

# Jacek R WiÅ›niewski

## List of Publications by Year in descending order

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122  
papers

18,522  
citations

44069

48  
h-index

19190

118  
g-index

127  
all docs

127  
docs citations

127  
times ranked

27908  
citing authors

#	ARTICLE	IF	CITATIONS
1	Universal sample preparation method for proteome analysis. <i>Nature Methods</i> , 2009, 6, 359-362.	19.0	6,678
2	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , 2011, 7, 548.	7.2	878
3	Ultradeep Human Phosphoproteome Reveals a Distinct Regulatory Nature of Tyr and Ser/Thr-Based Signaling. <i>Cell Reports</i> , 2014, 8, 1583-1594.	6.4	839
4	Integrated Analysis of Protein Composition, Tissue Diversity, and Gene Regulation in Mouse Mitochondria. <i>Cell</i> , 2003, 115, 629-640.	28.9	815
5	Precision Mapping of an In Vivo N-Glycoproteome Reveals Rigid Topological and Sequence Constraints. <i>Cell</i> , 2010, 141, 897-907.	28.9	789
6	A "Proteomic Ruler" for Protein Copy Number and Concentration Estimation without Spike-in Standards. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3497-3506.	3.8	530
7	Combination of FASP and StageTip-Based Fractionation Allows In-Depth Analysis of the Hippocampal Membrane Proteome. <i>Journal of Proteome Research</i> , 2009, 8, 5674-5678.	3.7	507
8	Super-SILAC mix for quantitative proteomics of human tumor tissue. <i>Nature Methods</i> , 2010, 7, 383-385.	19.0	480
9	Classification of Inhibitors of Hepatic Organic Anion Transporting Polypeptides (OATPs): Influence of Protein Expression on Drug-Drug Interactions. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 4740-4763.	6.4	299
10	High Recovery FASP Applied to the Proteomic Analysis of Microdissected Formalin Fixed Paraffin Embedded Cancer Tissues Retrieves Known Colon Cancer Markers. <i>Journal of Proteome Research</i> , 2011, 10, 3040-3049.	3.7	281
11	Consecutive Proteolytic Digestion in an Enzyme Reactor Increases Depth of Proteomic and Phosphoproteomic Analysis. <i>Analytical Chemistry</i> , 2012, 84, 2631-2637.	6.5	278
12	Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. <i>Nature Protocols</i> , 2011, 6, 147-157.	12.0	265
13	Brain Phosphoproteome Obtained by a FASP-Based Method Reveals Plasma Membrane Protein Topology. <i>Journal of Proteome Research</i> , 2010, 9, 3280-3289.	3.7	253
14	Mapping N-Glycosylation Sites across Seven Evolutionarily Distant Species Reveals a Divergent Substrate Proteome Despite a Common Core Machinery. <i>Molecular Cell</i> , 2012, 46, 542-548.	9.7	238
15	Fast and Sensitive Total Protein and Peptide Assays for Proteomic Analysis. <i>Analytical Chemistry</i> , 2015, 87, 4110-4116.	6.5	236
16	Extensive quantitative remodeling of the proteome between normal colon tissue and adenocarcinoma. <i>Molecular Systems Biology</i> , 2012, 8, 611.	7.2	221
17	Proteome, Phosphoproteome, and N-Glycoproteome Are Quantitatively Preserved in Formalin-Fixed Paraffin-Embedded Tissue and Analyzable by High-Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 3688-3700.	3.7	219
18	Quantitative Analysis of Human Red Blood Cell Proteome. <i>Journal of Proteome Research</i> , 2017, 16, 2752-2761.	3.7	216

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19	Mass Spectrometric Mapping of Linker Histone H1 Variants Reveals Multiple Acetylations, Methylations, and Phosphorylation as Well as Differences between Cell Culture and Tissue. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 72-87.	3.8	205
20	Proteasome machinery is instrumental in a common gain-of-function program of the p53 missense mutants in cancer. <i>Nature Cell Biology</i> , 2016, 18, 897-909.	10.3	205
21	Screening for N-glycosylated proteins by liquid chromatography mass spectrometry. <i>Proteomics</i> , 2004, 4, 454-465.	2.2	185
22	Quantitative Evaluation of Filter Aided Sample Preparation (FASP) and Multienzyme Digestion FASP Protocols. <i>Analytical Chemistry</i> , 2016, 88, 5438-5443.	6.5	184
23	Multi-enzyme digestion FASP and the "Total Protein Approach"™-based absolute quantification of the <i>Escherichia coli</i> proteome. <i>Journal of Proteomics</i> , 2014, 109, 322-331.	2.4	179
24	Comparison of ultrafiltration units for proteomic and N-glycoproteomic analysis by the filter-aided sample preparation method. <i>Analytical Biochemistry</i> , 2011, 410, 307-309.	2.4	166
25	N <sup>ε</sup> -Formylation of lysine is a widespread post-translational modification of nuclear proteins occurring at residues involved in regulation of chromatin function. <i>Nucleic Acids Research</i> , 2008, 36, 570-577.	14.5	152
26	Proteomic Mapping of Brain Plasma Membrane Proteins. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 402-408.	3.8	147
27	In-depth quantitative analysis and comparison of the human hepatocyte and hepatoma cell line HepG2 proteomes. <i>Journal of Proteomics</i> , 2016, 136, 234-247.	2.4	134
28	Proteomic workflow for analysis of archival formalin-fixed and paraffin-embedded clinical samples to a depth of 10 <sup>4</sup> proteins. <i>Proteomics - Clinical Applications</i> , 2013, 7, 225-233.	1.6	131
29	Variability in Mass Spectrometry-based Quantification of Clinically Relevant Drug Transporters and Drug Metabolizing Enzymes. <i>Molecular Pharmaceutics</i> , 2017, 14, 3142-3151.	4.6	102
30	Hepatic Uptake of Atorvastatin: Influence of Variability in Transporter Expression on Uptake Clearance and Drug-Drug Interactions. <i>Drug Metabolism and Disposition</i> , 2014, 42, 1210-1218.	3.3	98
31	Selective Roles of Vertebrate PCF11 in Premature and Full-Length Transcript Termination. <i>Molecular Cell</i> , 2019, 74, 158-172.e9.	9.7	95
32	Comparative Proteomic Analysis of Human Liver Tissue and Isolated Hepatocytes with a Focus on Proteins Determining Drug Exposure. <i>Journal of Proteome Research</i> , 2015, 14, 3305-3314.	3.7	92
33	HysTag™ A Novel Proteomic Quantification Tool Applied to Differential Display Analysis of Membrane Proteins From Distinct Areas of Mouse Brain. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 82-92.	3.8	88
34	A dual role of linker histone H1.4 Lys 34 acetylation in transcriptional activation. <i>Genes and Development</i> , 2012, 26, 797-802.	5.9	84
35	Analysis of the Mouse Liver Proteome Using Advanced Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 2963-2972.	3.7	83
36	Detergent-Based but Gel-Free Method Allows Identification of Several Hundred Membrane Proteins in Single LC-MS Runs. <i>Journal of Proteome Research</i> , 2008, 7, 5028-5032.	3.7	77

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37	Toward a Consensus on Applying Quantitative Liquid Chromatography-Tandem Mass Spectrometry Proteomics in Translational Pharmacology Research: A White Paper. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 525-543.	4.7	77
38	Absolute Proteome Analysis of Colorectal Mucosa, Adenoma, and Cancer Reveals Drastic Changes in Fatty Acid Metabolism and Plasma Membrane Transporters. <i>Journal of Proteome Research</i> , 2015, 14, 4005-4018.	3.7	74
39	<i>Caenorhabditis elegans</i> Has a Phosphoproteome Atypical for Metazoans That Is Enriched in Developmental and Sex Determination Proteins. <i>Journal of Proteome Research</i> , 2009, 8, 4039-4049.	3.7	66
40	Filter-Aided Sample Preparation for Proteome Analysis. <i>Methods in Molecular Biology</i> , 2018, 1841, 3-10.	0.9	62
41	Filter Aided Sample Preparation – A tutorial. <i>Analytica Chimica Acta</i> , 2019, 1090, 23-30.	5.4	61
42	Astrocyte-neuron crosstalk regulates the expression and subcellular localization of carbohydrate metabolism enzymes. <i>Glia</i> , 2015, 63, 328-340.	4.9	59
43	The Proteome of Filter-Grown Caco-2 Cells With a Focus on Proteins Involved in Drug Disposition. <i>Journal of Pharmaceutical Sciences</i> , 2016, 105, 817-827.	3.3	58
44	Comparative Proteomic Profiling of Membrane Proteins in Rat Cerebellum, Spinal Cord, and Sciatic Nerve. <i>Journal of Proteome Research</i> , 2009, 8, 2418-2425.	3.7	57
45	Differential Analysis of Membrane Proteins in Mouse Fore- and Hindbrain Using a Label-Free Approach. <i>Journal of Proteome Research</i> , 2006, 5, 2701-2710.	3.7	56
46	Constitutive Phosphorylation of the Acidic Tails of the High Mobility Group 1 Proteins by Casein Kinase II Alters Their Conformation, Stability, and DNA Binding Specificity. <i>Journal of Biological Chemistry</i> , 1999, 274, 20116-20122.	3.4	56
47	The Impact of High-Fat Diet on Metabolism and Immune Defense in Small Intestine Mucosa. <i>Journal of Proteome Research</i> , 2015, 14, 353-365.	3.7	53
48	Mutant p53 induces Golgi tubulo-vesiculation driving a prometastatic secretome. <i>Nature Communications</i> , 2020, 11, 3945.	12.8	52
49	A Proteomics Approach to the Protein Normalization Problem: Selection of Unvarying Proteins for MS-Based Proteomics and Western Blotting. <i>Journal of Proteome Research</i> , 2016, 15, 2321-2326.	3.7	51
50	Aging-associated changes in hippocampal glycogen metabolism in mice. Evidence for and against astrocyte-neuron lactate shuttle. <i>Glia</i> , 2018, 66, 1481-1495.	4.9	51
51	Proteomic Sample Preparation from Formalin Fixed and Paraffin Embedded Tissue. <i>Journal of Visualized Experiments</i> , 2013, , .	0.3	44
52	Constitutive and dynamic phosphorylation and acetylation sites on NUCKS, a hypermodified nuclear protein, studied by quantitative proteomics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 710-718.	2.6	43
53	Reply to “Spin filter”-based sample preparation for shotgun proteomics. <i>Nature Methods</i> , 2009, 6, 785-786.	19.0	42
54	Quantitative proteomic profiling of membrane proteins from the mouse brain cortex, hippocampus, and cerebellum using the HysTag reagent: Mapping of neurotransmitter receptors and ion channels. <i>Brain Research</i> , 2007, 1134, 95-106.	2.2	41

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55	Translating Proteomic Into Functional Data: An High Mobility Group A1 (HMGA1) Proteomic Signature Has Prognostic Value in Breast Cancer. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 109-123.	3.8	41
56	Global variability analysis of mRNA and protein concentrations across and within human tissues. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz010.	3.2	40
57	Absolute Quantitative Profiling of the Key Metabolic Pathways in Slow and Fast Skeletal Muscle. <i>Journal of Proteome Research</i> , 2015, 14, 1400-1411.	3.7	38
58	Novel Roles of <i>Caenorhabditis elegans</i> Heterochromatin Protein HP1 and Linker Histone in the Regulation of Innate Immune Gene Expression. <i>Molecular and Cellular Biology</i> , 2012, 32, 251-265.	2.3	34
59	Quantitative analysis of the <i>Escherichia coli</i> proteome. <i>Data in Brief</i> , 2014, 1, 7-11.	1.0	34
60	Integrating Proteomics and Enzyme Kinetics Reveals Tissue-Specific Types of the Glycolytic and Gluconeogenic Pathways. <i>Journal of Proteome Research</i> , 2015, 14, 3263-3273.	3.7	34
61	Cdc2 and Mitogen-activated Protein Kinases Modulate DNA Binding Properties of the Putative Transcriptional Regulator <i>Chironomus</i> High Mobility Group Protein I. <i>Journal of Biological Chemistry</i> , 1997, 272, 27476-27483.	3.4	33
62	High mobility group proteins cHMG 1a, cHMG 1b, and cHMGI are distinctly distributed in chromosomes and differentially expressed during ecdysone dependent cell differentiation. <i>Chromosoma</i> , 1997, 105, 369-379.	2.2	33
63	Quantifying the impact of transporters on cellular drug permeability. <i>Trends in Pharmacological Sciences</i> , 2015, 36, 255-262.	8.7	32
64	Immunohistochemical and Proteomic Evaluation of Nuclear Ubiquitous Casein and Cyclin-Dependent Kinases Substrate in Invasive Ductal Carcinoma of the Breast. <i>Journal of Biomedicine and Biotechnology</i> , 2009, 2009, 1-8.	3.0	31
65	Cell-type-resolved proteomic analysis of the human liver. <i>Liver International</i> , 2020, 40, 1770-1780.	3.9	31
66	Distinct Organization of DNA Complexes of Various HMGI/Y Family Proteins and Their Modulation upon Mitotic Phosphorylation. <i>Journal of Biological Chemistry</i> , 2001, 276, 1984-1992.	3.4	26
67	Subcellular fractionation of human liver reveals limits in global proteomic quantification from isolated fractions. <i>Analytical Biochemistry</i> , 2016, 509, 82-88.	2.4	25
68	Intracellular Drug Bioavailability: Effect of Neutral Lipids and Phospholipids. <i>Molecular Pharmaceutics</i> , 2018, 15, 2224-2233.	4.6	25
69	Differences in plasma fibrin clot composition in patients with thrombotic antiphospholipid syndrome compared with venous thromboembolism. <i>Scientific Reports</i> , 2018, 8, 17301.	3.3	25
70	Mapping of Lysine Monomethylation of Linker Histones in Human Breast and Its Cancer. <i>Journal of Proteome Research</i> , 2009, 8, 4207-4215.	3.7	24
71	Optimization of quantitative proteomic analysis of clots generated from plasma of patients with venous thromboembolism. <i>Clinical Proteomics</i> , 2017, 14, 38.	2.1	24
72	Plasma fibrin clot proteomics in healthy subjects: Relation to clot permeability and lysis time. <i>Journal of Proteomics</i> , 2019, 208, 103487.	2.4	24

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73	HMGA1 Modulates Gene Transcription Sustaining a Tumor Signalling Pathway Acting on the Epigenetic Status of Triple-Negative Breast Cancer Cells. <i>Cancers</i> , 2019, 11, 1105.	3.7	23
74	Comparison of Proteome Composition of Serum Enriched in Extracellular Vesicles Isolated from Polycythemia Vera Patients and Healthy Controls. <i>Proteomes</i> , 2019, 7, 20.	3.5	23
75	A simple approach for restoration of differentiation and function in cryopreserved human hepatocytes. <i>Archives of Toxicology</i> , 2019, 93, 819-829.	4.2	22
76	Consecutive Steps of Phosphorylation Affect Conformation and DNA Binding of the Chironomus High Mobility Group A Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 26012-26021.	3.4	21
77	In-Depth Quantitative Proteomic Analysis of Trophozoites and Pseudocysts of <i>Trichomonas vaginalis</i> . <i>Journal of Proteome Research</i> , 2018, 17, 3704-3718.	3.7	21
78	Multiple-Enzyme-Digestion Strategy Improves Accuracy and Sensitivity of Label- and Standard-Free Absolute Quantification to a Level That Is Achievable by Analysis with Stable Isotope-Labeled Standard Spiking. <i>Journal of Proteome Research</i> , 2018, 18, 217-224.	3.7	21
79	Beyond Linker Histones and High Mobility Group Proteins: A Global Profiling of Perchloric Acid Soluble Proteins. <i>Journal of Proteome Research</i> , 2006, 5, 925-934.	3.7	19
80	Ultrasonic-Based Filter Aided Sample Preparation as the General Method to Sample Preparation in Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 9164-9171.	6.5	19
81	Alterations in titer and distribution of high mobility group proteins during embryonic development of <i>Drosophila melanogaster</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2000, 1475, 99-108.	2.4	18
82	Homogenous Phase Enrichment of Cysteine-Containing Peptides for Improved Proteome Coverage. <i>Analytical Chemistry</i> , 2015, 87, 6861-6867.	6.5	18
83	Tools for phospho- and glycoproteomics of plasma membranes. <i>Amino Acids</i> , 2011, 41, 223-233.	2.7	17
84	Restoration of type 1 iodothyronine deiodinase expression in renal cancer cells downregulates oncoproteins and affects key metabolic pathways as well as anti-oxidative system. <i>PLoS ONE</i> , 2017, 12, e0190179.	2.5	17
85	Absolute protein quantification allows differentiation of cell-specific metabolic routes and functions. <i>Proteomics</i> , 2015, 15, 1316-1325.	2.2	16
86	Shotgun proteomic analyses without alkylation of cysteine. <i>Analytica Chimica Acta</i> , 2020, 1100, 131-137.	5.4	16
87	Mass Spectrometry-Based Proteomics: Principles, Perspectives, and Challenges. <i>Archives of Pathology and Laboratory Medicine</i> , 2008, 132, 1566-1569.	2.5	16
88	Drug Disposition Protein Quantification in Matched Human Jejunum and Liver From Donors With Obesity. <i>Clinical Pharmacology and Therapeutics</i> , 2022, 111, 1142-1154.	4.7	16
89	Proteomics-Informed Prediction of Rosuvastatin Plasma Profiles in Patients With a Wide Range of Body Weight. <i>Clinical Pharmacology and Therapeutics</i> , 2021, 109, 762-771.	4.7	15
90	Targeting of Protein Kinase CK2 in Acute Myeloid Leukemia Cells Using the Clinical-Grade Synthetic-Peptide CIGB-300. <i>Biomedicines</i> , 2021, 9, 766.	3.2	15

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91	Global quantitative TPA-based proteomics of mouse brain structures reveals significant alterations in expression of proteins involved in neuronal plasticity during aging. <i>Aging</i> , 2018, 10, 1682-1697.	3.1	15
92	Plasma fibrin clot proteomics in patients with acute pulmonary embolism: Association with clot properties. <i>Journal of Proteomics</i> , 2020, 229, 103946.	2.4	14
93	Staurosporine and NEM mainly impair WNK-SPAK/OSR1 mediated phosphorylation of KCC2 and NKCC1. <i>PLoS ONE</i> , 2020, 15, e0232967.	2.5	14
94	Evidence for Insertional RNA Editing in Humans. <i>Current Biology</i> , 2008, 18, 1760-1765.	3.9	12
95	Respiromics – An integrative analysis linking mitochondrial bioenergetics to molecular signatures. <i>Molecular Metabolism</i> , 2018, 9, 4-14.	6.5	12
96	Proteomics Unveils Fibroblast–Cardiomyocyte Lactate Shuttle and Hexokinase Paradox in Mouse Muscles. <i>Journal of Proteome Research</i> , 2016, 15, 2479-2490.	3.7	11
97	Identification and characterization of a novel ubiquitous nucleolar protein –NARR™ encoded by a gene overlapping the rab34 oncogene. <i>Nucleic Acids Research</i> , 2011, 39, 7103-7113.	14.5	10
98	In-depth quantitative proteomics uncovers specie-specific metabolic programs in <i>Leishmania (Viannia)</i> species. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008509.	3.0	10
99	Absolute Proteome Analysis of Hippocampus, Cortex and Cerebellum in Aged and Young Mice Reveals Changes in Energy Metabolism. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6188.	4.1	10
100	Insulin/IGF1-PI3K-dependent nucleolar localization of a glycolytic enzyme - phosphoglycerate mutase 2, is necessary for proper structure of nucleolus and RNA synthesis. <i>Oncotarget</i> , 2015, 6, 17237-17250.	1.8	10
101	Proteomic-Based Analysis of Hypoxia- and Physioxia-Responsive Proteins and Pathways in Diffuse Large B-Cell Lymphoma. <i>Cells</i> , 2021, 10, 2025.	4.1	8
102	Snap-heated freeze-free preservation and processing of the urine proteome using the combination of stabilizer-based technology and filter aided sample preparation. <i>Analytica Chimica Acta</i> , 2019, 1076, 82-90.	5.4	7
103	Phosphoproteomic Landscape of AML Cells Treated with the ATP-Competitive CK2 Inhibitor CX-4945. <i>Cells</i> , 2021, 10, 338.	4.1	7
104	Linking FOXO3, NCOA3, and TCF7L2 to Ras pathway phenotypes through a genome-wide forward genetic screen in human colorectal cancer cells. <i>Genome Medicine</i> , 2018, 10, 2.	8.2	6
105	Nitric Oxide Resistance in <i>Leishmania (Viannia) braziliensis</i> Involves Regulation of Glucose Consumption, Glutathione Metabolism and Abundance of Pentose Phosphate Pathway Enzymes. <i>Antioxidants</i> , 2022, 11, 277.	5.1	6
106	Pattern of Melanotransferrin Expression in Human Colorectal Tissues: An Immunohistochemical Study on Potential Clinical Application. <i>Anticancer Research</i> , 2015, 35, 6551-61.	1.1	6
107	Datasets: Sensitivity and protein digestion course of proteomic Filter Aided Sample Preparation. <i>Data in Brief</i> , 2019, 26, 104530.	1.0	5
108	Large-Scale Proteomic Analysis of Follicular Lymphoma Reveals Extensive Remodeling of Cell Adhesion Pathway and Identifies Hub Proteins Related to the Lymphomagenesis. <i>Cancers</i> , 2021, 13, 630.	3.7	5

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109	Compatibility of Distinct Label-Free Proteomic Workflows in Absolute Quantification of Proteins Linked to the Oocyte Quality in Human Follicular Fluid. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7415.	4.1	5
110	Absolute quantitative proteomics using the total protein approach to identify novel clinical immunohistochemical markers in renal neoplasms. <i>BMC Medicine</i> , 2021, 19, 196.	5.5	5
111	Label-Free Quantitative Analysis of Mitochondrial Proteomes Using the Multienzyme Digestion-Filter Aided Sample Preparation (MED-FASP) and "Total Protein Approach". <i>Methods in Molecular Biology</i> , 2017, 1567, 69-77.	0.9	4
112	CIGB-300-Regulated Proteome Reveals Common and Tailored Response Patterns of AML Cells to CK2 Inhibition. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 834814.	3.5	4
113	Glycation and acetylation sites on fibrinogen in plasma fibrin clot of patients with type 2 diabetes: Effects of low-dose acetylsalicylic acid. <i>Thrombosis Research</i> , 2021, 198, 93-98.	1.7	3
114	In-Depth Quantitative Proteomics Characterization of In Vitro Selected Miltefosine Resistance in <i>Leishmania infantum</i> . <i>Proteomes</i> , 2022, 10, 10.	3.5	2
115	Global Proteome Changes in Liver Tissue 6 Weeks after FOLFOX Treatment of Colorectal Cancer Liver Metastases. <i>Proteomes</i> , 2016, 4, 30.	3.5	1
116	Dilemmas With Absolute Quantification of Pharmacologically Relevant Proteins Using Mass Spectrometry. <i>Journal of Pharmaceutical Sciences</i> , 2021, 110, 17-21.	3.3	1
117	Gel electrophoresis/electroelution sorting fractionator combined with filter-aided sample preparation for deep proteomic analysis. <i>Journal of Separation Science</i> , 2022, 45, 1784-1796.	2.5	1
118	Proteomes: A New Proteomic Journal. <i>Proteomes</i> , 2013, 1, 1-2.	3.5	0
119	Title is missing!. , 2020, 14, e0008509.		0
120	Title is missing!. , 2020, 14, e0008509.		0
121	Title is missing!. , 2020, 14, e0008509.		0
122	Title is missing!. , 2020, 14, e0008509.		0