Martin Eisenacher

List of Publications by Year
in descending order

142 papers	17,177 citations	76326 40 h-index	18130 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. Nucleic Acids Research, 2019, 47, D442-D450.	14.5	6,449
2	The PRIDE database resources in 2022: a hub for mass spectrometry-based proteomics evidences. Nucleic Acids Research, 2022, 50, D543-D552.	14.5	2,766
3	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	17.5	2,505
4	Glucocorticoids induce differentiation of a specifically activated, anti-inflammatory subtype of human monocytes. Blood, 2007, 109, 1265-1274.	1.4	336
5	A HUPO test sample study reveals common problems in mass spectrometry–based proteomics. Nature Methods, 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. Laboratory Investigation, 2002, 82, 1525-1533.	3.7	221
7	Proteomics Characterization of Mouse Kidney Peroxisomes by Tandem Mass Spectrometry and Protein Correlation Profiling. Molecular and Cellular Proteomics, 2007, 6, 2045-2057.	3.8	210
8	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. Molecular and Cellular Proteomics, 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. Molecular and Cellular Proteomics, 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. British Journal of Cancer, 2009, 101, 80-90.	6.4	137
11	Comparison of label-free and label-based strategies for proteome analysis of hepatoma cell lines. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 967-976.	2.3	122
12	Reproducibility, Specificity and Accuracy of Relative Quantification Using Spectral Library-based Data-independent Acquisition. Molecular and Cellular Proteomics, 2020, 19, 181-197.	3.8	106
13	Lipidomic and proteomic characterization of platelet extracellular vesicle subfractions from senescent platelets. Transfusion, 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. Molecular and Cellular Proteomics, 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. PLoS ONE, 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. European Journal of Cancer, 2008, 44, 699-709.	2.8	87
17	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	3.7	87
18	Reporter Metabolite Analysis of Transcriptional Profiles of a Staphylococcus aureus Strain with Normal Phenotype and Its Isogenic hemB Mutant Displaying the Small-Colony-Variant Phenotype. Journal of Bacteriology, 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. Proteomics, 2008, 8, 1129-1137.	2.2	82
20	Study of Early Leaf Senescence in Arabidopsis thaliana by Quantitative Proteomics Using Reciprocal 14N/15N Labeling and Difference Gel Electrophoresis. Molecular and Cellular Proteomics, 2008, 7, 108-120.	3.8	79
21	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 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. Cancer Research, 2004, 64, 3395-3405.	0.9	73
23	PIA: An Intuitive Protein Inference Engine with a Web-Based User Interface. Journal of Proteome Research, 2015, 14, 2988-2997.	3.7	69
24	The mzQuantML Data Standard for Mass Spectrometry‐based Quantitative Studies in Proteomics. Molecular and Cellular Proteomics, 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. Journal of Proteome Research, 2015, 14, 2278-2286.	3.7	66
26	Gene expression in periodontal tissues following treatment. BMC Medical Genomics, 2008, 1, 30.	1.5	63
27	Proteomics of rimmed vacuoles define new risk allele in inclusion body myositis. Annals of Neurology, 2017, 81, 227-239.	5.3	59
28	Quantitative Tissue Proteomics Analysis Reveals Versican as Potential Biomarker for Early-Stage Hepatocellular Carcinoma. Journal of Proteome Research, 2016, 15, 38-47.	3.7	58
29	Distinction between Human Cytochrome P450 (CYP) Isoforms and Identification of New Phosphorylation Sites by Mass Spectrometry. Journal of Proteome Research, 2008, 7, 4678-4688.	3.7	57
30	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. Journal of Proteomics, 2017, 150, 170-182.	2.4	56
31	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular and Cellular Proteomics, 2017, 16, 1275-1285.	3.8	55
32	Development of data representation standards by the human proteome organization proteomics standards initiative. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 495-506.	4.4	54
33	Individual Profiling of Circulating Tumor Cell Composition and Therapeutic Outcome in Patients with Hepatocellular Carcinoma. Translational Oncology, 2013, 6, 420-428.	3.7	52
34	Low-bias phosphopeptide enrichment from scarce samples using plastic antibodies. Scientific Reports, 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. Scientific Reports, 2017, 7, 44829.	3.3	49
36	A practical data processing workflow for multi-OMICS projects. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 52-62.	2.3	48

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37	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. Journal of Proteomics, 2013, 95, 84-88.	2.4	46
38	The challenge of on-tissue digestion for MALDI MSIâ€" a comparison of different protocols to improve imaging experiments. Analytical and Bioanalytical Chemistry, 2015, 407, 2223-2243.	3.7	46
39	The Membrane Proteome of Sensory Cilia to the Depth of Olfactory Receptors. Molecular and Cellular Proteomics, 2014, 13, 1828-1843.	3.8	45
40	A proteomics sample metadata representation for multiomics integration and big data analysis. Nature Communications, 2021, 12, 5854.	12.8	45
41	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. Analytical Chemistry, 2019, 91, 3302-3310.	6.5	43
42	Sense and Nonsense of Pathway Analysis Software in Proteomics. Journal of Proteome Research, 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). Journal of Cell Science, 2013, 126, 2629-40.	2.0	42
44	Shotgun proteomic analysis of Yersinia ruckeri strains under normal and iron-limited conditions. Veterinary Research, 2016, 47, 100.	3.0	42
45	Peek a peak: a glance at statistics for quantitative label-free proteomics. Expert Review of Proteomics, 2010, 7, 249-261.	3.0	41
46	Using Laboratory Information Management Systems as central part of a proteomics data workflow. Proteomics, 2010, 10, 1230-1249.	2.2	39
47	Glyoxalase 1-knockdown in human aortic endothelial cells â€" effect on the proteome and endothelial function estimates. Scientific Reports, 2016, 6, 37737.	3.3	39
48	Integrated Fourier Transform Infrared Imaging and Proteomics for Identification of a Candidate Histochemical Biomarker in Bladder Cancer. American Journal of Pathology, 2019, 189, 619-631.	3.8	39
49	Diagnostic Value of the Impairment of Olfaction in Parkinson's Disease. PLoS ONE, 2013, 8, e64735.	2.5	39
50	Sampling Strategy for Intraoral Detection of Periodontal Pathogens Before and Following Periodontal Therapy. Journal of Periodontology, 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. PLoS ONE, 2014, 9, e89596.	2.5	37
52	Comparison of Alternative MS/MS and Bioinformatics Approaches for Confident Phosphorylation Site Localization. Journal of Proteome Research, 2014, 13, 1128-1137.	3.7	37
53	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. Biochimica Et Biophysica Acta - Proteins and Proteomics, 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. Journal of Translational Medicine, 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. Journal of Proteome Research, 2020, 19, 926-937.	3.7	36
56	Identification of Novel Biomarker Candidates for the Immunohistochemical Diagnosis of Cholangiocellular Carcinoma. Molecular and Cellular Proteomics, 2014, 13, 2661-2672.	3.8	35
57	Circulating U2 small nuclear RNA fragments as a diagnostic and prognostic biomarker in lung cancer patients. Journal of Cancer Research and Clinical Oncology, 2016, 142, 795-805.	2.5	34
58	Protein Inference Using PIA Workflows and PSI Standard File Formats. Journal of Proteome Research, 2019, 18, 741-747.	3.7	33
59	Differential interferon-α subtype induced immune signatures are associated with suppression of SARS-CoV-2 infection. Proceedings of the National Academy of Sciences of the United States of America, 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. Molecular and Cellular Proteomics, 2014, 13, 475-488.	3.8	31
61	Protein variability in cerebrospinal fluid and its possible implications for neurological protein biomarker research. PLoS ONE, 2018, 13, e0206478.	2.5	31
62	mzIdentML: An Open Community-Built Standard Format for the Results of Proteomics Spectrum Identification Algorithms. Methods in Molecular Biology, 2011, 696, 161-177.	0.9	31
63	Redox Proteomics Uncovers Peroxynitrite-sensitive Proteins That Help Escherichia coli to Overcome Nitrosative Stress. Journal of Biological Chemistry, 2013, 288, 19698-19714.	3.4	29
64	Differential proteomic and tissue expression analyses identify valuable diagnostic biomarkers of hepatocellular differentiation and hepatoid adenocarcinomas. Pathology, 2015, 47, 543-550.	0.6	28
65	Flow cytometric characterization of microglia in the offspring of PolyI:C treated mice. Brain Research, 2016, 1636, 172-182.	2.2	27
66	Characterization of Cerebrospinal Fluid via Data-Independent Acquisition Mass Spectrometry. Journal of Proteome Research, 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. Molecular and Cellular Proteomics, 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. Journal of Neuro-Oncology, 2018, 137, 463-468.	2.9	26
69	Activation of counter-regulatory mechanisms in a rat renal acute rejection model. BMC Genomics, 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. Antiviral Research, 2013, 100, 654-661.	4.1	23
71	A standardized framing for reporting protein identifications in mzIdentML 1.2. Proteomics, 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. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 641-650.	2.3	23

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73	PAA: an R/bioconductor package for biomarker discovery with protein microarrays. Bioinformatics, 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. Analytical Chemistry, 2017, 89, 4474-4479.	6.5	22
75	Proteomics Standards Initiative Extended FASTA Format. Journal of Proteome Research, 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. Journal of Cell Science, 2013, 126, 2480-92.	2.0	21
77	BioInfra.Prot: A comprehensive proteomics workflow including data standardization, protein inference, expression analysis and data publication. Journal of Biotechnology, 2017, 261, 116-125.	3.8	21
78	Improving the default data analysis workflow for large autoimmune biomarker discovery studies with ProtoArrays. Proteomics, 2013, 13, 2083-2087.	2.2	19
79	Intestinal Amino Acid Availability via PEPT-1 Affects TORC1/2 Signaling and the Unfolded Protein Response. Journal of Proteome Research, 2014, 13, 3685-3692.	3.7	19
80	Autoimmune profiling with protein microarrays in clinical applications. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 977-987.	2.3	19
81	The bacterial proteogenomic pipeline. BMC Genomics, 2014, 15, S19.	2.8	19
82	Quantitative proteome analysis reveals the correlation between endocytosis-associated proteins and hepatocellular carcinoma dedifferentiation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1579-1585.	2.3	19
83	Quantitative Secretome Analysis of Activated Jurkat Cells Using Click Chemistry-Based Enrichment of Secreted Glycoproteins. Journal of Proteome Research, 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. Briefings in Bioinformatics, 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. Mucosal Immunology, 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. Proteomics - Clinical Applications, 2017, 11, 1700014.	1.6	16
87	Advanced Fiber Type-Specific Protein Profiles Derived from Adult Murine Skeletal Muscle. Proteomes, 2021, 9, 28.	3.5	16
88	Getting a grip on proteomics data â€" Proteomics Data Collection (ProDaC). Proteomics, 2009, 9, 3928-3933.	2.2	15
89	Proteome Analysis of a Hepatocyte-Specific BIRC5 (Survivin)-Knockout Mouse Model during Liver Regeneration. Journal of Proteome Research, 2014, 13, 2771-2782.	3.7	15
90	Novel immunohistochemical markers differentiate intrahepatic cholangiocarcinoma from benign bile duct lesions. Journal of Clinical Pathology, 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. Glia, 2007, 55, 189-201.	4.9	14
92	ProCon â€" PROteomics CONversion tool. Journal of Proteomics, 2015, 129, 56-62.	2.4	14
93	Automated Calculation of Unique PeptideSequencesforUnambiguous Identification of HighlyHomologousProteins byMassSpectrometry. Journal of Proteomics and Bioinformatics, 2008, 01, 006-010.	0.4	14
94	Important Issues in Planning a Proteomics Experiment: Statistical Considerations of Quantitative Proteomic Data. Methods in Molecular Biology, 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. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2017, 470, 537-543.	2.8	13
96	A community proposal to integrate proteomics activities in ELIXIR. F1000Research, 2017, 6, 875.	1.6	13
97	Data handling and processing in proteomics. Expert Review of Proteomics, 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. Journal of Neurochemistry, 2009, 110, 935-946.	3.9	12
99	Quality meets quantity â€" quality control, data standards and repositories. Proteomics, 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. Journal of Proteome Research, 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?. PLoS ONE, 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. Clinical and Molecular Hepatology, 2019, 25, 42-51.	8.9	12
103	IGFBP1in epithelial circulating tumor cells as a potential response marker to selective internal radiation therapy in hepatocellular carcinoma. Biomarkers in Medicine, 2014, 8, 687-698.	1.4	11
104	The impact of the COVID-19 pandemic on non-COVID induced sepsis survival. BMC Anesthesiology, 2022, 22, 12.	1.8	11
105	A Current Encyclopedia of Bioinformatics Tools, Data Formats and Resources for Mass Spectrometry Lipidomics. Metabolites, 2022, 12, 584.	2.9	10
106	Search and Decoy: The Automatic Identification of Mass Spectra. Methods in Molecular Biology, 2012, 893, 445-488.	0.9	9
107	Noninvasive diagnosis of urothelial cancer in urine using DNA hypermethylation signaturesâ€"Gender matters. International Journal of Cancer, 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. Oncology Reports, 2007, 17, 399-407.	2.6	9

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109	Transcriptome and Proteome Analysis in LUHMES Cells Overexpressing Alpha-Synuclein. Frontiers in Neurology, 2022, 13, 787059.	2.4	9
110	Maintaining standardization: an update of the HUPO Brain Proteome Project. Expert Review of Proteomics, 2008, 5, 165-173.	3.0	8
111	Modeling and Managing Experimental Data Using FuGE. OMICS A Journal of Integrative Biology, 2009, 13, 239-251.	2.0	8
112	Comprehensive proteomic analysis of <i>Penicillium verrucosum</i>. Proteomics, 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. Journal of Proteomics, 2017, 154, 13-21.	2.4	8
114	Tissue-based quantitative proteome analysis of human hepatocellular carcinoma using tandem mass tags. Biomarkers, 2017, 22, 113-122.	1.9	8
115	Adjusted Confidence Intervals for the Expression Change of Proteins Observed in 2-Dimensional Difference Gel Electrophoresis. Journal of Proteomics and Bioinformatics, 2009, 02, 078-087.	0.4	8
116	MicroRNAs from urinary exosomes as alternative biomarkers in the differentiation of benign and malignant prostate diseases. Journal of Circulating Biomarkers, 2022, 11, 5-13.	1.3	8
117	Functional metagenomics of the thioredoxin superfamily. Journal of Biological Chemistry, 2021, 296, 100247.	3.4	7
118	NTRK1/TrkA Signaling in Neuroblastoma Cells Induces Nuclear Reorganization and Intra-Nuclear Aggregation of Lamin A/C. Cancers, 2021, 13, 5293.	3.7	7
119	Detection of Patient Subgroups with Differential Expression in Omics Data: A Comprehensive Comparison of Univariate Measures. PLoS ONE, 2013, 8, e79380.	2.5	6
120	MaCPepDB: A Database to Quickly Access All Tryptic Peptides of the UniProtKB. Journal of Proteome Research, 2021, 20, 2145-2150.	3.7	6
121	CalibraCurve: A Tool for Calibration of Targeted MSâ€Based Measurements. Proteomics, 2020, 20, e1900143.	2.2	5
122	Important Issues in Planning a Proteomics Experiment: Statistical Considerations of Quantitative Proteomic Data. Methods in Molecular Biology, 2021, 2228, 1-20.	0.9	5
123	Establishing a Custom-Fit Data-Independent Acquisition Method for Label-Free Proteomics. Methods in Molecular Biology, 2021, 2228, 307-325.	0.9	5
124	BIONDA: a free database for a fast information on published biomarkers. Bioinformatics Advances, 2021, 1, .	2.4	5
125	Mass Analysis Peptide Sequence Prediction (MAPSP). Bioinformatics, 2006, 22, 1002-1003.	4.1	4
126	Inter-Lab Proteomics: Data Mining in Collaborative Projects on the Basis of the HUPO Brain Proteome Projectâ€™s Pilot Studies. Methods in Molecular Biology, 2011, 696, 235-246.	0.9	4

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127	Proteomics Data Collection – 4th ProDaC Workshop 15 August 2008, Amsterdam, The Netherlands. Proteomics, 2009, 9, 218-222.	2.2	3
128	Toward a Successful Clinical Neuroproteomics The 11th HUPO Brain Proteome Project Workshop 3 March, 2009, Kolymbari, Greece. Proteomics - Clinical Applications, 2009, 3, 1012-1016.	1.6	3
129	Find Pairs: The Module for Protein Quantification of the PeakQuant Software Suite. OMICS A Journal of Integrative Biology, 2012, 16, 457-467.	2.0	3
130	A combination of two electrophoretical approaches for detailed proteome-based characterization of SCLC subtypes. Archives of Physiology and Biochemistry, 2013, 119, 114-125.	2.1	3
131	The amino acid's backup bone — Storage solutions for proteomics facilities. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 2-11.	2.3	3
132	Boolean modeling techniques for protein co-expression networks in systems medicine. Expert Review of Proteomics, 2016, 13, 555-569.	3.0	3
133	Proteomics Data Collection (ProDaC): Publishing and Collecting Proteomics Data Sets in Public Repositories Using Standard Formats. Methods in Molecular Biology, 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. Journal of Visualized Experiments, 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. Oncology Reports, 2007, 17, 399.	2.6	2
136	Proteomics today: Bioinformatics at its best. Proteomics and Bioinformatics — an inseparable couple. Proteomics, 2008, 8, 4616-4617.	2.2	2
137	Quantitative analysis of proteome dynamics in a mouse model of asthma. Clinical and Experimental Allergy, 2021, 51, 1471-1481.	2.9	2
138	Creation of Reusable Bioinformatics Workflows for Reproducible Analysis of LC-MS Proteomics Data. Neuromethods, 2017, , 305-324.	0.3	2
139	Computational proteomics in the post-identification era. Biochimica Et Biophysica Acta - Proteins and Proteomics, 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. Briefings in Bioinformatics, 2019, 20, 1215-1221.	6.5	1
141	Let me infuse this for you — A way to solve the first YPIC challenge. EuPA Open Proteomics, 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. Data in Brief, 2022, 43, 108435.	1.0	0