.4	5
95	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
96	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
97	Interactions Affected by Arginine Methylation in the Yeast Protein-Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3184-3198.	3.8	33
98	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
99	Analysis of the Proteome of <i>Saccharomyces cerevisiae</i> for Methylarginine. <i>Journal of Proteome Research</i> , 2013, 12, 3884-3899.	3.7	26
100	VAN: an R package for identifying biologically perturbed networks via differential variability analysis. <i>BMC Research Notes</i> , 2013, 6, 430.	1.4	9
101	Molecular interaction networks for the analysis of human disease: Utility, limitations, and considerations. <i>Proteomics</i> , 2013, 13, 3393-3405.	2.2	17
102	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
103	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
104	Protein arginine methylation in <i>Saccharomyces cerevisiae</i> . <i>FEBS Journal</i> , 2012, 279, 4423-4443.	4.7	45
105	Dynamic Hubs Show Competitive and Static Hubs Non-Competitive Regulation of Their Interaction Partners. <i>PLoS ONE</i> , 2012, 7, e48209.	2.5	7
106	The methylproteome and the intracellular methylation network. <i>Proteomics</i> , 2012, 12, 564-586.	2.2	73
107	Visualization of the interactome: What are we looking at?. <i>Proteomics</i> , 2012, 12, 1669-1686.	2.2	10
108	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

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109	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
110	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
111	Four-dimensional visualisation and analysis of protein-protein interaction networks. <i>Proteomics</i> , 2011, 11, 2672-2682.	2.2	16
112	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
113	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
114	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
115	Response of <i>Helicobacter hepaticus</i> to Bovine Bile. <i>Journal of Proteome Research</i> , 2010, 9, 1374-1384.	3.7	6
116	Hares and tortoises: The high-versus low-throughput proteomic race. <i>Electrophoresis</i> , 2009, 30, S150-5.	2.4	14
117	Micropreparative fractionation of the complexome by blue native continuous elution electrophoresis. <i>Proteomics</i> , 2009, 9, 2494-2502.	2.2	5
118	The Interactorium: Visualising proteins, complexes and interaction networks in a virtual 3D cell. <i>Proteomics</i> , 2009, 9, 5309-5315.	2.2	8
119	Proteomics data mining. <i>Expert Review of Proteomics</i> , 2009, 6, 599-603.	3.0	61
120	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
121	Sticking together? Falling apart? Exploring the dynamics of the interactome. <i>Trends in Biochemical Sciences</i> , 2008, 33, 195-200.	7.5	35
122	Interactive Three-Dimensional Visualization and Contextual Analysis of Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2008, 7, 104-112.	3.7	37
123	Information management for proteomics: a perspective. <i>Expert Review of Proteomics</i> , 2008, 5, 663-678.	3.0	10
124	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	17.5	694
125	Guidelines for the next 10 years of proteomics. <i>Proteomics</i> , 2006, 6, 4-8.	2.2	314
126	Characterisation of organellar proteomes: A guide to subcellular proteomic fractionation and analysis. <i>Proteomics</i> , 2006, 6, 5746-5757.	2.2	34

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127	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
128	Unseen Proteome: 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
129	Automatic Poisson peak harvesting for high throughput protein identification. <i>Electrophoresis</i> , 2000, 21, 2243-2251.	2.4	90
130	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
131	A Molecular Scanner To Automate Proteomic Research and To Display Proteome Images. <i>Analytical Chemistry</i> , 1999, 71, 4981-4988.	6.5	127
132	Two-dimensional gel electrophoresis for proteome projects: The effects of protein hydrophobicity and copy number. <i>Electrophoresis</i> , 1998, 19, 1501-1505.	2.4	196
133	Towards an automated approach for protein identification in proteome projects. <i>Electrophoresis</i> , 1998, 19, 1941-1949.	2.4	100
134	'98Escherichia coli SWISS-2DPAGE database update. <i>Electrophoresis</i> , 1998, 19, 1960-1971.	2.4	90
135	Multiple parameter cross-species protein identification using Multident - a world-wide web accessible tool. <i>Electrophoresis</i> , 1998, 19, 3199-3206.	2.4	60
136	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
137	Elevation of apolipoprotein E in the CSF of cattle affected by BSE. <i>FEBS Letters</i> , 1997, 416, 161-163.	2.8	27
138	Translationally controlled tumor protein: A protein identified in several nontumoral cells including erythrocytes. <i>Electrophoresis</i> , 1997, 18, 150-155.	2.4	141
139	Improved and simplified in-gel sample application using reswelling of dry immobilized pH gradients. <i>Electrophoresis</i> , 1997, 18, 324-327.	2.4	319
140	Detailed peptide characterization using PEPTIDEMASS - a World-Wide-Web-accessible tool. <i>Electrophoresis</i> , 1997, 18, 403-408.	2.4	334
141	TheDictyostelium discoideum proteome - the SWISS-2DPAGE database of the multicellular aggregate (slug). <i>Electrophoresis</i> , 1997, 18, 491-497.	2.4	29
142	Large-scale protein modelling and integration with the SWISS-PROT and SWISS-2DPAGE databases: The example ofEscherichia coli. <i>Electrophoresis</i> , 1997, 18, 498-501.	2.4	59
143	Renal cell carcinoma and normal kidney protein expression. <i>Electrophoresis</i> , 1997, 18, 599-604.	2.4	131
144	Simultaneous analysis of cyclin and oncogene expression using multiple monoclonal antibody immunoblots. <i>Electrophoresis</i> , 1997, 18, 638-641.	2.4	35

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145	A role for Edman degradation in proteome studies. <i>Electrophoresis</i> , 1997, 18, 1068-1072.	2.4	45
146	A two-dimensional protein map of human amniotic fluid at 17 weeks' gestation. <i>Electrophoresis</i> , 1997, 18, 2816-2822.	2.4	49
147	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
148	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
149	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
150	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
151	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
152	Characterization of Human Plasma Glycoproteins Separated by Two-Dimensional Gel Electrophoresis. <i>Nature Biotechnology</i> , 1996, 14, 66-70.	17.5	21
153	Progress with geneâ€product mapping of the Mollicutes: <i>Mycoplasma genitalium</i> . <i>Electrophoresis</i> , 1995, 16, 1090-1094.	2.4	892