

Albert Sickmann

List of Publications by Year in descending order

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295
papers

18,350
citations

9756

73
h-index

18075

120
g-index

302
all docs

302
docs citations

302
times ranked

20870
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.	3.3	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.	0.6	623
3	PeptideShaker enables reanalysis of MS-derived proteomics data sets. <i>Nature Biotechnology</i> , 2015, 33, 22-24.	9.4	460
4	Global Analysis of the Mitochondrial N-Proteome Identifies a Processing Peptidase Critical for Protein Stability. <i>Cell</i> , 2009, 139, 428-439.	13.5	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.	1.8	341
6	State-of-the-art in phosphoproteomics. <i>Proteomics</i> , 2005, 5, 4052-4061.	1.3	335
7	SearchGUI: An open-source graphical user interface for simultaneous OMSSA and X!Tandem searches. <i>Proteomics</i> , 2011, 11, 996-999.	1.3	331
8	The Protein Import Machinery of Mitochondria A Regulatory Hub in Metabolism, Stress, and Disease. <i>Cell Metabolism</i> , 2014, 19, 357-372.	7.2	316
9	Mitochondrial Presequence Translocase: Switching between TOM Tethering and Motor Recruitment Involves Tim21 and Tim17. <i>Cell</i> , 2005, 120, 817-829.	13.5	315
10	Multiple pathways for sorting mitochondrial precursor proteins. <i>EMBO Reports</i> , 2008, 9, 42-49.	2.0	282
11	Protein Insertion into the Mitochondrial Inner Membrane by a Twin-Pore Translocase. <i>Science</i> , 2003, 299, 1747-1751.	6.0	272
12	Endothelial Nitric-oxide Synthase (Type III) Is Activated and Becomes Calcium Independent upon Phosphorylation by Cyclic Nucleotide-dependent Protein Kinases. <i>Journal of Biological Chemistry</i> , 2000, 275, 5179-5187.	1.6	256
13	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.	1.2	243
14	The Mitochondrial Presequence Translocase. <i>Cell</i> , 2002, 111, 507-518.	13.5	241
15	Pex8p: An Intraperoxisomal Organizer of the Peroxisomal Import Machinery. <i>Molecular Cell</i> , 2003, 11, 635-646.	4.5	232
16	Regulation of Mitochondrial Protein Import by Cytosolic Kinases. <i>Cell</i> , 2011, 144, 227-239.	13.5	218
17	Application of electron transfer dissociation (ETD) for the analysis of posttranslational modifications. <i>Proteomics</i> , 2008, 8, 4466-4483.	1.3	209
18	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.	0.9	192

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19	A J-protein is an essential subunit of the presequence translocase-associated protein import motor of mitochondria. <i>Journal of Cell Biology</i> , 2003, 163, 707-713.	2.3	191
20	Pam16 has an essential role in the mitochondrial protein import motor. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 226-233.	3.6	189
21	An Assembly Chaperone Collaborates with the SMN Complex to Generate Spliceosomal SnRNPs. <i>Cell</i> , 2008, 135, 497-509.	13.5	189
22	Role of thioredoxin reductase 1 and thioredoxin interacting protein in prognosis of breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R44.	2.2	180
23	Amyloid- β Peptide Induces Mitochondrial Dysfunction by Inhibition of Preprotein Maturation. <i>Cell Metabolism</i> , 2014, 20, 662-669.	7.2	176
24	Challenges in mass spectrometry-based proteomics. <i>Proteomics</i> , 2004, 4, 3686-3703.	1.3	164
25	Phosphoamino acid analysis. <i>Proteomics</i> , 2001, 1, 200-206.	1.3	155
26	Protein Import Channel of the Outer Mitochondrial Membrane: a Highly Stable Tom40-Tom22 Core Structure Differentially Interacts with Preproteins, Small Tom Proteins, and Import Receptors. <i>Molecular and Cellular Biology</i> , 2001, 21, 2337-2348.	1.1	154
27	Phosphoproteome of Resting Human Platelets. <i>Journal of Proteome Research</i> , 2008, 7, 526-534.	1.8	154
28	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. <i>Cell Metabolism</i> , 2018, 28, 866-880.e15.	7.2	154
29	The La-related protein LARP7 is a component of the 7SK ribonucleoprotein and affects transcription of cellular and viral polymerase II genes. <i>EMBO Reports</i> , 2008, 9, 569-575.	2.0	152
30	Current strategies and findings in clinically relevant post-translational modification-specific proteomics. <i>Expert Review of Proteomics</i> , 2015, 12, 235-253.	1.3	147
31	The Human Platelet Membrane Proteome Reveals Several New Potential Membrane Proteins. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1754-1761.	2.5	143
32	Composition and Topology of the Endoplasmic Reticulum-Mitochondria Encounter Structure. <i>Journal of Molecular Biology</i> , 2011, 413, 743-750.	2.0	143
33	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.	2.5	142
34	Defective glycosylation of coagulation factor XII underlies hereditary angioedema type III. <i>Journal of Clinical Investigation</i> , 2015, 125, 3132-3146.	3.9	138
35	Elucidation of N-Glycosylation Sites on Human Platelet Proteins. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 226-233.	2.5	137
36	Intermembrane Space Proteome of Yeast Mitochondria. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1840-1852.	2.5	134

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37	The Mitochondrial Proteome: From Inventory to Function. <i>Cell</i> , 2008, 134, 22-24.	13.5	129
38	A Comprehensive Interaction Map of the Human Survival of Motor Neuron (SMN) Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 5825-5833.	1.6	123
39	Landscape of submitochondrial protein distribution. <i>Nature Communications</i> , 2017, 8, 290.	5.8	123
40	Inhibition of proinflammatory and innate immune signaling pathways by a cytomegalovirus RIP1-interacting protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3094-3099.	3.3	121
41	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.	4.5	121
42	RioK1, a New Interactor of Protein Arginine Methyltransferase 5 (PRMT5), Competes with pICln for Binding and Modulates PRMT5 Complex Composition and Substrate Specificity. <i>Journal of Biological Chemistry</i> , 2011, 286, 1976-1986.	1.6	120
43	Platelet membrane proteomics: a novel repository for functional research. <i>Blood</i> , 2009, 114, e10-e19.	0.6	114
44	Cytoskeleton assembly at endothelial cell-cell contacts is regulated by β -II-spectrin-VASP complexes. <i>Journal of Cell Biology</i> , 2008, 180, 205-219.	2.3	110
45	STEAP1 Is Associated with the Invasive and Oxidative Stress Phenotype of Ewing Tumors. <i>Molecular Cancer Research</i> , 2012, 10, 52-65.	1.5	109
46	Overexpression of LASP-1 mediates migration and proliferation of human ovarian cancer cells and influences zyxin localisation. <i>British Journal of Cancer</i> , 2007, 96, 296-305.	2.9	107
47	Pam17 Is Required for Architecture and Translocation Activity of the Mitochondrial Protein Import Motor. <i>Molecular and Cellular Biology</i> , 2005, 25, 7449-7458.	1.1	104
48	The Bruchpilot cytomatrix determines the size of the readily releasable pool of synaptic vesicles. <i>Journal of Cell Biology</i> , 2013, 202, 667-683.	2.3	101
49	Simultaneous Metabolite, Protein, Lipid Extraction (SIMPLEX): A Combinatorial Multimolecular Omics Approach for Systems Biology. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1435-1466.	2.5	99
50	Precise protein quantification based on peptide quantification using iTRAQ. <i>BMC Bioinformatics</i> , 2007, 8, 214.	1.2	97
51	What Can Proteomics Tell Us About Platelets?. <i>Circulation Research</i> , 2014, 114, 1204-1219.	2.0	97
52	Temporal quantitative phosphoproteomics of ADP stimulation reveals novel central nodes in platelet activation and inhibition. <i>Blood</i> , 2017, 129, e1-e12.	0.6	97
53	Identification of peroxisomal membrane proteins of <i>Saccharomyces cerevisiae</i> by mass spectrometry. <i>Electrophoresis</i> , 2001, 22, 2955-2968.	1.3	96
54	Proteomic Analysis of Brain Plasma Membranes Isolated by Affinity Two-phase Partitioning. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 390-400.	2.5	96

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55	Silver- and Coomassie-staining protocols: Detection limits and compatibility with ESI MS. <i>Electrophoresis</i> , 2007, 28, 2095-2099.	1.3	96
56	Antimicrobial Poly(2-methylloxazoline)s with Bioswitchable Activity through Satellite Group Modification. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 3830-3834.	7.2	96
57	Peptide and protein quantification: A map of the minefield. <i>Proteomics</i> , 2010, 10, 650-670.	1.3	95
58	The multisubunit chloroplast RNA polymerase- ϵ A from mustard (<i>Sinapis alba</i> L.). <i>FEBS Journal</i> , 2000, 267, 253-261.	0.2	94
59	Conformational Switch and Role of Phosphorylation in PAK Activation. <i>Molecular and Cellular Biology</i> , 2001, 21, 5179-5189.	1.1	94
60	Why phosphoproteomics is still a challenge. <i>Molecular BioSystems</i> , 2015, 11, 1487-1493.	2.9	94
61	Identification of proteins from human cerebrospinal fluid, separated by two-dimensional polyacrylamide gel electrophoresis. <i>Electrophoresis</i> , 2000, 21, 2721-2728.	1.3	92
62	Evolution of an RNP assembly system: A minimal SMN complex facilitates formation of UsnRNPs in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10045-10050.	3.3	92
63	Catch me if you can: Mass spectrometry-based phosphoproteomics and quantification strategies. <i>Proteomics</i> , 2011, 11, 554-570.	1.3	90
64	IGHMBP2 is a ribosome-associated helicase inactive in the neuromuscular disorder distal SMA type 1 (DSMA1). <i>Human Molecular Genetics</i> , 2009, 18, 1288-1300.	1.4	88
65	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.	2.9	88
66	Tyrosine Phosphorylation Modulates the Activity of TRPV4 in Response to Defined Stimuli. <i>Journal of Biological Chemistry</i> , 2009, 284, 2923-2933.	1.6	87
67	compomics-utilities: an open-source Java library for computational proteomics. <i>BMC Bioinformatics</i> , 2011, 12, 70.	1.2	86
68	Phosphorylation-Independent Activity of Atypical Response Regulators of <i>Helicobacter pylori</i> . <i>Journal of Bacteriology</i> , 2005, 187, 3100-3109.	1.0	84
69	Targeting early stages of cardiotoxicity from anti-PD1 immune checkpoint inhibitor therapy. <i>European Heart Journal</i> , 2022, 43, 316-329.	1.0	84
70	Towards a high resolution separation of human cerebrospinal fluid. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002, 771, 167-196.	1.2	82
71	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.	1.8	82
72	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.	0.6	80

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73	Ribosome-associated Complex Binds to Ribosomes in Close Proximity of Rpl31 at the Exit of the Polypeptide Tunnel in Yeast. <i>Molecular Biology of the Cell</i> , 2008, 19, 5279-5288.	0.9	78
74	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.	1.2	77
75	O-GlcNAcylation of Histone Deacetylase 4 Protects the Diabetic Heart From Failure. <i>Circulation</i> , 2019, 140, 580-594.	1.6	77
76	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.	2.5	76
77	The Wuerzburg Hybridoma Library against <i>Drosophila</i> Brain. <i>Journal of Neurogenetics</i> , 2009, 23, 78-91.	0.6	76
78	Identification of key lipids critical for platelet activation by comprehensive analysis of the platelet lipidome. <i>Blood</i> , 2018, 132, e1-e12.	0.6	76
79	The Catalytic Activity of Protein-disulfide Isomerase Requires a Conformationally Flexible Molecule. <i>Journal of Biological Chemistry</i> , 2008, 283, 33630-33640.	1.6	75
80	ms_lims, a simple yet powerful open source laboratory information management system for MS-driven proteomics. <i>Proteomics</i> , 2010, 10, 1261-1264.	1.3	73
81	Purification and Characterization of a Magnesium-dependent Neutral Sphingomyelinase from Bovine Brain. <i>Journal of Biological Chemistry</i> , 2000, 275, 7641-7647.	1.6	71
82	Platelet Protein Interactions. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2008, 28, 1326-1331.	1.1	70
83	Conjugation of Ciprofloxacin with Poly(2-oxazoline)s and Polyethylene Glycol via End Groups. <i>Bioconjugate Chemistry</i> , 2015, 26, 1950-1962.	1.8	69
84	Detecting post-translational modification signatures as potential biomarkers in clinical mass spectrometry. <i>Expert Review of Proteomics</i> , 2018, 15, 515-535.	1.3	69
85	Modificomics: Posttranslational modifications beyond protein phosphorylation and glycosylation. <i>New Biotechnology</i> , 2007, 24, 169-177.	2.7	68
86	Two-dimensional benzyltrimethyl-n-hexadecylammonium chloride/SDS-PAGE for membrane proteomics. <i>Proteomics</i> , 2005, 5, 3581-3588.	1.3	66
87	An alternative NFAT-activation pathway mediated by IL-7 is critical for early thymocyte development. <i>Nature Immunology</i> , 2013, 14, 127-135.	7.0	65
88	Multidimensional nano-HPLC for analysis of protein complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 1003-1011.	1.2	64
89	Proteome analysis of <i>Apis mellifera</i> royal jelly. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 1087-1093.	1.9	64
90	Identification of a Protein Kinase C-dependent phosphorylation site involved in sensitization of TRPV4 channel. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 1721-1725.	1.0	61

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91	A proteomic approach to analysing spheroid formation of two human thyroid cell lines cultured on a random positioning machine. <i>Proteomics</i> , 2011, 11, 2095-2104.	1.3	61
92	Laser-Induced Dissociation/High-Energy Collision-Induced Dissociation Fragmentation Using MALDI-TOF/TOF-MS Instrumentation for the Analysis of Neutral and Acidic Oligosaccharides. <i>Analytical Chemistry</i> , 2005, 77, 3274-3283.	3.2	59
93	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, 20652-20663.	1.6	58
94	Identification of Major Tyrosine Phosphorylation Sites in the Human Insulin Receptor Substrate Gab-1 by Insulin Receptor Kinase in Vitro. <i>Biochemistry</i> , 2000, 39, 10898-10907.	1.2	56
95	eIF5A hypusination, boosted by dietary spermidine, protects from premature brain aging and mitochondrial dysfunction. <i>Cell Reports</i> , 2021, 35, 108941.	2.9	56
96	Method and platform standardization in MRM-based quantitative plasma proteomics. <i>Journal of Proteomics</i> , 2013, 95, 66-76.	1.2	55
97	Identification of new tyrosine phosphorylated proteins in rat brain mitochondria. <i>FEBS Letters</i> , 2008, 582, 1104-1110.	1.3	54
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.	3.3	54
99	Proteomic analysis of cathepsin B and L-deficient mouse brain lysosomes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 1237-1246.	1.1	53
100	Identification of Major ERK-Related Phosphorylation Sites in Gab1. <i>Biochemistry</i> , 2004, 43, 12133-12140.	1.2	52
101	iTRAQ protein quantification: A quality-controlled workflow. <i>Proteomics</i> , 2011, 11, 1125-1134.	1.3	52
102	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.	2.5	52
103	Identification of Novel Centrosomal Proteins in <i>Dictyostelium discoideum</i> by Comparative Proteomic Approaches. <i>Journal of Proteome Research</i> , 2006, 5, 589-598.	1.8	51
104	A stimulatory role for the La-related protein 4B in translation. <i>Rna</i> , 2010, 16, 1488-1499.	1.6	51
105	A Complex Standard for Protein Identification, Designed by Evolution. <i>Journal of Proteome Research</i> , 2012, 11, 5065-5071.	1.8	51
106	Application of free-flow IEF to identify protein candidates changing under microgravity conditions. <i>Proteomics</i> , 2010, 10, 904-913.	1.3	50
107	Nuclear import of LASP-1 is regulated by phosphorylation and dynamic protein-protein interactions. <i>Oncogene</i> , 2013, 32, 2107-2113.	2.6	50
108	Identification of proteins involved in inhibition of spheroid formation under microgravity. <i>Proteomics</i> , 2015, 15, 2945-2952.	1.3	50

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109	LILY-lipidome isotope labeling of yeast: in vivo synthesis of ¹³ C labeled reference lipids for quantification by mass spectrometry. <i>Analyst</i> , 2017, 142, 1891-1899.	1.7	49
110	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020, 11, 5248.	5.8	49
111	Identification of Novel in Vivo Phosphorylation Sites of the Human Proapoptotic Protein BAD. <i>Journal of Biological Chemistry</i> , 2009, 284, 28004-28020.	1.6	48
112	XTandem Parser: An open-source library to parse and analyse XTandem MS/MS search results. <i>Proteomics</i> , 2010, 10, 1522-1524.	1.3	48
113	Cytomegalovirus Downregulates IRE1 to Repress the Unfolded Protein Response. <i>PLoS Pathogens</i> , 2013, 9, e1003544.	2.1	48
114	Activity-based protein profiling as a robust method for enzyme identification and screening in extremophilic Archaea. <i>Nature Communications</i> , 2017, 8, 15352.	5.8	45
115	Understanding platelets. <i>Thrombosis and Haemostasis</i> , 2005, 94, 916-925.	1.8	43
116	Current methods for global proteome identification. <i>Expert Review of Proteomics</i> , 2012, 9, 519-532.	1.3	43
117	Cannabinoid synthases and osmoprotective metabolites accumulate in the exudates of <i>Cannabis sativa</i> L. glandular trichomes. <i>Plant Science</i> , 2019, 284, 108-116.	1.7	43
118	Identification of Modified Proteins by Mass Spectrometry. <i>IUBMB Life</i> , 2002, 54, 51-57.	1.5	41
119	Peptide identification quality control. <i>Proteomics</i> , 2011, 11, 2105-2114.	1.3	41
120	Phosphorylation of CalDAG-GEFI by protein kinase A prevents Rap1b activation. <i>Journal of Thrombosis and Haemostasis</i> , 2013, 11, 1574-1582.	1.9	41
121	Investigation of charge variants of rViscumin by two-dimensional gel electrophoresis and mass spectrometry. <i>Electrophoresis</i> , 2001, 22, 2888-2897.	1.3	40
122	thermo-msf-parser: An Open Source Java Library to Parse and Visualize Thermo Proteome Discoverer <i>msf</i> Files. <i>Journal of Proteome Research</i> , 2011, 10, 3840-3843.	1.8	40
123	Combination of Proteogenomics with Peptide <i>De Novo</i> Sequencing Identifies New Genes and Hidden Posttranscriptional Modifications. <i>MBio</i> , 2019, 10, .	1.8	40
124	Assessment of a complete and classified platelet proteome from genome-wide transcripts of human platelets and megakaryocytes covering platelet functions. <i>Scientific Reports</i> , 2021, 11, 12358.	1.6	40
125	Mass spectrometry-based peptide quantification: applications and limitations. <i>Expert Review of Proteomics</i> , 2005, 2, 381-392.	1.3	39
126	The Human TRPV6 Channel Protein Is Associated with Cyclophilin B in Human Placenta. <i>Journal of Biological Chemistry</i> , 2008, 283, 18086-18098.	1.6	39

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127	Herpesviruses induce aggregation and selective autophagy of host signalling proteins NEMO and RIPK1 as an immune-evasion mechanism. <i>Nature Microbiology</i> , 2020, 5, 331-342.	5.9	39
128	Lymphocyte transformation test: History and current approaches. <i>Journal of Immunological Methods</i> , 2021, 493, 113036.	0.6	38
129	Identification of phosphorylation and acetylation sites in γ A-crystallin of the eye lens (mus musculus) after two-dimensional gel electrophoresis. <i>Analytical and Bioanalytical Chemistry</i> , 2003, 376, 966-972.	1.9	37
130	Glycosylation Site Analysis of Human Platelets by Electrostatic Repulsion Hydrophilic Interaction Chromatography. <i>Clinical Proteomics</i> , 2008, 4, 25-36.	1.1	36
131	The Hsp70 homolog Ssb is essential for glucose sensing via the SNF1 kinase network. <i>Genes and Development</i> , 2009, 23, 2102-2115.	2.7	36
132	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.	2.7	36
133	Proteomic differences between microvascular endothelial cells and the EA.hy926 cell line forming three-dimensional structures. <i>Proteomics</i> , 2014, 14, 689-698.	1.3	36
134	Simple, scalable, and ultrasensitive tip-based identification of protease substrates. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 826-834.	2.5	36
135	Identification of post-translationally modified proteins in proteome studies. <i>Electrophoresis</i> , 2001, 22, 1669-1676.	1.3	35
136	Phosphoproteomics of human platelets: A quest for novel activation pathways. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1963-1976.	1.1	35
137	Aqueous Polymer Two-Phase Systems for the Proteomic Analysis of Plasma Membranes from Minute Brain Samples. <i>Journal of Proteome Research</i> , 2008, 7, 432-442.	1.8	35
138	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.	1.6	35
139	Homologous desensitization of guanylyl cyclase α , the receptor for atrial natriuretic peptide, is associated with a complex phosphorylation pattern. <i>FEBS Journal</i> , 2010, 277, 2440-2453.	2.2	34
140	Highly Sensitive Phosphoproteomics by Tailoring Solid-Phase Extraction to Electrostatic Repulsion-Hydrophilic Interaction Chromatography. <i>Analytical Chemistry</i> , 2015, 87, 1596-1604.	3.2	34
141	Omics-based responses induced by bosentan in human hepatoma HepaRG cell cultures. <i>Archives of Toxicology</i> , 2018, 92, 1939-1952.	1.9	34
142	Novel manifestations of immune dysregulation and granule defects in gray platelet syndrome. <i>Blood</i> , 2020, 136, 1956-1967.	0.6	34
143	Improving Identification of In-organello Protein-Protein Interactions Using an Affinity-enrichable, Isotopically Coded, and Mass Spectrometry-cleavable Chemical Crosslinker. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 624-639.	2.5	34
144	Intersection of Proteomics and Genomics to Solve the Unsolved in Rare Disorders such as Neurodegenerative and Neuromuscular Diseases. <i>Proteomics - Clinical Applications</i> , 2018, 12, 1700073.	0.8	33

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145	Identification of an obeche (<i>Triplochiton scleroxylon</i>) wood allergen as a class I chitinase. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2005, 60, 808-814.	2.7	32
146	Analysis of the membrane proteome of canine pancreatic rough microsomes identifies a novel Hsp40, termed ERj7. <i>Proteomics</i> , 2009, 9, 3463-3473.	1.3	32
147	N-glycoproteomics: mass spectrometry-based glycosylation site annotation. <i>Biological Chemistry</i> , 2012, 393, 249-258.	1.2	32
148	Phosphoproteomicsâ€”More than meets the eye. <i>Electrophoresis</i> , 2013, 34, 1483-1492.	1.3	32
149	OMSSA Parser: An openâ€”source library to parse and extract data from OMSSA MS/MS search results. <i>Proteomics</i> , 2009, 9, 3772-3774.	1.3	31
150	Quality control of nanoâ€”LCâ€”MS systems using stable isotopeâ€”coded peptides. <i>Proteomics</i> , 2011, 11, 1049-1057.	1.3	31
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