

# RenÃ© P Zahedi

## List of Publications by Year in descending order

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156  
papers

9,533  
citations

41339

49  
h-index

43886

91  
g-index

161  
all docs

161  
docs citations

161  
times ranked

13149  
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 13207-13212.	7.1	839
2	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-e82.	1.4	623
3	PeptideShaker enables reanalysis of MS-derived proteomics data sets. <i>Nature Biotechnology</i> , 2015, 33, 22-24.	17.5	460
4	Global Analysis of the Mitochondrial N-Proteome Identifies a Processing Peptidase Critical for Protein Stability. <i>Cell</i> , 2009, 139, 428-439.	28.9	434
5	Toward the Complete Yeast Mitochondrial Proteome: A Multidimensional Separation Techniques for Mitochondrial Proteomics. <i>Journal of Proteome Research</i> , 2006, 5, 1543-1554.	3.7	341
6	The Protein Import Machinery of Mitochondria is a Regulatory Hub in Metabolism, Stress, and Disease. <i>Cell Metabolism</i> , 2014, 19, 357-372.	16.2	316
7	The next level of complexity: Crosstalk of posttranslational modifications. <i>Proteomics</i> , 2014, 14, 513-524.	2.2	246
8	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, 1454-1462.	2.4	243
9	Regulation of Mitochondrial Protein Import by Cytosolic Kinases. <i>Cell</i> , 2011, 144, 227-239.	28.9	218
10	Proteomic Analysis of the Yeast Mitochondrial Outer Membrane Reveals Accumulation of a Subclass of Preproteins. <i>Molecular Biology of the Cell</i> , 2006, 17, 1436-1450.	2.1	192
11	Amyloid- $\beta$ Peptide Induces Mitochondrial Dysfunction by Inhibition of Preprotein Maturation. <i>Cell Metabolism</i> , 2014, 20, 662-669.	16.2	176
12	Phosphoproteome of Resting Human Platelets. <i>Journal of Proteome Research</i> , 2008, 7, 526-534.	3.7	154
13	Current strategies and findings in clinically relevant post-translational modification-specific proteomics. <i>Expert Review of Proteomics</i> , 2015, 12, 235-253.	3.0	147
14	The Human Platelet Membrane Proteome Reveals Several New Potential Membrane Proteins. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1754-1761.	3.8	143
15	Profiling Phosphoproteins of Yeast Mitochondria Reveals a Role of Phosphorylation in Assembly of the ATP Synthase. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1896-1906.	3.8	142
16	Intermembrane Space Proteome of Yeast Mitochondria. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1840-1852.	3.8	134
17	Landscape of submitochondrial protein distribution. <i>Nature Communications</i> , 2017, 8, 290.	12.8	123
18	Dual Function of Sdh3 in the Respiratory Chain and TIM22 Protein Translocase of the Mitochondrial Inner Membrane. <i>Molecular Cell</i> , 2011, 44, 811-818.	9.7	121

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19	Protein carbamylation: In vivo modification or in vitro artefact?. <i>Proteomics</i> , 2013, 13, 941-944.	2.2	118
20	Platelet membrane proteomics: a novel repository for functional research. <i>Blood</i> , 2009, 114, e10-e19.	1.4	114
21	PARL mediates Smac proteolytic maturation in mitochondria to promote apoptosis. <i>Nature Cell Biology</i> , 2017, 19, 318-328.	10.3	111
22	Gene network activity in cultivated primary hepatocytes is highly similar to diseased mammalian liver tissue. <i>Archives of Toxicology</i> , 2016, 90, 2513-2529.	4.2	100
23	Simultaneous Metabolite, Protein, Lipid Extraction (SIMPLEX): A Combinatorial Multimolecular Omics Approach for Systems Biology. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1435-1466.	3.8	99
24	What Can Proteomics Tell Us About Platelets?. <i>Circulation Research</i> , 2014, 114, 1204-1219.	4.5	97
25	Temporal quantitative phosphoproteomics of ADP stimulation reveals novel central nodes in platelet activation and inhibition. <i>Blood</i> , 2017, 129, e1-e12.	1.4	97
26	Why phosphoproteomics is still a challenge. <i>Molecular BioSystems</i> , 2015, 11, 1487-1493.	2.9	94
27	Targeting Drug Resistance in EGFR with Covalent Inhibitors: A Structure-Based Design Approach. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 6844-6863.	6.4	92
28	Catch me if you can: Mass spectrometry-based phosphoproteomics and quantification strategies. <i>Proteomics</i> , 2011, 11, 554-570.	2.2	90
29	The mTOR and PP2A Pathways Regulate PHD2 Phosphorylation to Fine-Tune HIF1 $\pm$ Levels and Colorectal Cancer Cell Survival under Hypoxia. <i>Cell Reports</i> , 2017, 18, 1699-1712.	6.4	88
30	Targeted and Untargeted Proteomics Approaches in Biomarker Development. <i>Proteomics</i> , 2020, 20, e1900029.	2.2	83
31	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, 3823-3830.	3.7	82
32	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.	1.4	80
33	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.	2.7	77
34	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, 1933-1941.	3.8	76
35	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, 2458-2469.	2.2	72
36	Detecting post-translational modification signatures as potential biomarkers in clinical mass spectrometry. <i>Expert Review of Proteomics</i> , 2018, 15, 515-535.	3.0	69

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37	Mutations in INPP5K , Encoding a Phosphoinositide 5-Phosphatase, Cause Congenital Muscular Dystrophy with Cataracts and Mild Cognitive Impairment. American Journal of Human Genetics, 2017, 100, 523-536.	6.2	67
38	Two-dimensional benzyltrimethyl-n-hexadecylammonium chloride/SDS-PAGE for membrane proteomics. Proteomics, 2005, 5, 3581-3588.	2.2	66
39	Proteome-wide detection of S-nitrosylation targets and motifs using bioorthogonal cleavable-linker-based enrichment and switch technique. Nature Communications, 2019, 10, 2195.	12.8	66
40	An alternative NFAT-activation pathway mediated by IL-7 is critical for early thymocyte development. Nature Immunology, 2013, 14, 127-135.	14.5	65
41	A Unique Morphological Phenotype in Chemoresistant Triple-Negative Breast Cancer Reveals Metabolic Reprogramming and PLIN4 Expression as a Molecular Vulnerability. Molecular Cancer Research, 2019, 17, 2492-2507.	3.4	63
42	Protein lipid modificationsâ€”More than just a greasy ballast. Proteomics, 2016, 16, 759-782.	2.2	62
43	Impact of Digestion Conditions on Phosphoproteomics. Journal of Proteome Research, 2014, 13, 2761-2770.	3.7	59
44	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. Journal of Biological Chemistry, 2012, 287, 20652-20663.	3.4	58
45	pymzML v2.0: introducing a highly compressed and seekable gzip format. Bioinformatics, 2018, 34, 2513-2514.	4.1	56
46	Drugging the catalytically inactive state of RET kinase in RET-rearranged tumors. Science Translational Medicine, 2017, 9, .	12.4	55
47	Insight into the Inhibition of Drugâ€”Resistant Mutants of the Receptor Tyrosine Kinase EGFR. Angewandte Chemie - International Edition, 2016, 55, 10909-10912.	13.8	54
48	The FERM protein EPB41L5 regulates actomyosin contractility and focal adhesion formation to maintain the kidney filtration barrier. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4621-E4630.	7.1	54
49	Taking the stock of granule cargo: Platelet releasate proteomics. Platelets, 2017, 28, 119-128.	2.3	53
50	Effective Assignment of $\pm 2,3$ Sialic Acid Isomers by LCâ€”MS/MSâ€”Based Glycoproteomics. Angewandte Chemie - International Edition, 2018, 57, 9320-9324.	13.8	53
51	iTRAQ protein quantification: A qualityâ€”controlled workflow. Proteomics, 2011, 11, 1125-1134.	2.2	52
52	Combined Quantification of the Global Proteome, Phosphoproteome, and Proteolytic Cleavage to Characterize Altered Platelet Functions in the Human Scott Syndrome. Molecular and Cellular Proteomics, 2016, 15, 3154-3169.	3.8	52
53	A Complex Standard for Protein Identification, Designed by Evolution. Journal of Proteome Research, 2012, 11, 5065-5071.	3.7	51
54	Myopathy in Marinescoâ€”SjÃ¶gren syndrome links endoplasmic reticulum chaperone dysfunction to nuclear envelope pathology. Acta Neuropathologica, 2014, 127, 761-777.	7.7	51

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55	Identification of Novel in Vivo Phosphorylation Sites of the Human Proapoptotic Protein BAD. <i>Journal of Biological Chemistry</i> , 2009, 284, 28004-28020.	3.4	48
56	Cytomegalovirus Downregulates IRE1 to Repress the Unfolded Protein Response. <i>PLoS Pathogens</i> , 2013, 9, e1003544.	4.7	48
57	<sc>D</sc>â€score: A search engine independent <sc>MD</sc>â€score. <i>Proteomics</i> , 2013, 13, 1036-1041.	2.2	46
58	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, 2691-2708.	4.8	46
59	TRPM7 Kinase Controls Calcium Responses in Arterial Thrombosis and Stroke in Mice. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 344-352.	2.4	42
60	Peptide identification quality control. <i>Proteomics</i> , 2011, 11, 2105-2114.	2.2	41
61	Phosphorylation of CalDAGâ€GEFI by protein kinase A prevents Rap1b activation. <i>Journal of Thrombosis and Haemostasis</i> , 2013, 11, 1574-1582.	3.8	41
62	PKA-RII subunit phosphorylation precedes activation by cAMP and regulates activity termination. <i>Journal of Cell Biology</i> , 2018, 217, 2167-2184.	5.2	40
63	Glycosylation Site Analysis of Human Platelets by Electrostatic Repulsion Hydrophilic Interaction Chromatography. <i>Clinical Proteomics</i> , 2008, 4, 25-36.	2.1	36
64	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-e276.	6.3	36
65	Simple, scalable, and ultrasensitive tip-based identification of protease substrates. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 826-834.	3.8	36
66	Phosphoproteomics of human platelets: A quest for novel activation pathways. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1963-1976.	2.3	35
67	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, 27239-27254.	3.4	35
68	Homologous desensitization of guanylyl cyclaseâ€fA, the receptor for atrial natriuretic peptide, is associated with a complex phosphorylation pattern. <i>FEBS Journal</i> , 2010, 277, 2440-2453.	4.7	34
69	Highly Sensitive Phosphoproteomics by Tailoring Solid-Phase Extraction to Electrostatic Repulsion-Hydrophilic Interaction Chromatography. <i>Analytical Chemistry</i> , 2015, 87, 1596-1604.	6.5	34
70	Omics-based responses induced by bosentan in human hepatoma HepaRG cell cultures. <i>Archives of Toxicology</i> , 2018, 92, 1939-1952.	4.2	34
71	Analysis of the membrane proteome of canine pancreatic rough microsomes identifies a novel Hsp40, termed ERj7. <i>Proteomics</i> , 2009, 9, 3463-3473.	2.2	32
72	Phosphoproteomicsâ€”More than meets the eye. <i>Electrophoresis</i> , 2013, 34, 1483-1492.	2.4	32

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73	Enrichment of Cross-Linked Peptides Using Charge-Based Fractional Diagonal Chromatography (ChaFRADIC). <i>Journal of Proteome Research</i> , 2017, 16, 459-469.	3.7	31
74	Cellular Signature of SIL1 Depletion: Disease Pathogenesis due to Alterations in Protein Composition Beyond the ER Machinery. <i>Molecular Neurobiology</i> , 2016, 53, 5527-5541.	4.0	30
75	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.	2.4	29
76	Hypoxia-induced p38 MAPK activation reduces Mcl-1 expression and facilitates sensitivity towards BH3 mimetics in chronic lymphocytic leukemia. <i>Leukemia</i> , 2015, 29, 981-984.	7.2	28
77	Human Platelet Protein Ubiquitylation and Changes following GPVI Activation. <i>Thrombosis and Haemostasis</i> , 2019, 119, 104-116.	3.4	28
78	Comparative proteomic analysis of biofilm and planktonic cells of <i>Neisseria meningitidis</i> . <i>Proteomics</i> , 2010, 10, 4512-4521.	2.2	27
79	The good, the bad, the ugly: Validating the mass spectrometric analysis of modified peptides. <i>Proteomics</i> , 2011, 11, 1099-1109.	2.2	26
80	Revealing phosphoproteins playing role in tobacco pollen activated in vitro. <i>Proteomics</i> , 2012, 12, 3229-3250.	2.2	26
81	Mutations in glycyl-tRNA synthetase impair mitochondrial metabolism in neurons. <i>Human Molecular Genetics</i> , 2018, 27, 2187-2204.	2.9	26
82	Mass spectrometry-based protein analysis to unravel the tissue pathophysiology in Duchenne muscular dystrophy. <i>Proteomics - Clinical Applications</i> , 2018, 12, 1700071.	1.6	26
83	Integral Quantification Accuracy Estimation for Reporter Ion-based Quantitative Proteomics (iQuARI). <i>Journal of Proteome Research</i> , 2012, 11, 5072-5080.	3.7	25
84	Inhibition of osimertinib-resistant epidermal growth factor receptor EGFR-T790M/C797S. <i>Chemical Science</i> , 2019, 10, 10789-10801.	7.4	25
85	Recent advances in yeast organelle and membrane proteomics. <i>Proteomics</i> , 2009, 9, 4731-4743.	2.2	24
86	Phosphoproteomics Profiling of Tobacco Mature Pollen and Pollen Activated in vitro. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1338-1350.	3.8	24
87	High spatial and temporal resolution cell manipulation techniques in microchannels. <i>Analyst</i> , The, 2016, 141, 1888-1905.	3.5	24
88	Two Birds with One Stone: Parallel Quantification of Proteome and Phosphoproteome Using iTRAQ. <i>Methods in Molecular Biology</i> , 2016, 1394, 25-41.	0.9	24
89	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.	3.4	23
90	Mild proteasomal stress improves photosynthetic performance in <i>Arabidopsis</i> chloroplasts. <i>Nature Communications</i> , 2020, 11, 1662.	12.8	23

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91	The proteome of baker's yeast mitochondria. <i>Mitochondrion</i> , 2017, 33, 15-21.	3.4	22
92	Assembly of nuclear pore complexes mediated by major vault protein. <i>Journal of Cell Science</i> , 2009, 122, 780-786.	2.0	21
93	Response: platelet transcriptome and proteomeâ€™relation rather than correlation. <i>Blood</i> , 2013, 121, 5257-5258.	1.4	21
94	Shedding light on black boxes in protein identification. <i>Proteomics</i> , 2014, 14, 1001-1005.	2.2	20
95	Multidimensional electrostatic repulsionâ€™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, 460-468.	2.3	20
96	How iMALDI can improve clinical diagnostics. <i>Analyst, The</i> , 2018, 143, 2197-2203.	3.5	20
97	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, 4550-4563.	3.7	19
98	Bottom-up proteomics suggests an association between differential expression of mitochondrial proteins and chronic fatigue syndrome. <i>Translational Psychiatry</i> , 2016, 6, e904-e904.	4.8	19
99	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, .	3.4	18
100	Comprehensive Mutational Analysis Reveals p6 <sup>Gag</sup> Phosphorylation To Be Dispensable for HIV-1 Morphogenesis and Replication. <i>Journal of Virology</i> , 2013, 87, 724-734.	3.4	17
101	Clinical and research strategies for limbâ€™girdle congenital myasthenic syndromes. <i>Annals of the New York Academy of Sciences</i> , 2018, 1412, 102-112.	3.8	17
102	Protease Specificity Profiling in a Pipet Tip Using â€™Charge-Synchronizedâ€™ Proteome-Derived Peptide Libraries. <i>Journal of Proteome Research</i> , 2018, 17, 1923-1933.	3.7	16
103	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.	3.3	16
104	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, 472.	4.1	16
105	In-depth phenotyping of lymphoblastoid cells suggests selective cellular vulnerability in Marinesco-SjÃ¶gren syndrome. <i>Oncotarget</i> , 2017, 8, 68493-68516.	1.8	16
106	Tracking Effects of SIL1 Increase: Taking a Closer Look Beyond the Consequences of Elevated Expression Level. <i>Molecular Neurobiology</i> , 2018, 55, 2524-2546.	4.0	15
107	Integration of polycarbonate membranes in microfluidic free-flow electrophoresis. <i>Analyst, The</i> , 2017, 142, 4228-4239.	3.5	14
108	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.	3.7	14

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109	Combined inhibition of receptor tyrosine and p21-activated kinases as a therapeutic strategy in childhood ALL. <i>Blood Advances</i> , 2018, 2, 2554-2567.	5.2	14
110	MARCKS affects cell motility and response to BTK inhibitors in CLL. <i>Blood</i> , 2021, 138, 544-556.	1.4	14
111	Two-Dimensional BAC/SDS-PAGE for Membrane Proteomics. , 2007, 43, 13-20.		14
112	Quantifying Missing (Phospho)Proteome Regions with the Broad-Specificity Protease Subtilisin. <i>Analytical Chemistry</i> , 2017, 89, 13137-13145.	6.5	13
113	Mild hyperlipidemia in mice aggravates platelet responsiveness in thrombus formation and exploration of platelet proteome and lipidome. <i>Scientific Reports</i> , 2020, 10, 21407.	3.3	13
114	Phosphoproteome Analysis of the Platelet Plasma Membrane. <i>Methods in Molecular Biology</i> , 2011, 728, 279-290.	0.9	12
115	Unraveling the Phosphocholination Mechanism of the <i>Legionella pneumophila</i> Enzyme AnkX. <i>Biochemistry</i> , 2016, 55, 4375-4385.	2.5	12
116	Proteogenomics of Colorectal Cancer Liver Metastases: Complementing Precision Oncology with Phenotypic Data. <i>Cancers</i> , 2019, 11, 1907.	3.7	12
117	The RhoA regulators Myo9b and GEFH1 are targets of cyclic nucleotide-dependent kinases in platelets. <i>Journal of Thrombosis and Haemostasis</i> , 2020, 18, 3002-3012.	3.8	12
118	Fast, Efficient, and Quality-Controlled Phosphopeptide Enrichment from Minute Sample Amounts Using Titanium Dioxide. <i>Methods in Molecular Biology</i> , 2014, 1156, 417-430.	0.9	12
119	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.	6.5	11
120	Variable Digestion Strategies for Phosphoproteomics Analysis. <i>Methods in Molecular Biology</i> , 2016, 1355, 225-239.	0.9	10
121	The potential of fractional diagonal chromatography strategies for the enrichment of post-translational modifications. <i>EuPA Open Proteomics</i> , 2014, 4, 165-170.	2.5	9
122	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, 945-955.	3.7	9
123	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.	1.6	9
124	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.	5.4	8
125	Phosphorylation of eIF4E in the stroma drives the production and spatial organisation of collagen type I in the mammary gland. <i>Matrix Biology</i> , 2022, 111, 264-288.	3.6	8
126	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.	2.5	7

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127	Free Flow Electrophoresis Separation of Proteins and DNA Using Microfluidics and Polycarbonate Membranes. <i>Procedia Engineering</i> , 2016, 168, 1382-1385.	1.2	7
128	Joining forces: studying multiple post-translational modifications to understand dynamic disease mechanisms. <i>Expert Review of Proteomics</i> , 2016, 13, 1055-1057.	3.0	7
129	Phosphoproteomics of short-term hedgehog signaling in human medulloblastoma cells. <i>Cell Communication and Signaling</i> , 2020, 18, 99.	6.5	7
130	INPP5K and SIL1 associated pathologies with overlapping clinical phenotypes converge through dysregulation of PHGDH. <i>Brain</i> , 2021, 144, 2427-2442.	7.6	7
131	Precise Quantitation of PTEN by Immuno-MRM: A Tool To Resolve the Breast Cancer Biomarker Controversy. <i>Analytical Chemistry</i> , 2021, 93, 10816-10824.	6.5	7
132	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, 21, 100212.	3.8	7
133	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, 4443.	4.1	7
134	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.	1.6	6
135	Advanced tools for the analysis of protein phosphorylation in yeast mitochondria. <i>Analytical Biochemistry</i> , 2018, 554, 23-27.	2.4	6
136	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.	4.9	6
137	Phosphorylation of the Bruchpilot N-terminus unlocks axonal transport of active zone building blocks. <i>Journal of Cell Science</i> , 2019, 132, .	2.0	5
138	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, 2000034.	1.6	5
139	Nuclear envelopes from amphibian oocytes " from morphology to protein inventory. <i>European Journal of Cell Biology</i> , 2005, 84, 151-162.	3.6	4
140	Analysis of Post-translational Modifications. <i>Proteomics</i> , 2013, 13, 901-903.	2.2	4
141	Inhibition wirkstoffresistenter Mutationsvarianten der Rezeptortyrosinkinase EGFR. <i>Angewandte Chemie</i> , 2016, 128, 11069-11073.	2.0	4
142	Immuno-MALDI-TOF-MS in the Clinic. <i>Clinical Chemistry</i> , 2018, 64, 1271-1272.	3.2	4
143	Cyclin Y Is Expressed in Platelets and Modulates Integrin Outside-in Signaling. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8239.	4.1	4
144	Platelet Proteomics: Essentials for Understanding and Application. <i>Transfusion Medicine and Hemotherapy</i> , 2006, 33, 227-235.	1.6	3

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145	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, 35237-35252.	3.4	3
146	High Temporal Resolution Study of Phosphorylation Events in HEK Cells Using a Micromixer Microfluidic Device. <i>Procedia Engineering</i> , 2016, 168, 1430-1433.	1.2	3
147	Proteomics - moving from inventory to personalized medicine?. <i>Proteomics</i> , 2014, 14, 1953-1953.	2.2	2
148	Subcellular Analysis of the Platelet Proteome. <i>Current Proteomics</i> , 2011, 8, 181-192.	0.3	1
149	Effective Assignment of $\alpha$ 2,3/ $\alpha$ 2,6-Sialic Acid Isomers by LC-MS/MS-Based Glycoproteomics. <i>Angewandte Chemie</i> , 2018, 130, 9464-9468.	2.0	1
150	Simple Targeted Assays for Metabolic Pathways and Signaling: A Powerful Tool for Targeted Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 13672-13676.	6.5	1
151	A multiplexed, automated immuno-matrix assisted laser desorption/ionization mass spectrometry assay for simultaneous and precise quantitation of PTEN and p110 $\beta$ in cell lines and tumor tissues. <i>Analyst</i> , 2021, 146, 6566-6575.	3.5	1
152	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.	4.9	1
153	196. <i>Cytokine</i> , 2013, 63, 289.	3.2	0
154	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.	1.4	0
155	Integrated Proteomic and Phosphoproteomic Analysis Reveal Novel Targets and Suggest Rationale for Ibrutinib Efficacy in UM-CLL. <i>Blood</i> , 2018, 132, 583-583.	1.4	0
156	BIM Regulation Is BTK Dependent and Can be Targeted By Entospletinib in Ibrutinib Refractory Mutants. <i>Blood</i> , 2019, 134, 1765-1765.	1.4	0