

Ren P Zahedi

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

151
papers

7,487
citations

43
h-index

83
g-index

161
ext. papers

8,706
ext. citations

7.3
avg, IF

5.86
L-index

#	Paper	IF	Citations
151	The proteome of <i>Saccharomyces cerevisiae</i> mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 13207-12	11.5	753
150	The first comprehensive and quantitative analysis of human platelet protein composition allows the comparative analysis of structural and functional pathways. <i>Blood</i> , 2012 , 120, e73-82	2.2	485
149	Global analysis of the mitochondrial N-proteome identifies a processing peptidase critical for protein stability. <i>Cell</i> , 2009 , 139, 428-39	56.2	351
148	PeptideShaker enables reanalysis of MS-derived proteomics data sets. <i>Nature Biotechnology</i> , 2015 , 33, 22-4	44.5	344
147	Toward the complete yeast mitochondrial proteome: multidimensional separation techniques for mitochondrial proteomics. <i>Journal of Proteome Research</i> , 2006 , 5, 1543-54	5.6	311
146	The protein import machinery of mitochondria-a regulatory hub in metabolism, stress, and disease. <i>Cell Metabolism</i> , 2014 , 19, 357-72	24.6	257
145	Systematic and quantitative comparison of digest efficiency and specificity reveals the impact of trypsin quality on MS-based proteomics. <i>Journal of Proteomics</i> , 2012 , 75, 1454-62	3.9	194
144	Regulation of mitochondrial protein import by cytosolic kinases. <i>Cell</i> , 2011 , 144, 227-39	56.2	186
143	The next level of complexity: crosstalk of posttranslational modifications. <i>Proteomics</i> , 2014 , 14, 513-24	4.8	176
142	Proteomic analysis of the yeast mitochondrial outer membrane reveals accumulation of a subclass of preproteins. <i>Molecular Biology of the Cell</i> , 2006 , 17, 1436-50	3.5	174
141	Phosphoproteome of resting human platelets. <i>Journal of Proteome Research</i> , 2008 , 7, 526-34	5.6	140
140	Amyloid- β peptide induces mitochondrial dysfunction by inhibition of preprotein maturation. <i>Cell Metabolism</i> , 2014 , 20, 662-9	24.6	137
139	The human platelet membrane proteome reveals several new potential membrane proteins. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1754-61	7.6	129
138	Profiling phosphoproteins of yeast mitochondria reveals a role of phosphorylation in assembly of the ATP synthase. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1896-906	7.6	124
137	Current strategies and findings in clinically relevant post-translational modification-specific proteomics. <i>Expert Review of Proteomics</i> , 2015 , 12, 235-53	4.2	123
136	Intermembrane space proteome of yeast mitochondria. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1840-52	12.0	120
135	Platelet membrane proteomics: a novel repository for functional research. <i>Blood</i> , 2009 , 114, e10-9	2.2	106

134	Protein carbamylation: in vivo modification or in vitro artefact?. <i>Proteomics</i> , 2013 , 13, 941-4	4.8	98
133	Dual function of Sdh3 in the respiratory chain and TIM22 protein translocase of the mitochondrial inner membrane. <i>Molecular Cell</i> , 2011 , 44, 811-8	17.6	96
132	Catch me if you can: mass spectrometry-based phosphoproteomics and quantification strategies. <i>Proteomics</i> , 2011 , 11, 554-70	4.8	84
131	Landscape of submitochondrial protein distribution. <i>Nature Communications</i> , 2017 , 8, 290	17.4	82
130	Targeting Drug Resistance in EGFR with Covalent Inhibitors: A Structure-Based Design Approach. <i>Journal of Medicinal Chemistry</i> , 2015 , 58, 6844-63	8.3	76
129	What can proteomics tell us about platelets?. <i>Circulation Research</i> , 2014 , 114, 1204-19	15.7	76
128	PARL mediates Smac proteolytic maturation in mitochondria to promote apoptosis. <i>Nature Cell Biology</i> , 2017 , 19, 318-328	23.4	75
127	Novel highly sensitive, specific, and straightforward strategy for comprehensive N-terminal proteomics reveals unknown substrates of the mitochondrial peptidase Icp55. <i>Journal of Proteome Research</i> , 2013 , 12, 3823-30	5.6	72
126	Time-resolved characterization of cAMP/PKA-dependent signaling reveals that platelet inhibition is a concerted process involving multiple signaling pathways. <i>Blood</i> , 2014 , 123, e1-e10	2.2	71
125	Enhanced N-glycosylation site analysis of sialoglycopeptides by strong cation exchange prefractionation applied to platelet plasma membranes. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1933-41	7.6	70
124	Temporal quantitative phosphoproteomics of ADP stimulation reveals novel central nodes in platelet activation and inhibition. <i>Blood</i> , 2017 , 129, e1-e12	2.2	68
123	Simultaneous Metabolite, Protein, Lipid Extraction (SIMPLEX): A Combinatorial Multimolecular Omics Approach for Systems Biology. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1453-66	7.6	65
122	Two-dimensional benzyldimethyl-n-hexadecylammonium chloride/SDS-PAGE for membrane proteomics. <i>Proteomics</i> , 2005 , 5, 3581-8	4.8	64
121	Why phosphoproteomics is still a challenge. <i>Molecular BioSystems</i> , 2015 , 11, 1487-93		63
120	The mTOR and PP2A Pathways Regulate PHD2 Phosphorylation to Fine-Tune HIF1 α Levels and Colorectal Cancer Cell Survival under Hypoxia. <i>Cell Reports</i> , 2017 , 18, 1699-1712	10.6	60
119	An improved workflow for quantitative N-terminal charge-based fractional diagonal chromatography (ChaFRADIC) to study proteolytic events in <i>Arabidopsis thaliana</i> . <i>Proteomics</i> , 2015 , 15, 2458-69	4.8	59
118	Gene network activity in cultivated primary hepatocytes is highly similar to diseased mammalian liver tissue. <i>Archives of Toxicology</i> , 2016 , 90, 2513-29	5.8	57
117	Protein lipid modifications--More than just a greasy ballast. <i>Proteomics</i> , 2016 , 16, 759-82	4.8	54

116	Effects of the NO/soluble guanylate cyclase/cGMP system on the functions of human platelets. <i>Nitric Oxide - Biology and Chemistry</i> , 2018 , 76, 71-80	5	49
115	Impact of digestion conditions on phosphoproteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 2761-70	5.6	49
114	iTRAQ protein quantification: a quality-controlled workflow. <i>Proteomics</i> , 2011 , 11, 1125-34	4.8	47
113	Myopathy in Marinesco-Sjögren syndrome links endoplasmic reticulum chaperone dysfunction to nuclear envelope pathology. <i>Acta Neuropathologica</i> , 2014 , 127, 761-77	14.3	46
112	An alternative NFAT-activation pathway mediated by IL-7 is critical for early thymocyte development. <i>Nature Immunology</i> , 2013 , 14, 127-35	19.1	45
111	Cytomegalovirus downregulates IRE1 to repress the unfolded protein response. <i>PLoS Pathogens</i> , 2013 , 9, e1003544	7.6	44
110	D-score: a search engine independent MD-score. <i>Proteomics</i> , 2013 , 13, 1036-41	4.8	44
109	Detecting post-translational modification signatures as potential biomarkers in clinical mass spectrometry. <i>Expert Review of Proteomics</i> , 2018 , 15, 515-535	4.2	43
108	Proteomic and metabolomic analyses of mitochondrial complex I-deficient mouse model generated by spontaneous B2 short interspersed nuclear element (SINE) insertion into NADH dehydrogenase (ubiquinone) Fe-S protein 4 (Ndufs4) gene. <i>Journal of Biological Chemistry</i> , 2012 , 287, 20652-63	5.4	42
107	Drugging the catalytically inactive state of RET kinase in RET-rearranged tumors. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	41
106	Mutations in INPP5K, Encoding a Phosphoinositide 5-Phosphatase, Cause Congenital Muscular Dystrophy with Cataracts and Mild Cognitive Impairment. <i>American Journal of Human Genetics</i> , 2017 , 100, 523-536	11	40
105	Identification of novel in vivo phosphorylation sites of the human proapoptotic protein BAD: pore-forming activity of BAD is regulated by phosphorylation. <i>Journal of Biological Chemistry</i> , 2009 , 284, 28004-28020	5.4	39
104	Insight into the Inhibition of Drug-Resistant Mutants of the Receptor Tyrosine Kinase EGFR. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 10909-12	16.4	38
103	Identification of cleavage sites and substrate proteins for two mitochondrial intermediate peptidases in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2015 , 66, 2691-708	7	37
102	Phosphorylation of CalDAG-GEFI by protein kinase A prevents Rap1b activation. <i>Journal of Thrombosis and Haemostasis</i> , 2013 , 11, 1574-82	15.4	37
101	Peptide identification quality control. <i>Proteomics</i> , 2011 , 11, 2105-14	4.8	35
100	Proteome-wide detection of S-nitrosylation targets and motifs using bioorthogonal cleavable-linker-based enrichment and switch technique. <i>Nature Communications</i> , 2019 , 10, 2195	17.4	34
99	Highly sensitive phosphoproteomics by tailoring solid-phase extraction to electrostatic repulsion-hydrophilic interaction chromatography. <i>Analytical Chemistry</i> , 2015 , 87, 1596-604	7.8	34

98	The FERM protein EPB41L5 regulates actomyosin contractility and focal adhesion formation to maintain the kidney filtration barrier. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E4621-E4630	11.5	33
97	A complex standard for protein identification, designed by evolution. <i>Journal of Proteome Research</i> , 2012 , 11, 5065-71	5.6	33
96	Targeted and Untargeted Proteomics Approaches in Biomarker Development. <i>Proteomics</i> , 2020 , 20, e190029	4.0	33
95	Phosphoproteomics--more than meets the eye. <i>Electrophoresis</i> , 2013 , 34, 1483-92	3.6	32
94	Glycosylation Site Analysis of Human Platelets by Electrostatic Repulsion Hydrophilic Interaction Chromatography. <i>Clinical Proteomics</i> , 2008 , 4, 25-36	5	32
93	Simple, scalable, and ultrasensitive tip-based identification of protease substrates. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 826-834	7.6	31
92	Combined Quantification of the Global Proteome, Phosphoproteome, and Proteolytic Cleavage to Characterize Altered Platelet Functions in the Human Scott Syndrome. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 3154-3169	7.6	31
91	A Unique Morphological Phenotype in Chemoresistant Triple-Negative Breast Cancer Reveals Metabolic Reprogramming and PLIN4 Expression as a Molecular Vulnerability. <i>Molecular Cancer Research</i> , 2019 , 17, 2492-2507	6.6	31
90	pymzML v2.0: introducing a highly compressed and seekable gzip format. <i>Bioinformatics</i> , 2018 , 34, 2513-2514	2.1	29
89	Homologous desensitization of guanylyl cyclase A, the receptor for atrial natriuretic peptide, is associated with a complex phosphorylation pattern. <i>FEBS Journal</i> , 2010 , 277, 2440-53	5.7	29
88	Analysis of the membrane proteome of canine pancreatic rough microsomes identifies a novel Hsp40, termed ERj7. <i>Proteomics</i> , 2009 , 9, 3463-73	4.8	29
87	Raf kinases mediate the phosphorylation of eukaryotic translation elongation factor 1A and regulate its stability in eukaryotic cells. <i>Cell Death and Disease</i> , 2012 , 3, e276	9.8	29
86	Taking the stock of granule cargo: Platelet releasate proteomics. <i>Platelets</i> , 2017 , 28, 119-128	3.6	28
85	Phosphoproteomics of human platelets: A quest for novel activation pathways. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006 , 1764, 1963-76	4	28
84	Effective Assignment of α ,3/ α ,6-Sialic Acid Isomers by LC-MS/MS-Based Glycoproteomics. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 9320-9324	16.4	27
83	TRPM7 Kinase Controls Calcium Responses in Arterial Thrombosis and Stroke in Mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018 , 38, 344-352	9.4	26
82	The good, the bad, the ugly: validating the mass spectrometric analysis of modified peptides. <i>Proteomics</i> , 2011 , 11, 1099-109	4.8	25
81	Positive regulation of A-RAF by phosphorylation of isoform-specific hinge segment and identification of novel phosphorylation sites. <i>Journal of Biological Chemistry</i> , 2008 , 283, 27239-54	5.4	25

80	Hypoxia-induced p38 MAPK activation reduces Mcl-1 expression and facilitates sensitivity towards BH3 mimetics in chronic lymphocytic leukemia. <i>Leukemia</i> , 2015 , 29, 981-4	10.7	24
79	Comparative proteomic analysis of biofilm and planktonic cells of <i>Neisseria meningitidis</i> . <i>Proteomics</i> , 2010 , 10, 4512-21	4.8	24
78	Cellular Signature of SIL1 Depletion: Disease Pathogenesis due to Alterations in Protein Composition Beyond the ER Machinery. <i>Molecular Neurobiology</i> , 2016 , 53, 5527-41	6.2	23
77	Enrichment of Cross-Linked Peptides Using Charge-Based Fractional Diagonal Chromatography (ChaFRADIC). <i>Journal of Proteome Research</i> , 2017 , 16, 459-469	5.6	23
76	PKA-RII subunit phosphorylation precedes activation by cAMP and regulates activity termination. <i>Journal of Cell Biology</i> , 2018 , 217, 2167-2184	7.3	23
75	Integral quantification accuracy estimation for reporter ion-based quantitative proteomics (iQuARI). <i>Journal of Proteome Research</i> , 2012 , 11, 5072-80	5.6	22
74	Recent advances in yeast organelle and membrane proteomics. <i>Proteomics</i> , 2009 , 9, 4731-43	4.8	22
73	High spatial and temporal resolution cell manipulation techniques in microchannels. <i>Analyst, The</i> , 2016 , 141, 1888-905	5	21
72	Revealing phosphoproteins playing role in tobacco pollen activated in vitro. <i>Proteomics</i> , 2012 , 12, 3229-508	5.08	21
71	Omics-based responses induced by bosentan in human hepatoma HepaRG cell cultures. <i>Archives of Toxicology</i> , 2018 , 92, 1939-1952	5.8	21
70	Multidimensional electrostatic repulsion-hydrophilic interaction chromatography (ERLIC) for quantitative analysis of the proteome and phosphoproteome in clinical and biomedical research. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 460-8	4	20
69	Assembly of nuclear pore complexes mediated by major vault protein. <i>Journal of Cell Science</i> , 2009 , 122, 780-6	5.3	19
68	Phosphoproteomics Profiling of Tobacco Mature Pollen and Pollen Activated in vitro. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1338-50	7.6	19
67	Multi-OMICS: a critical technical perspective on integrative lipidomics approaches. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2017 , 1862, 808-811	5	18
66	Quantitative Profiling for Substrates of the Mitochondrial Presequence Processing Protease Reveals a Set of Nonsubstrate Proteins Increased upon Proteotoxic Stress. <i>Journal of Proteome Research</i> , 2015 , 14, 4550-63	5.6	18
65	Response: platelet transcriptome and proteome--relation rather than correlation. <i>Blood</i> , 2013 , 121, 5257-8	5.8	18
64	The proteome of baker's yeast mitochondria. <i>Mitochondrion</i> , 2017 , 33, 15-21	4.9	18
63	Mass spectrometry-based protein analysis to unravel the tissue pathophysiology in Duchenne muscular dystrophy. <i>Proteomics - Clinical Applications</i> , 2018 , 12, 1700071	3.1	17

62	Shedding light on black boxes in protein identification. <i>Proteomics</i> , 2014 , 14, 1001-5	4.8	17
61	Alterations of the platelet proteome in type I Glanzmann thrombasthenia caused by different homozygous delG frameshift mutations in ITGA2B. <i>Thrombosis and Haemostasis</i> , 2017 , 117, 556-569	7	17
60	How iMALDI can improve clinical diagnostics. <i>Analyst, The</i> , 2018 , 143, 2197-2203	5	16
59	Comprehensive mutational analysis reveals p6Gag phosphorylation to be dispensable for HIV-1 morphogenesis and replication. <i>Journal of Virology</i> , 2013 , 87, 724-34	6.6	16
58	Human Platelet Protein Ubiquitylation and Changes following GPVI Activation. <i>Thrombosis and Haemostasis</i> , 2019 , 119, 104-116	7	16
57	Mutations in glycyl-tRNA synthetase impair mitochondrial metabolism in neurons. <i>Human Molecular Genetics</i> , 2018 , 27, 2187-2204	5.6	15
56	Bottom-up proteomics suggests an association between differential expression of mitochondrial proteins and chronic fatigue syndrome. <i>Translational Psychiatry</i> , 2016 , 6, e904	8.6	15
55	In-depth phenotyping of lymphoblastoid cells suggests selective cellular vulnerability in Marinesco-Sjögren syndrome. <i>Oncotarget</i> , 2017 , 8, 68493-68516	3.3	14
54	Inhibition of osimertinib-resistant epidermal growth factor receptor EGFR-T790M/C797S. <i>Chemical Science</i> , 2019 , 10, 10789-10801	9.4	14
53	The Ubiquitin-Specific Protease Usp7, a Novel Merkel Cell Polyomavirus Large T-Antigen Interaction Partner, Modulates Viral DNA Replication. <i>Journal of Virology</i> , 2020 , 94,	6.6	12
52	Tracking Effects of SIL1 Increase: Taking a Closer Look Beyond the Consequences of Elevated Expression Level. <i>Molecular Neurobiology</i> , 2018 , 55, 2524-2546	6.2	12
51	Phosphoproteome analysis of the platelet plasma membrane. <i>Methods in Molecular Biology</i> , 2011 , 728, 279-90	1.4	12
50	Two-dimensional BAC/SDS-PAGE for membrane proteomics. <i>Sub-Cellular Biochemistry</i> , 2007 , 43, 13-20	5.5	12
49	Protease Specificity Profiling in a Pipet Tip Using "Charge-Synchronized" Proteome-Derived Peptide Libraries. <i>Journal of Proteome Research</i> , 2018 , 17, 1923-1933	5.6	11
48	Fast, efficient, and quality-controlled phosphopeptide enrichment from minute sample amounts using titanium dioxide. <i>Methods in Molecular Biology</i> , 2014 , 1156, 417-30	1.4	11
47	Mild proteasomal stress improves photosynthetic performance in Arabidopsis chloroplasts. <i>Nature Communications</i> , 2020 , 11, 1662	17.4	10
46	Combining De Novo Peptide Sequencing Algorithms, A Synergistic Approach to Boost Both Identifications and Confidence in Bottom-up Proteomics. <i>Journal of Proteome Research</i> , 2017 , 16, 3209-3218	5.6	10
45	Combined inhibition of receptor tyrosine and p21-activated kinases as a therapeutic strategy in childhood ALL. <i>Blood Advances</i> , 2018 , 2, 2554-2567	7.8	10

44	Integration of polycarbonate membranes in microfluidic free-flow electrophoresis. <i>Analyst, The</i> , 2017 , 142, 4228-4239	5	9
43	Clinical and research strategies for limb-girdle congenital myasthenic syndromes. <i>Annals of the New York Academy of Sciences</i> , 2018 , 1412, 102-112	6.5	9
42	Proteome Profiling and Ultrastructural Characterization of the Human RCMH Cell Line: Myoblastic Properties and Suitability for Myopathological Studies. <i>Journal of Proteome Research</i> , 2016 , 15, 945-55	5.6	9
41	Quantifying Missing (Phospho)Proteome Regions with the Broad-Specificity Protease Subtilisin. <i>Analytical Chemistry</i> , 2017 , 89, 13137-13145	7.8	9
40	Variable Digestion Strategies for Phosphoproteomics Analysis. <i>Methods in Molecular Biology</i> , 2016 , 1355, 225-39	1.4	9
39	The RhoA regulators Myo9b and GEF-H1 are targets of cyclic nucleotide-dependent kinases in platelets. <i>Journal of Thrombosis and Haemostasis</i> , 2020 , 18, 3002-3012	15.4	9
38	Unraveling the Phosphocholination Mechanism of the Legionella pneumophila Enzyme AnkX. <i>Biochemistry</i> , 2016 , 55, 4375-85	3.2	8
37	The potential of fractional diagonal chromatography strategies for the enrichment of post-translational modifications. <i>EuPA Open Proteomics</i> , 2014 , 4, 165-170	0.1	8
36	Impaired iloprost-induced platelet inhibition and phosphoproteome changes in patients with confirmed pseudohypoparathyroidism type Ia, linked to genetic mutations in GNAS. <i>Scientific Reports</i> , 2020 , 10, 11389	4.9	8
35	Using Two Peptide Isotopologues as Internal Standards for the Streamlined Quantification of Low-Abundance Proteins by Immuno-MRM and Immuno-MALDI. <i>Analytical Chemistry</i> , 2020 , 92, 12407-12414	7.8	8
34	The Cell Cycle Checkpoint System MAST(L)-ENSA/ARPP19-PP2A is Targeted by cAMP/PKA and cGMP/PKG in Anucleate Human Platelets. <i>Cells</i> , 2020 , 9,	7.9	7
33	Two Birds with One Stone: Parallel Quantification of Proteome and Phosphoproteome Using iTRAQ. <i>Methods in Molecular Biology</i> , 2016 , 1394, 25-41	1.4	7
32	Proteogenomics of Colorectal Cancer Liver Metastases: Complementing Precision Oncology with Phenotypic Data. <i>Cancers</i> , 2019 , 11,	6.6	7
31	Proteomic insights into non-small cell lung cancer: New ideas for cancer diagnosis and therapy from a functional viewpoint. <i>EuPA Open Proteomics</i> , 2014 , 4, 25-39	0.1	6
30	The Caveolin-3 G56S sequence variant of unknown significance: Muscle biopsy findings and functional cell biological analysis. <i>Proteomics - Clinical Applications</i> , 2017 , 11, 1600007	3.1	6
29	Advanced tools for the analysis of protein phosphorylation in yeast mitochondria. <i>Analytical Biochemistry</i> , 2018 , 554, 23-27	3.1	6
28	An LC-MRM assay for the quantification of metanephrines from dried blood spots for the diagnosis of pheochromocytomas and paragangliomas. <i>Analytica Chimica Acta</i> , 2020 , 1128, 140-148	6.6	5
27	Free Flow Electrophoresis Separation of Proteins and DNA Using Microfluidics and Polycarbonate Membranes. <i>Procedia Engineering</i> , 2016 , 168, 1382-1385		5

26	Phosphoproteomics of short-term hedgehog signaling in human medulloblastoma cells. <i>Cell Communication and Signaling</i> , 2020 , 18, 99	7.5	4
25	Systematic Optimization of the iMALDI Workflow for the Robust and Straightforward Quantification of Signaling Proteins in Cancer Cells. <i>Proteomics - Clinical Applications</i> , 2020 , 14, e2000034 ¹	7.1	4
24	Direct and Precise Measurement of Bevacizumab Levels in Human Plasma Based on Controlled Methionine Oxidation and Multiple Reaction Monitoring. <i>ACS Pharmacology and Translational Science</i> , 2020 , 3, 1304-1309	5.9	4
23	Inhibition wirkstoffresistenter Mutationsvarianten der Rezeptortyrosinkinase EGFR. <i>Angewandte Chemie</i> , 2016 , 128, 11069-11073	3.6	4
22	Platelet Proteomics: Essentials for Understanding and Application. <i>Transfusion Medicine and Hemotherapy</i> , 2006 , 33, 227-235	4.2	3
21	Nuclear envelopes from amphibian oocytes--from morphology to protein inventory. <i>European Journal of Cell Biology</i> , 2005 , 84, 151-62	6.1	3
20	High Temporal Resolution Study of Phosphorylation Events in HEK Cells Using a Micromixer Microfluidic Device. <i>Procedia Engineering</i> , 2016 , 168, 1430-1433		3
19	Cyclin Y is expressed in Platelets and Modulates Integrin Outside-in Signaling. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	2
18	Tyr728 in the kinase domain of the murine kinase suppressor of RAS 1 regulates binding and activation of the mitogen-activated protein kinase kinase. <i>Journal of Biological Chemistry</i> , 2013 , 288, 35237-52	5.4	2
17	MARCKS affects cell motility and response to BTK inhibitors in CLL. <i>Blood</i> , 2021 , 138, 544-556	2.2	2
16	INPP5K and SIL1 associated pathologies with overlapping clinical phenotypes converge through dysregulation of PHGDH. <i>Brain</i> , 2021 , 144, 2427-2442	11.2	2
15	Precise Quantitation of PTEN by Immuno-MRM: A Tool To Resolve the Breast Cancer Biomarker Controversy. <i>Analytical Chemistry</i> , 2021 , 93, 10816-10824	7.8	2
14	Phosphorylation of the Bruchpilot N-terminus in unlocks axonal transport of active zone building blocks. <i>Journal of Cell Science</i> , 2019 , 132,	5.3	2
13	Multiple reaction monitoring-mass spectrometry enables robust quantitation of plasma proteins regardless of whole blood processing delays that may occur in the clinic.. <i>Molecular and Cellular Proteomics</i> , 2022 , 100212	7.6	2
12	Mild hyperlipidemia in mice aggravates platelet responsiveness in thrombus formation and exploration of platelet proteome and lipidome. <i>Scientific Reports</i> , 2020 , 10, 21407	4.9	1
11	Direct and Precise Measurement of Bevacizumab Levels in Human Plasma Based on Controlled Methionine Oxidation and Multiple Reaction Monitoring. <i>ACS Pharmacology and Translational Science</i> , 2020 , 3, 1304-1309	5.9	1
10	Utility, promise, and limitations of liquid chromatography-mass spectrometry-based therapeutic drug monitoring in precision medicine. <i>Journal of Mass Spectrometry</i> , 2021 , 56, e4788	2.2	1
9	Simple Targeted Assays for Metabolic Pathways and Signaling: A Powerful Tool for Targeted Proteomics. <i>Analytical Chemistry</i> , 2020 , 92, 13672-13676	7.8	1

8	Effective Assignment of α ,3/ α ,6-Sialic Acid Isomers by LC-MS/MS-Based Glycoproteomics. <i>Angewandte Chemie</i> , 2018 , 130, 9464-9468	3.6	1
7	A Non-Hazardous Deparaffinization Protocol Enables Quantitative Proteomics of Core Needle Biopsy-Sized Formalin-Fixed and Paraffin-Embedded (FFPE) Tissue Specimens.. <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	1
6	A multiplexed, automated immuno-matrix assisted laser desorption/ionization mass spectrometry assay for simultaneous and precise quantitation of PTEN and p110 β in cell lines and tumor tissues. <i>Analyst, The</i> , 2021 , 146, 6566-6575	5	0
5	Subcellular Analysis of the Platelet Proteome. <i>Current Proteomics</i> , 2011 , 8, 181-192	0.7	
4	Post-Translational Modifications317-342		
3	Integrated Proteomic and Phosphoproteomic Analysis Reveal Novel Targets and Suggest Rationale for Ibrutinib Efficacy in UM-CLL. <i>Blood</i> , 2018 , 132, 583-583	2.2	
2	BIM Regulation Is BTK Dependent and Can be Targeted By Entospletinib in Ibrutinib Refractory Mutants. <i>Blood</i> , 2019 , 134, 1765-1765	2.2	
1	p38 MAPK Controls Sensitivity Towards BH3 Mimetics By Regulating Mcl-1 Expression of Chronic Lymphocytic Leukemia in Hypoxia and Acquired Resistance. <i>Blood</i> , 2014 , 124, 1947-1947	2.2	