

Martin Eisenacher

List of Publications by Year in descending order

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142
papers

17,177
citations

76322

40
h-index

18128

120
g-index

166
all docs

166
docs citations

166
times ranked

32399
citing authors

#	ARTICLE	IF	CITATIONS
1	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , 2019, 47, D442-D450.	14.5	6,449
2	The PRIDE database resources in 2022: a hub for mass spectrometry-based proteomics evidences. <i>Nucleic Acids Research</i> , 2022, 50, D543-D552.	14.5	2,766
3	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	17.5	2,505
4	Glucocorticoids induce differentiation of a specifically activated, anti-inflammatory subtype of human monocytes. <i>Blood</i> , 2007, 109, 1265-1274.	1.4	336
5	A HUPO test sample study reveals common problems in mass spectrometry-based proteomics. <i>Nature Methods</i> , 2009, 6, 423-430.	19.0	316
6	Cytogenetic Alterations and Cytokeratin Expression Patterns in Breast Cancer: Integrating a New Model of Breast Differentiation into Cytogenetic Pathways of Breast Carcinogenesis. <i>Laboratory Investigation</i> , 2002, 82, 1525-1533.	3.7	221
7	Proteomics Characterization of Mouse Kidney Peroxisomes by Tandem Mass Spectrometry and Protein Correlation Profiling. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 2045-2057.	3.8	210
8	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014381-1-M111.014381-10.	3.8	175
9	PRIDE Inspector Toolsuite: Moving Toward a Universal Visualization Tool for Proteomics Data Standard Formats and Quality Assessment of ProteomeXchange Datasets. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 305-317.	3.8	140
10	Stable interference of EWS-FLI1 in an Ewing sarcoma cell line impairs IGF-1/IGF-1R signalling and reveals TOPK as a new target. <i>British Journal of Cancer</i> , 2009, 101, 80-90.	6.4	137
11	Comparison of label-free and label-based strategies for proteome analysis of hepatoma cell lines. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 967-976.	2.3	122
12	Reproducibility, Specificity and Accuracy of Relative Quantification Using Spectral Library-based Data-independent Acquisition. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 181-197.	3.8	106
13	Lipidomic and proteomic characterization of platelet extracellular vesicle subfractions from senescent platelets. <i>Transfusion</i> , 2015, 55, 507-521.	1.6	101
14	Proteomic Differences Between Hepatocellular Carcinoma and Nontumorous Liver Tissue Investigated by a Combined Gel-based and Label-free Quantitative Proteomics Study. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2006-2020.	3.8	100
15	The Proteome of Human Liver Peroxisomes: Identification of Five New Peroxisomal Constituents by a Label-Free Quantitative Proteomics Survey. <i>PLoS ONE</i> , 2013, 8, e57395.	2.5	89
16	Microarray analysis of Ewing's sarcoma family of tumours reveals characteristic gene expression signatures associated with metastasis and resistance to chemotherapy. <i>European Journal of Cancer</i> , 2008, 44, 699-709.	2.8	87
17	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	3.7	87
18	Reporter Metabolite Analysis of Transcriptional Profiles of a <i>Staphylococcus aureus</i> Strain with Normal Phenotype and Its Isogenic hemB Mutant Displaying the Small-Colony-Variant Phenotype. <i>Journal of Bacteriology</i> , 2006, 188, 7765-7777.	2.2	84

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19	An easy-to-use Decoy Database Builder software tool, implementing different decoy strategies for false discovery rate calculation in automated MS/MS protein identifications. <i>Proteomics</i> , 2008, 8, 1129-1137.	2.2	82
20	Study of Early Leaf Senescence in <i>Arabidopsis thaliana</i> by Quantitative Proteomics Using Reciprocal 14N/15N Labeling and Difference Gel Electrophoresis. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 108-120.	3.8	79
21	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat009-bat009.	3.0	76
22	Expression Profiling of t(12;22) Positive Clear Cell Sarcoma of Soft Tissue Cell Lines Reveals Characteristic Up-Regulation of Potential New Marker Genes Including ERBB3. <i>Cancer Research</i> , 2004, 64, 3395-3405.	0.9	73
23	PIA: An Intuitive Protein Inference Engine with a Web-Based User Interface. <i>Journal of Proteome Research</i> , 2015, 14, 2988-2997.	3.7	69
24	The mzQuantML Data Standard for Mass Spectrometry-based Quantitative Studies in Proteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2332-2340.	3.8	66
25	Analysis of Disease-Associated Protein Expression Using Quantitative Proteomics-Fibulin-5 Is Expressed in Association with Hepatic Fibrosis. <i>Journal of Proteome Research</i> , 2015, 14, 2278-2286.	3.7	66
26	Gene expression in periodontal tissues following treatment. <i>BMC Medical Genomics</i> , 2008, 1, 30.	1.5	63
27	Proteomics of rimmed vacuoles define new risk allele in inclusion body myositis. <i>Annals of Neurology</i> , 2017, 81, 227-239.	5.3	59
28	Quantitative Tissue Proteomics Analysis Reveals Versican as Potential Biomarker for Early-Stage Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2016, 15, 38-47.	3.7	58
29	Distinction between Human Cytochrome P450 (CYP) Isoforms and Identification of New Phosphorylation Sites by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2008, 7, 4678-4688.	3.7	57
30	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , 2017, 150, 170-182.	2.4	56
31	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1275-1285.	3.8	55
32	Development of data representation standards by the human proteome organization proteomics standards initiative. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 495-506.	4.4	54
33	Individual Profiling of Circulating Tumor Cell Composition and Therapeutic Outcome in Patients with Hepatocellular Carcinoma. <i>Translational Oncology</i> , 2013, 6, 420-428.	3.7	52
34	Low-bias phosphopeptide enrichment from scarce samples using plastic antibodies. <i>Scientific Reports</i> , 2015, 5, 11438.	3.3	51
35	Spatial and molecular resolution of diffuse malignant mesothelioma heterogeneity by integrating label-free FTIR imaging, laser capture microdissection and proteomics. <i>Scientific Reports</i> , 2017, 7, 44829.	3.3	49
36	A practical data processing workflow for multi-OMICS projects. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 52-62.	2.3	48

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37	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. <i>Journal of Proteomics</i> , 2013, 95, 84-88.	2.4	46
38	The challenge of on-tissue digestion for MALDI MSI – a comparison of different protocols to improve imaging experiments. <i>Analytical and Bioanalytical Chemistry</i> , 2015, 407, 2223-2243.	3.7	46
39	The Membrane Proteome of Sensory Cilia to the Depth of Olfactory Receptors. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1828-1843.	3.8	45
40	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	12.8	45
41	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. <i>Analytical Chemistry</i> , 2019, 91, 3302-3310.	6.5	43
42	Sense and Nonsense of Pathway Analysis Software in Proteomics. <i>Journal of Proteome Research</i> , 2011, 10, 5398-5408.	3.7	42
43	Factor Inhibiting HIF-1 (FIH-1) modulates protein interactions of Apoptosis-Stimulating p53 binding Protein 2 (ASPP2). <i>Journal of Cell Science</i> , 2013, 126, 2629-40.	2.0	42
44	Shotgun proteomic analysis of <i>Yersinia ruckeri</i> strains under normal and iron-limited conditions. <i>Veterinary Research</i> , 2016, 47, 100.	3.0	42
45	Peek a peak: a glance at statistics for quantitative label-free proteomics. <i>Expert Review of Proteomics</i> , 2010, 7, 249-261.	3.0	41
46	Using Laboratory Information Management Systems as central part of a proteomics data workflow. <i>Proteomics</i> , 2010, 10, 1230-1249.	2.2	39
47	Glyoxalase 1-knockdown in human aortic endothelial cells – effect on the proteome and endothelial function estimates. <i>Scientific Reports</i> , 2016, 6, 37737.	3.3	39
48	Integrated Fourier Transform Infrared Imaging and Proteomics for Identification of a Candidate Histochemical Biomarker in Bladder Cancer. <i>American Journal of Pathology</i> , 2019, 189, 619-631.	3.8	39
49	Diagnostic Value of the Impairment of Olfaction in Parkinson's Disease. <i>PLoS ONE</i> , 2013, 8, e64735.	2.5	39
50	Sampling Strategy for Intraoral Detection of Periodontal Pathogens Before and Following Periodontal Therapy. <i>Journal of Periodontology</i> , 2006, 77, 1323-1332.	3.4	38
51	Highly Immunoreactive IgG Antibodies Directed against a Set of Twenty Human Proteins in the Sera of Patients with Amyotrophic Lateral Sclerosis Identified by Protein Array. <i>PLoS ONE</i> , 2014, 9, e89596.	2.5	37
52	Comparison of Alternative MS/MS and Bioinformatics Approaches for Confident Phosphorylation Site Localization. <i>Journal of Proteome Research</i> , 2014, 13, 1128-1137.	3.7	37
53	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 98-107.	2.3	36
54	Evaluation of the biomarker candidate MFAP4 for non-invasive assessment of hepatic fibrosis in hepatitis C patients. <i>Journal of Translational Medicine</i> , 2016, 14, 201.	4.4	36

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55	Systematic Comparison of Label-Free, SILAC, and TMT Techniques to Study Early Adaption toward Inhibition of EGFR Signaling in the Colorectal Cancer Cell Line DiFi. <i>Journal of Proteome Research</i> , 2020, 19, 926-937.	3.7	36
56	Identification of Novel Biomarker Candidates for the Immunohistochemical Diagnosis of Cholangiocellular Carcinoma. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2661-2672.	3.8	35
57	Circulating U2 small nuclear RNA fragments as a diagnostic and prognostic biomarker in lung cancer patients. <i>Journal of Cancer Research and Clinical Oncology</i> , 2016, 142, 795-805.	2.5	34
58	Protein Inference Using PIA Workflows and PSI Standard File Formats. <i>Journal of Proteome Research</i> , 2019, 18, 741-747.	3.7	33
59	Differential interferon- λ subtype induced immune signatures are associated with suppression of SARS-CoV-2 infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	33
60	Amyloid Beta A4 Precursor Protein-binding Family B Member 1 (FE65) Interactomics Revealed Synaptic Vesicle Glycoprotein 2A (SV2A) and Sarcoplasmic/Endoplasmic Reticulum Calcium ATPase 2 (SERCA2) as New Binding Proteins in the Human Brain. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 475-488.	3.8	31
61	Protein variability in cerebrospinal fluid and its possible implications for neurological protein biomarker research. <i>PLoS ONE</i> , 2018, 13, e0206478.	2.5	31
62	mzIdentML: An Open Community-Built Standard Format for the Results of Proteomics Spectrum Identification Algorithms. <i>Methods in Molecular Biology</i> , 2011, 696, 161-177.	0.9	31
63	Redox Proteomics Uncovers Peroxynitrite-sensitive Proteins That Help Escherichia coli to Overcome Nitrosative Stress. <i>Journal of Biological Chemistry</i> , 2013, 288, 19698-19714.	3.4	29
64	Differential proteomic and tissue expression analyses identify valuable diagnostic biomarkers of hepatocellular differentiation and hepatoid adenocarcinomas. <i>Pathology</i> , 2015, 47, 543-550.	0.6	28
65	Flow cytometric characterization of microglia in the offspring of Poly:I:C treated mice. <i>Brain Research</i> , 2016, 1636, 172-182.	2.2	27
66	Characterization of Cerebrospinal Fluid via Data-Independent Acquisition Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 3418-3430.	3.7	27
67	Immunohistochemical Markers Distinguishing Cholangiocellular Carcinoma (CCC) from Pancreatic Ductal Adenocarcinoma (PDAC) Discovered by Proteomic Analysis of Microdissected Cells. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1072-1082.	3.8	26
68	MicroRNA-30c as a novel diagnostic biomarker for primary and secondary B-cell lymphoma of the CNS. <i>Journal of Neuro-Oncology</i> , 2018, 137, 463-468.	2.9	26
69	Activation of counter-regulatory mechanisms in a rat renal acute rejection model. <i>BMC Genomics</i> , 2008, 9, 71.	2.8	24
70	Identification of proteins that mediate the pro-viral functions of the interferon stimulated gene 15 in hepatitis C virus replication. <i>Antiviral Research</i> , 2013, 100, 654-661.	4.1	23
71	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014, 14, 2389-2399.	2.2	23
72	A structured proteomic approach identifies 14-3-3Sigma as a novel and reliable protein biomarker in panel based differential diagnostics of liver tumors. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 641-650.	2.3	23

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73	PAA: an R/bioconductor package for biomarker discovery with protein microarrays. <i>Bioinformatics</i> , 2016, 32, 1577-1579.	4.1	22
74	The Human Proteome Organizationâ€“Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 4474-4479.	6.5	22
75	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	3.7	22
76	FE65 regulates and interacts with the Bloom syndrome protein in dynamic nuclear spheres â€“ potential relevance to Alzheimer's disease. <i>Journal of Cell Science</i> , 2013, 126, 2480-92.	2.0	21
77	BiInfra.Prot: A comprehensive proteomics workflow including data standardization, protein inference, expression analysis and data publication. <i>Journal of Biotechnology</i> , 2017, 261, 116-125.	3.8	21
78	Improving the default data analysis workflow for large autoimmune biomarker discovery studies with ProtoArrays. <i>Proteomics</i> , 2013, 13, 2083-2087.	2.2	19
79	Intestinal Amino Acid Availability via PEPT-1 Affects TORC1/2 Signaling and the Unfolded Protein Response. <i>Journal of Proteome Research</i> , 2014, 13, 3685-3692.	3.7	19
80	Autoimmune profiling with protein microarrays in clinical applications. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 977-987.	2.3	19
81	The bacterial proteogenomic pipeline. <i>BMC Genomics</i> , 2014, 15, S19.	2.8	19
82	Quantitative proteome analysis reveals the correlation between endocytosis-associated proteins and hepatocellular carcinoma dedifferentiation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1579-1585.	2.3	19
83	Quantitative Secretome Analysis of Activated Jurkat Cells Using Click Chemistry-Based Enrichment of Secreted Glycoproteins. <i>Journal of Proteome Research</i> , 2017, 16, 137-146.	3.7	19
84	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	18
85	Spatial proteomics revealed a CX3CL1-dependent crosstalk between the urothelium and relocated macrophages through IL-6 during an acute bacterial infection in the urinary bladder. <i>Mucosal Immunology</i> , 2020, 13, 702-714.	6.0	17
86	Quantitative proteome analysis of plasma microparticles for the characterization of HCVâ€“induced hepatic cirrhosis and hepatocellular carcinoma. <i>Proteomics - Clinical Applications</i> , 2017, 11, 1700014.	1.6	16
87	Advanced Fiber Type-Specific Protein Profiles Derived from Adult Murine Skeletal Muscle. <i>Proteomes</i> , 2021, 9, 28.	3.5	16
88	Getting a grip on proteomics data â€“ Proteomics Data Collection (ProDaC). <i>Proteomics</i> , 2009, 9, 3928-3933.	2.2	15
89	Proteome Analysis of a Hepatocyte-Specific BIRC5 (Survivin)-Knockout Mouse Model during Liver Regeneration. <i>Journal of Proteome Research</i> , 2014, 13, 2771-2782.	3.7	15
90	Novel immunohistochemical markers differentiate intrahepatic cholangiocarcinoma from benign bile duct lesions. <i>Journal of Clinical Pathology</i> , 2016, 69, 619-626.	2.0	15

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91	Transformation of adult retina from the regenerative to the axonogenesis state activates specific genes in various subsets of neurons and glial cells. <i>Glia</i> , 2007, 55, 189-201.	4.9	14
92	ProCon – PROteomics CONversion tool. <i>Journal of Proteomics</i> , 2015, 129, 56-62.	2.4	14
93	Automated Calculation of Unique Peptide Sequences for Unambiguous Identification of Highly Homologous Proteins by Mass Spectrometry. <i>Journal of Proteomics and Bioinformatics</i> , 2008, 01, 006-010.	0.4	14
94	Important Issues in Planning a Proteomics Experiment: Statistical Considerations of Quantitative Proteomic Data. <i>Methods in Molecular Biology</i> , 2012, 893, 3-21.	0.9	13
95	Annexin A10 optimally differentiates between intrahepatic cholangiocarcinoma and hepatic metastases of pancreatic ductal adenocarcinoma: a comparative study of immunohistochemical markers and panels. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2017, 470, 537-543.	2.8	13
96	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	1.6	13
97	Data handling and processing in proteomics. <i>Expert Review of Proteomics</i> , 2009, 6, 217-219.	3.0	12
98	Varying survival of motoneurons and activation of distinct molecular mechanism in response to altered peripheral myelin protein 22 gene dosage. <i>Journal of Neurochemistry</i> , 2009, 110, 935-946.	3.9	12
99	Quality meets quantity – quality control, data standards and repositories. <i>Proteomics</i> , 2011, 11, 1031-1036.	2.2	12
100	Dynamic Changes of the <i>Caenorhabditis elegans</i> Proteome during Ontogenesis Assessed by Quantitative Analysis with ¹⁵ N Metabolic Labeling. <i>Journal of Proteome Research</i> , 2012, 11, 4594-4604.	3.7	12
101	Small RNAs as biomarkers to differentiate benign and malign prostate diseases: An alternative for transrectal punch biopsy of the prostate?. <i>PLoS ONE</i> , 2021, 16, e0247930.	2.5	12
102	Direct-acting antivirals-based therapy decreases hepatic fibrosis serum biomarker microfibrillar-associated protein 4 in hepatitis C patients. <i>Clinical and Molecular Hepatology</i> , 2019, 25, 42-51.	8.9	12
103	IGFBP1 in epithelial circulating tumor cells as a potential response marker to selective internal radiation therapy in hepatocellular carcinoma. <i>Biomarkers in Medicine</i> , 2014, 8, 687-698.	1.4	11
104	The impact of the COVID-19 pandemic on non-COVID induced sepsis survival. <i>BMC Anesthesiology</i> , 2022, 22, 12.	1.8	11
105	A Current Encyclopedia of Bioinformatics Tools, Data Formats and Resources for Mass Spectrometry Lipidomics. <i>Metabolites</i> , 2022, 12, 584.	2.9	10
106	Search and Decoy: The Automatic Identification of Mass Spectra. <i>Methods in Molecular Biology</i> , 2012, 893, 445-488.	0.9	9
107	Noninvasive diagnosis of urothelial cancer in urine using DNA hypermethylation signatures – Gender matters. <i>International Journal of Cancer</i> , 2019, 145, 2861-2872.	5.1	9
108	Expression analysis of pancreatic cancer cell lines reveals association of enhanced gene transcription and genomic amplifications at the 8q22.1 and 8q24.22 loci. <i>Oncology Reports</i> , 2007, 17, 399-407.	2.6	9

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109	Transcriptome and Proteome Analysis in LUHMES Cells Overexpressing Alpha-Synuclein. <i>Frontiers in Neurology</i> , 2022, 13, 787059.	2.4	9
110	Maintaining standardization: an update of the HUPO Brain Proteome Project. <i>Expert Review of Proteomics</i> , 2008, 5, 165-173.	3.0	8
111	Modeling and Managing Experimental Data Using FuGE. <i>OMICS A Journal of Integrative Biology</i> , 2009, 13, 239-251.	2.0	8
112	Comprehensive proteomic analysis of <i>Penicillium verrucosum</i> . <i>Proteomics</i> , 2017, 17, 1600467.	2.2	8
113	One Sample, One Shot - Evaluation of sample preparation protocols for the mass spectrometric proteome analysis of human bile fluid without extensive fractionation. <i>Journal of Proteomics</i> , 2017, 154, 13-21.	2.4	8
114	Tissue-based quantitative proteome analysis of human hepatocellular carcinoma using tandem mass tags. <i>Biomarkers</i> , 2017, 22, 113-122.	1.9	8
115	Adjusted Confidence Intervals for the Expression Change of Proteins Observed in 2-Dimensional Difference Gel Electrophoresis. <i>Journal of Proteomics and Bioinformatics</i> , 2009, 02, 078-087.	0.4	8
116	MicroRNAs from urinary exosomes as alternative biomarkers in the differentiation of benign and malignant prostate diseases. <i>Journal of Circulating Biomarkers</i> , 2022, 11, 5-13.	1.3	8
117	Functional metagenomics of the thioredoxin superfamily. <i>Journal of Biological Chemistry</i> , 2021, 296, 100247.	3.4	7
118	NTRK1/TrkA Signaling in Neuroblastoma Cells Induces Nuclear Reorganization and Intra-Nuclear Aggregation of Lamin A/C. <i>Cancers</i> , 2021, 13, 5293.	3.7	7
119	Detection of Patient Subgroups with Differential Expression in Omics Data: A Comprehensive Comparison of Univariate Measures. <i>PLoS ONE</i> , 2013, 8, e79380.	2.5	6
120	MaCPepDB: A Database to Quickly Access All Tryptic Peptides of the UniProtKB. <i>Journal of Proteome Research</i> , 2021, 20, 2145-2150.	3.7	6
121	CalibraCurve: A Tool for Calibration of Targeted MS-Based Measurements. <i>Proteomics</i> , 2020, 20, e1900143.	2.2	5
122	Important Issues in Planning a Proteomics Experiment: Statistical Considerations of Quantitative Proteomic Data. <i>Methods in Molecular Biology</i> , 2021, 2228, 1-20.	0.9	5
123	Establishing a Custom-Fit Data-Independent Acquisition Method for Label-Free Proteomics. <i>Methods in Molecular Biology</i> , 2021, 2228, 307-325.	0.9	5
124	BIONDA: a free database for a fast information on published biomarkers. <i>Bioinformatics Advances</i> , 2021, 1, .	2.4	5
125	Mass Analysis Peptide Sequence Prediction (MAPSP). <i>Bioinformatics</i> , 2006, 22, 1002-1003.	4.1	4
126	Inter-Lab Proteomics: Data Mining in Collaborative Projects on the Basis of the HUPO Brain Proteome Project's Pilot Studies. <i>Methods in Molecular Biology</i> , 2011, 696, 235-246.	0.9	4

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127	Proteomics Data Collection – ProDaC Workshop 15 August 2008, Amsterdam, The Netherlands. <i>Proteomics</i> , 2009, 9, 218-222.	2.2	3
128	Toward a Successful Clinical Neuroproteomics The 11th HUPO Brain Proteome Project Workshop 3 March, 2009, Kolybari, Greece. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1012-1016.	1.6	3
129	Find Pairs: The Module for Protein Quantification of the PeakQuant Software Suite. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 457-467.	2.0	3
130	A combination of two electrophoretical approaches for detailed proteome-based characterization of SCLC subtypes. <i>Archives of Physiology and Biochemistry</i> , 2013, 119, 114-125.	2.1	3
131	The amino acid's backup bone – Storage solutions for proteomics facilities. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 2-11.	2.3	3
132	Boolean modeling techniques for protein co-expression networks in systems medicine. <i>Expert Review of Proteomics</i> , 2016, 13, 555-569.	3.0	3
133	Proteomics Data Collection (ProDaC): Publishing and Collecting Proteomics Data Sets in Public Repositories Using Standard Formats. <i>Methods in Molecular Biology</i> , 2010, 604, 345-368.	0.9	3
134	Laser Microdissection-Based Protocol for the LC-MS/MS Analysis of the Proteomic Profile of Neuromelanin Granules. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	3
135	Expression analysis of pancreatic cancer cell lines reveals association of enhanced gene transcription and genomic amplifications at the 8q22.1 and 8q24.22 loci. <i>Oncology Reports</i> , 2007, 17, 399.	2.6	2
136	Proteomics today: Bioinformatics at its best. <i>Proteomics and Bioinformatics – an inseparable couple</i> . <i>Proteomics</i> , 2008, 8, 4616-4617.	2.2	2
137	Quantitative analysis of proteome dynamics in a mouse model of asthma. <i>Clinical and Experimental Allergy</i> , 2021, 51, 1471-1481.	2.9	2
138	Creation of Reusable Bioinformatics Workflows for Reproducible Analysis of LC-MS Proteomics Data. <i>Neuromethods</i> , 2017, , 305-324.	0.3	2
139	Computational proteomics in the post-identification era. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1.	2.3	1
140	A generally applicable lightweight method for calculating a value structure for tools and services in bioinformatics infrastructure projects. <i>Briefings in Bioinformatics</i> , 2019, 20, 1215-1221.	6.5	1
141	Let me infuse this for you – A way to solve the first YPIC challenge. <i>EuPA Open Proteomics</i> , 2019, 22-23, 19-21.	2.5	0
142	Dataset containing physiological amounts of spike-in proteins into murine C2C12 background as a ground truth quantitative LC-MS/MS reference. <i>Data in Brief</i> , 2022, 43, 108435.	1.0	0