

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	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
2	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
3	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
4	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
5	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
6	Dilemmas With Absolute Quantification of Pharmacologically Relevant Proteins Using Mass Spectrometry. <i>Journal of Pharmaceutical Sciences</i> , 2021, 110, 17-21.	3.3	1
7	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
8	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
9	Phosphoproteomic Landscape of AML Cells Treated with the ATP-Competitive CK2 Inhibitor CX-4945. <i>Cells</i> , 2021, 10, 338.	4.1	7
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	Shotgun proteomic analyses without alkylation of cysteine. <i>Analytica Chimica Acta</i> , 2020, 1100, 131-137.	5.4	16
18	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

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19	Mutant p53 induces Golgi tubulo-vesiculation driving a prometastatic secretome. <i>Nature Communications</i> , 2020, 11, 3945.	12.8	52
20	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
21	Staurosporine and NEM mainly impair WNK-SPAK/OSR1 mediated phosphorylation of KCC2 and NKCC1. <i>PLoS ONE</i> , 2020, 15, e0232967.	2.5	14
22	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
23	Cell-type-resolved proteomic analysis of the human liver. <i>Liver International</i> , 2020, 40, 1770-1780.	3.9	31
24	Title is missing!. , 2020, 14, e0008509.		0
25	Title is missing!. , 2020, 14, e0008509.		0
26	Title is missing!. , 2020, 14, e0008509.		0
27	Title is missing!. , 2020, 14, e0008509.		0
28	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
29	Filter Aided Sample Preparation " A tutorial. <i>Analytica Chimica Acta</i> , 2019, 1090, 23-30.	5.4	61
30	Datasets: Sensitivity and protein digestion course of proteomic Filter Aided Sample Preparation. <i>Data in Brief</i> , 2019, 26, 104530.	1.0	5
31	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
32	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
33	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
34	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
35	Selective Roles of Vertebrate PCF11 in Premature and Full-Length Transcript Termination. <i>Molecular Cell</i> , 2019, 74, 158-172.e9.	9.7	95
36	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

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37	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
38	Respiromics – An integrative analysis linking mitochondrial bioenergetics to molecular signatures. <i>Molecular Metabolism</i> , 2018, 9, 4-14.	6.5	12
39	Intracellular Drug Bioavailability: Effect of Neutral Lipids and Phospholipids. <i>Molecular Pharmaceutics</i> , 2018, 15, 2224-2233.	4.6	25
40	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
41	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
42	Filter-Aided Sample Preparation for Proteome Analysis. <i>Methods in Molecular Biology</i> , 2018, 1841, 3-10.	0.9	62
43	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
44	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
45	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
46	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
47	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
48	Quantitative Analysis of Human Red Blood Cell Proteome. <i>Journal of Proteome Research</i> , 2017, 16, 2752-2761.	3.7	216
49	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
50	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
51	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
52	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
53	Quantitative Evaluation of Filter Aided Sample Preparation (FASP) and Multienzyme Digestion FASP Protocols. <i>Analytical Chemistry</i> , 2016, 88, 5438-5443.	6.5	184
54	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

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55	Proteomics Unveils Fibroblastâ€“Cardiomyocyte Lactate Shuttle and Hexokinase Paradox in Mouse Muscles. <i>Journal of Proteome Research</i> , 2016, 15, 2479-2490.	3.7	11
56	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
57	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
58	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
59	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
60	Homogenous Phase Enrichment of Cysteine-Containing Peptides for Improved Proteome Coverage. <i>Analytical Chemistry</i> , 2015, 87, 6861-6867.	6.5	18
61	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
62	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
63	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
64	Absolute protein quantification allows differentiation of cell-specific metabolic routes and functions. <i>Proteomics</i> , 2015, 15, 1316-1325.	2.2	16
65	Quantifying the impact of transporters on cellular drug permeability. <i>Trends in Pharmacological Sciences</i> , 2015, 36, 255-262.	8.7	32
66	Fast and Sensitive Total Protein and Peptide Assays for Proteomic Analysis. <i>Analytical Chemistry</i> , 2015, 87, 4110-4116.	6.5	236
67	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
68	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
69	Astrocyteâ€“neuron crosstalk regulates the expression and subcellular localization of carbohydrate metabolism enzymes. <i>Glia</i> , 2015, 63, 328-340.	4.9	59
70	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
71	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
72	Ultra-deep 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

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73	Hepatic Uptake of Atorvastatin: Influence of Variability in Transporter Expression on Uptake Clearance and Drug-Drug Interactions<sup />. Drug Metabolism and Disposition, 2014, 42, 1210-1218.	3.3	98
74	A â€œProteomic Rulerâ€ for Protein Copy Number and Concentration Estimation without Spike-in Standards. Molecular and Cellular Proteomics, 2014, 13, 3497-3506.	3.8	530
75	Quantitative analysis of the Escherichia coli proteome. Data in Brief, 2014, 1, 7-11.	1.0	34
76	Multi-enzyme digestion FASP and the â€Total Protein Approachâ€™-based absolute quantification of the Escherichia coli proteome. Journal of Proteomics, 2014, 109, 322-331.	2.4	179
77	Proteomic workflow for analysis of archival formalinâ€fixed and paraffinâ€embedded clinical samples to a depth of 10â€™000 proteins. Proteomics - Clinical Applications, 2013, 7, 225-233.	1.6	131
78	Proteomic Sample Preparation from Formalin Fixed and Paraffin Embedded Tissue. Journal of Visualized Experiments, 2013, , .	0.3	44
79	Proteomes: A New Proteomic Journal. Proteomes, 2013, 1, 1-2.	3.5	0
80	Novel Roles of Caenorhabditis elegans Heterochromatin Protein HP1 and Linker Histone in the Regulation of Innate Immune Gene Expression. Molecular and Cellular Biology, 2012, 32, 251-265.	2.3	34
81	Consecutive Proteolytic Digestion in an Enzyme Reactor Increases Depth of Proteomic and Phosphoproteomic Analysis. Analytical Chemistry, 2012, 84, 2631-2637.	6.5	278
82	Extensive quantitative remodeling of the proteome between normal colon tissue and adenocarcinoma. Molecular Systems Biology, 2012, 8, 611.	7.2	221
83	Mapping N-Glycosylation Sites across Seven Evolutionarily Distant Species Reveals a Divergent Substrate Proteome Despite a Common Core Machinery. Molecular Cell, 2012, 46, 542-548.	9.7	238
84	Classification of Inhibitors of Hepatic Organic Anion Transporting Polypeptides (OATPs): Influence of Protein Expression on Drugâ€Drug Interactions. Journal of Medicinal Chemistry, 2012, 55, 4740-4763.	6.4	299
85	A dual role of linker histone H1.4 Lys 34 acetylation in transcriptional activation. Genes and Development, 2012, 26, 797-802.	5.9	84
86	Deep proteome and transcriptome mapping of a human cancer cell line. Molecular Systems Biology, 2011, 7, 548.	7.2	878
87	High Recovery FASP Applied to the Proteomic Analysis of Microdissected Formalin Fixed Paraffin Embedded Cancer Tissues Retrieves Known Colon Cancer Markers. Journal of Proteome Research, 2011, 10, 3040-3049.	3.7	281
88	Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. Nature Protocols, 2011, 6, 147-157.	12.0	265
89	Tools for phospho- and glycoproteomics of plasma membranes. Amino Acids, 2011, 41, 223-233.	2.7	17
90	Comparison of ultrafiltration units for proteomic and N-glycoproteomic analysis by the filter-aided sample preparation method. Analytical Biochemistry, 2011, 410, 307-309.	2.4	166

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91	Identification and characterization of a novel ubiquitous nucleolar protein $\hat{\text{NARR}}^{\text{TM}}$ encoded by a gene overlapping the rab34 oncogene. <i>Nucleic Acids Research</i> , 2011, 39, 7103-7113.	14.5	10
92	Super-SILAC mix for quantitative proteomics of human tumor tissue. <i>Nature Methods</i> , 2010, 7, 383-385.	19.0	480
93	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
94	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
95	Precision Mapping of an In Vivo N-Glycoproteome Reveals Rigid Topological and Sequence Constraints. <i>Cell</i> , 2010, 141, 897-907.	28.9	789
96	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
97	Universal sample preparation method for proteome analysis. <i>Nature Methods</i> , 2009, 6, 359-362.	19.0	6,678
98	Reply to $\hat{\text{Spin filter}}$ -based sample preparation for shotgun proteomics. <i>Nature Methods</i> , 2009, 6, 785-786.	19.0	42
99	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
100	<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
101	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
102	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
103	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
104	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
105	Evidence for Insertional RNA Editing in Humans. <i>Current Biology</i> , 2008, 18, 1760-1765.	3.9	12
106	N $\hat{\mu}$ -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
107	Mass Spectrometry-Based Proteomics: Principles, Perspectives, and Challenges. <i>Archives of Pathology and Laboratory Medicine</i> , 2008, 132, 1566-1569.	2.5	16
108	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

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109	Analysis of the Mouse Liver Proteome Using Advanced Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 2963-2972.	3.7	83
110	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
111	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
112	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
113	Proteomic Mapping of Brain Plasma Membrane Proteins. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 402-408.	3.8	147
114	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
115	Screening for N-glycosylated proteins by liquid chromatography mass spectrometry. <i>Proteomics</i> , 2004, 4, 454-465.	2.2	185
116	Integrated Analysis of Protein Composition, Tissue Diversity, and Gene Regulation in Mouse Mitochondria. <i>Cell</i> , 2003, 115, 629-640.	28.9	815
117	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
118	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
119	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
120	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
121	Cdc2 and Mitogen-activated Protein Kinases Modulate DNA Binding Properties of the Putative Transcriptional Regulator Chironomus High Mobility Group Protein I. <i>Journal of Biological Chemistry</i> , 1997, 272, 27476-27483.	3.4	33
122	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