

Boris Macek

List of Publications by Year in descending order

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172
papers

16,654
citations

24978

57
h-index

16605

123
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191
all docs

191
docs citations

191
times ranked

21716
citing authors

#	ARTICLE	IF	CITATIONS
1	Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. <i>Cell</i> , 2006, 127, 635-648.	13.5	3,201
2	Parts per Million Mass Accuracy on an Orbitrap Mass Spectrometer via Lock Mass Injection into a C-trap. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 2010-2021.	2.5	1,395
3	Higher-energy C-trap dissociation for peptide modification analysis. <i>Nature Methods</i> , 2007, 4, 709-712.	9.0	844
4	SHARPIN forms a linear ubiquitin ligase complex regulating NF- κ B activity and apoptosis. <i>Nature</i> , 2011, 471, 637-641.	13.7	655
5	Metabolic priming by a secreted fungal effector. <i>Nature</i> , 2011, 478, 395-398.	13.7	509
6	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007, 8, R250.	13.9	410
7	Phosphoproteome Analysis of <i>E. coli</i> Reveals Evolutionary Conservation of Bacterial Ser/Thr/Tyr Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 299-307.	2.5	385
8	Global and Site-Specific Quantitative Phosphoproteomics: Principles and Applications. <i>Annual Review of Pharmacology and Toxicology</i> , 2009, 49, 199-221.	4.2	382
9	The Serine/Threonine/Tyrosine Phosphoproteome of the Model Bacterium <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2007, 6, 697-707.	2.5	359
10	In Vivo Identification of Human Small Ubiquitin-like Modifier Polymerization Sites by High Accuracy Mass Spectrometry and an in Vitro to in Vivo Strategy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 132-144.	2.5	251
11	C-Mannosylation and O-Fucosylation of the Thrombospondin Type 1 Module. <i>Journal of Biological Chemistry</i> , 2001, 276, 6485-6498.	1.6	228
12	Protein post-translational modifications in bacteria. <i>Nature Reviews Microbiology</i> , 2019, 17, 651-664.	13.6	223
13	Fast-Forward Genetics Identifies Plant CPL Phosphatases as Regulators of miRNA Processing Factor HYL1. <i>Cell</i> , 2012, 151, 859-870.	13.5	219
14	Initial Quantitative Proteomic Map of 28 Mouse Tissues Using the SILAC Mouse. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1709-1722.	2.5	204
15	MapZ marks the division sites and positions FtsZ rings in <i>Streptococcus pneumoniae</i> . <i>Nature</i> , 2014, 516, 259-262.	13.7	194
16	Proteomic analysis of the acid-soluble organic matrix of the chicken calcified eggshell layer. <i>Proteomics</i> , 2006, 6, 3801-3810.	1.3	182
17	Top-down Protein Sequencing and MS3 on a Hybrid Linear Quadrupole Ion Trap-Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 949-958.	2.5	179
18	Interplay of the Serine/Threonine-Kinase StkP and the Paralogs DivIVA and GpsB in Pneumococcal Cell Elongation and Division. <i>PLoS Genetics</i> , 2014, 10, e1004275.	1.5	166

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19	WIPI3 and WIPI4 \hat{I}^2 -propellers are scaffolds for LKB1-AMPK-TSC signalling circuits in the control of autophagy. <i>Nature Communications</i> , 2017, 8, 15637.	5.8	156
20	Proteogenomics of <i>Pristionchus pacificus</i> reveals distinct proteome structure of nematode models. <i>Genome Research</i> , 2010, 20, 837-846.	2.4	155
21	Structure of the core of the type III secretion system export apparatus. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 583-590.	3.6	153
22	The Ser/Thr/Tyr phosphoproteome of <i>Lactococcus lactis</i> IL1403 reveals multiply phosphorylated proteins. <i>Proteomics</i> , 2008, 8, 3486-3493.	1.3	145
23	Absolute Proteome and Phosphoproteome Dynamics during the Cell Cycle of <i>Schizosaccharomyces pombe</i> (Fission Yeast). <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1925-1936.	2.5	141
24	The neuropeptide complement of the marine annelid <i>Platynereis dumerilii</i> . <i>BMC Genomics</i> , 2013, 14, 906.	1.2	139
25	Solid Tumor Proteome and Phosphoproteome Analysis by High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2008, 7, 5314-5326.	1.8	132
26	Bacterial single-stranded DNA-binding proteins are phosphorylated on tyrosine. <i>Nucleic Acids Research</i> , 2006, 34, 1588-1596.	6.5	122
27	Characterization of the <i>E. coli</i> proteome and its modifications during growth and ethanol stress. <i>Frontiers in Microbiology</i> , 2015, 6, 103.	1.5	118
28	IAPs regulate the plasticity of cell migration by directly targeting Rac1 for degradation. <i>EMBO Journal</i> , 2012, 31, 14-28.	3.5	117
29	Global Dynamics of the <i>Escherichia coli</i> Proteome and Phosphoproteome During Growth in Minimal Medium. <i>Journal of Proteome Research</i> , 2013, 12, 2611-2621.	1.8	110
30	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) Applied to Quantitative Proteomics of <i>Bacillus subtilis</i> . <i>Journal of Proteome Research</i> , 2010, 9, 3638-3646.	1.8	108
31	Protein Kinase CK1 \hat{I} ± Regulates Erythrocyte Survival. <i>Cellular Physiology and Biochemistry</i> , 2012, 29, 171-180.	1.1	108
32	Multi-omics discovery of exome-derived neoantigens in hepatocellular carcinoma. <i>Genome Medicine</i> , 2019, 11, 28.	3.6	107
33	C-Mannosylation and O-Fucosylation of Thrombospondin Type 1 Repeats. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 11-18.	2.5	106
34	Mitotic Substrates of the Kinase Aurora with Roles in Chromatin Regulation Identified Through Quantitative Phosphoproteomics of Fission Yeast. <i>Science Signaling</i> , 2011, 4, rs6.	1.6	105
35	Human NACHT, LRR, and PYD domain-containing protein 3 (NLRP3) inflammasome activity is regulated by and potentially targetable through Bruton tyrosine kinase. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 1054-1067.e10.	1.5	105
36	Dimerization and direct membrane interaction of Nup53 contribute to nuclear pore complex assembly. <i>EMBO Journal</i> , 2012, 31, 4072-4084.	3.5	104

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37	Phosphoproteins of the chicken eggshell calcified layer. <i>Proteomics</i> , 2007, 7, 106-115.	1.3	102
38	Quantitative Proteomics Reveals That Hsp90 Inhibition Preferentially Targets Kinases and the DNA Damage Response. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014654.	2.5	91
39	PLEKHM1 Regulates Salmonella-Containing Vacuole Biogenesis and Infection. <i>Cell Host and Microbe</i> , 2015, 17, 58-71.	5.1	89
40	Impact of phosphoproteomics on studies of bacterial physiology. <i>FEMS Microbiology Reviews</i> , 2012, 36, 877-892.	3.9	86
41	Toll-like receptor 2 activation depends on lipopeptide shedding by bacterial surfactants. <i>Nature Communications</i> , 2016, 7, 12304.	5.8	86
42	Ser/Thr/Tyr Protein Phosphorylation in the Archaeon <i>Halobacterium salinarum</i> – A Representative of the Third Domain of Life. <i>PLoS ONE</i> , 2009, 4, e4777.	1.1	84
43	Proteome Analysis of Erythrocytes Lacking AMP-Activated Protein Kinase Reveals a Role of PAK2 Kinase in Eryptosis. <i>Journal of Proteome Research</i> , 2011, 10, 1690-1697.	1.8	83
44	Mouse urinary peptides provide a molecular basis for genotype discrimination by nasal sensory neurons. <i>Nature Communications</i> , 2013, 4, 1616.	5.8	81
45	Quantitative Phosphoproteome Analysis of <i>Bacillus subtilis</i> Reveals Novel Substrates of the Kinase PrkC and Phosphatase PrpC. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1965-1978.	2.5	81
46	Phosphoproteome of the cyanobacterium <i>Synechocystis</i> sp. PCC 6803 and its dynamics during nitrogen starvation. <i>Frontiers in Microbiology</i> , 2015, 6, 248.	1.5	79
47	Global Detection of Protein Kinase D-dependent Phosphorylation Events in Nocodazole-treated Human Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 160-170.	2.5	77
48	The fungal ligand chitin directly binds <sc>TLR</sc> 2 and triggers inflammation dependent on oligomer size. <i>EMBO Reports</i> , 2018, 19, .	2.0	75
49	Differential Rac1 signalling by guanine nucleotide exchange factors implicates FLII in regulating Rac1-driven cell migration. <i>Nature Communications</i> , 2016, 7, 10664.	5.8	72
50	Cytosolic Hsp70 and Hsp40 chaperones enable the biogenesis of mitochondrial β -barrel proteins. <i>Journal of Cell Biology</i> , 2018, 217, 3091-3108.	2.3	72
51	Deep Coverage of the <i>Escherichia coli</i> Proteome Enables the Assessment of False Discovery Rates in Simple Proteogenomic Experiments. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3420-3430.	2.5	71
52	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. <i>Nucleic Acids Research</i> , 2007, 35, D771-D779.	6.5	69
53	Cross-phosphorylation of bacterial serine/threonine and tyrosine protein kinases on key regulatory residues. <i>Frontiers in Microbiology</i> , 2014, 5, 495.	1.5	69
54	NetPhosBac – A predictor for Ser/Thr phosphorylation sites in bacterial proteins. <i>Proteomics</i> , 2009, 9, 116-125.	1.3	67

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55	Proteomics reveals evidence of cross-talk between protein modifications in bacteria: focus on acetylation and phosphorylation. <i>Current Opinion in Microbiology</i> , 2012, 15, 357-363.	2.3	67
56	Regulation of the opposing (p)ppGpp synthetase and hydrolase activities in a bifunctional RelA/SpotT homologue from <i>Staphylococcus aureus</i> . <i>PLoS Genetics</i> , 2018, 14, e1007514.	1.5	67
57	Structural and Functional Characterization of the Bacterial Type III Secretion Export Apparatus. <i>PLoS Pathogens</i> , 2016, 12, e1006071.	2.1	66
58	Bone morphogenetic protein (BMP)1-3 enhances bone repair. <i>Biochemical and Biophysical Research Communications</i> , 2011, 408, 25-31.	1.0	61
59	<i>Bacillus subtilis</i> BYâ€kinase PtkA controls enzyme activity and localization of its protein substrates. <i>Molecular Microbiology</i> , 2010, 77, 287-299.	1.2	60
60	The cytosolic cochaperone Sti1 is relevant for mitochondrial biogenesis and morphology. <i>FEBS Journal</i> , 2016, 283, 3338-3352.	2.2	60
61	Internally tagged ubiquitin: a tool to identify linear polyubiquitin-modified proteins by mass spectrometry. <i>Nature Methods</i> , 2017, 14, 504-512.	9.0	59
62	The Signal Transduction Protein PII Controls Ammonium, Nitrate and Urea Uptake in Cyanobacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 1428.	1.5	59
63	DRP1 interacts directly with BAX to induce its activation and apoptosis. <i>EMBO Journal</i> , 2022, 41, e108587.	3.5	59
64	Determination of the Stoichiometry of the Complete Bacterial Type III Secretion Needle Complex Using a Combined Quantitative Proteomic Approach. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1598-1609.	2.5	58
65	Î²-Actin mRNA interactome mapping by proximity biotinylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12863-12872.	3.3	58
66	Circulating Bone Morphogenetic Protein 1â€™3 Isoform Increases Renal Fibrosis. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 681-692.	3.0	55
67	Cell-selective labeling using amino acid precursors for proteomic studies of multicellular environments. <i>Nature Methods</i> , 2013, 10, 768-773.	9.0	55
68	Siteâ€™specific analysis of bacterial phosphoproteomes. <i>Proteomics</i> , 2011, 11, 3002-3011.	1.3	54
69	A flagellum-specific chaperone facilitates assembly of the core type III export apparatus of the bacterial flagellum. <i>PLoS Biology</i> , 2017, 15, e2002267.	2.6	54
70	High Accuracy Mass Spectrometry in Large-Scale Analysis of Protein Phosphorylation. <i>Methods in Molecular Biology</i> , 2009, 492, 131-142.	0.4	54
71	The kinases HipA and HipA7 phosphorylate different substrate pools in <i>Escherichia coli</i> to promote multidrug tolerance. <i>Science Signaling</i> , 2018, 11, .	1.6	52
72	The novel P_{II}-interactor PirC identifies phosphoglycerate mutase as key control point of carbon storage metabolism in cyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	52

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73	Fucosylation and Galactosylation of IgG Heavy Chains Differ between Acute and Remission Phases of Juvenile Chronic Arthritis. <i>Clinical Chemistry and Laboratory Medicine</i> , 1998, 36, 99-102.	1.4	49
74	The phosphoproteome and its physiological dynamics in <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2014, 304, 121-132.	1.5	48
75	Post-translational Serine/Threonine Phosphorylation and Lysine Acetylation: A Novel Regulatory Aspect of the Global Nitrogen Response Regulator GlnR in <i>S. coelicolor</i> M145. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 38.	1.6	48
76	The U1 snRNP Subunit LUC7 Modulates Plant Development and Stress Responses via Regulation of Alternative Splicing. <i>Plant Cell</i> , 2018, 30, 2838-2854.	3.1	48
77	Chlorosis as a Developmental Program in Cyanobacteria: The Proteomic Fundament for Survival and Awakening. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1650-1669.	2.5	47
78	Interaction of NCOR/SMRT Repressor Complexes with Papillomavirus E8 ^{E2C} Proteins Inhibits Viral Replication. <i>PLoS Pathogens</i> , 2016, 12, e1005556.	2.1	44
79	A Nexus Consisting of Beta-Catenin and Stat3 Attenuates BRAF Inhibitor Efficacy and Mediates Acquired Resistance to Vemurafenib. <i>EBioMedicine</i> , 2016, 8, 132-149.	2.7	44
80	Extending SILAC to Proteomics of Plant Cell Lines. <i>Plant Cell</i> , 2011, 23, 1701-1705.	3.1	42
81	Direct determination of glycosylation sites in O-fucosylated glycopeptides using nano-electrospray quadrupole time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 771-777.	0.7	41
82	TORC1 and TORC2 converge to regulate the SAGA coactivator in response to nutrient availability. <i>EMBO Reports</i> , 2017, 18, 2197-2218.	2.0	39
83	The translational regulator FMRP controls lipid and glucose metabolism in mice and humans. <i>Molecular Metabolism</i> , 2019, 21, 22-35.	3.0	39
84	Phosphorylation of SUMO-1 Occurs <i>in Vivo</i> and Is Conserved through Evolution. <i>Journal of Proteome Research</i> , 2008, 7, 4050-4057.	1.8	36
85	Mass spectrometry at the interface of proteomics and genomics. <i>Molecular BioSystems</i> , 2011, 7, 284-291.	2.9	36
86	The tomato receptor CuRe1 senses a cell wall protein to identify <i>Cuscuta</i> as a pathogen. <i>Nature Communications</i> , 2020, 11, 5299.	5.8	36
87	A bacterial effector counteracts host autophagy by promoting degradation of an autophagy component. <i>EMBO Journal</i> , 2022, 41, .	3.5	36
88	Proteome-wide measurement of non-canonical bacterial mistranslation by quantitative mass spectrometry of protein modifications. <i>Scientific Reports</i> , 2016, 6, 28631.	1.6	34
89	Structural studies on protein O-fucosylation by electron capture dissociation. <i>International Journal of Mass Spectrometry</i> , 2004, 234, 11-21.	0.7	32
90	Arabidopsis RNA processing factor SERRATE regulates the transcription of intronless genes. <i>ELife</i> , 2018, 7, .	2.8	32

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91	Deprivation of the Periplasmic Chaperone SurA Reduces Virulence and Restores Antibiotic Susceptibility of Multidrug-Resistant <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 100.	1.5	31
92	Detection of bone and cartilage-related proteins in plasma of patients with a bone fracture using liquid chromatography–mass spectrometry. <i>International Orthopaedics</i> , 2007, 31, 743-751.	0.9	30
93	Phosphoproteome of <i>Pristionchus pacificus</i> Provides Insights into Architecture of Signaling Networks in Nematode Models. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1631-1639.	2.5	30
94	Arginine dephosphorylation propels spore germination in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14228-14237.	3.3	30
95	Quantitative Phosphoproteomics of Murine <i>Fmr1</i> -KO Cell Lines Provides New Insights into FMRP-Dependent Signal Transduction Mechanisms. <i>Journal of Proteome Research</i> , 2014, 13, 4388-4397.	1.8	29
96	Identification of new chicken egg proteins by mass spectrometry-based proteomic analysis. <i>World's Poultry Science Journal</i> , 2008, 64, 209-218.	1.4	28
97	A Trimeric Lipoprotein Assists in Trimeric Autotransporter Biogenesis in Enterobacteria. <i>Journal of Biological Chemistry</i> , 2014, 289, 7388-7398.	1.6	28
98	Quantitative Proteomics of the Human Skin Secretome Reveal a Reduction in Immune Defense Mediators in Ectodermal Dysplasia Patients. <i>Journal of Investigative Dermatology</i> , 2015, 135, 759-767.	0.3	28
99	A single class of ARF GTPase activated by several pathway-specific ARF-GEFs regulates essential membrane traffic in Arabidopsis. <i>PLoS Genetics</i> , 2018, 14, e1007795.	1.5	28
100	The polarity protein Scribble positions DLC3 at adherens junctions to regulate Rho signaling. <i>Journal of Cell Science</i> , 2016, 129, 3583-3596.	1.2	27
101	Ubiquitin-independent regulation of MEK2/3 and MEK5/ERK5 signaling module by XIAP and cIAP1. <i>EMBO Journal</i> , 2014, 33, 1784-1801.	3.5	26
102	Proteomic analysis of Rac1 signaling regulation by guanine nucleotide exchange factors. <i>Cell Cycle</i> , 2016, 15, 1961-1974.	1.3	26
103	Identifying components required for OMP biogenesis as novel targets for antiinfective drugs. <i>Virulence</i> , 2017, 8, 1170-1188.	1.8	26
104	Analysis of a photosynthetic cyanobacterium rich in internal membrane systems via gradient profiling by sequencing (Grad-seq). <i>Plant Cell</i> , 2021, 33, 248-269.	3.1	26
105	Phosphoproteome dynamics mediate revival of bacterial spores. <i>BMC Biology</i> , 2015, 13, 76.	1.7	25
106	Control of Morphological Differentiation of <i>Streptomyces coelicolor</i> A3(2) by Phosphorylation of MreC and PBP2. <i>PLoS ONE</i> , 2015, 10, e0125425.	1.1	25
107	Serine-Threonine Kinases Encoded by Split <i>hipA</i> Homologs Inhibit Tryptophanyl-tRNA Synthetase. <i>MBio</i> , 2019, 10, .	1.8	25
108	Quantitative Proteomics Links the Intermediate Filament Nestin to Resistance to Targeted BRAF Inhibition in Melanoma Cells. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1096-1109.	2.5	25

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109	Discovery of a small protein factor involved in the coordinated degradation of phycobilisomes in cyanobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
110	Stable Isotope Labeling by Amino Acids Applied to Bacterial Cell Culture. Methods in Molecular Biology, 2014, 1188, 9-22.	0.4	25
111	Activation of <i>Bacillus subtilis</i> Ugd by the BY-Kinase PtkA Proceeds via Phosphorylation of Its Residue Tyrosine 70. Journal of Molecular Microbiology and Biotechnology, 2009, 17, 83-89.	1.0	23
112	GIT1 Phosphorylation on Serine 46 by PKD3 Regulates Paxillin Trafficking and Cellular Protrusive Activity. Journal of Biological Chemistry, 2012, 287, 34604-34613.	1.6	23
113	Ubiquitin-dependent regulation of Cdc42 by XIAP. Cell Death and Disease, 2017, 8, e2900-e2900.	2.7	23
114	<i>Staphylococcus aureus</i> Lpl protein triggers human host cell invasion via activation of Hsp90 receptor. Cellular Microbiology, 2020, 22, e13111.	1.1	23
115	Phosphorylation of Ser 402 impedes phosphatase activity of slingshot 1. EMBO Reports, 2011, 12, 527-533.	2.0	22
116	In-depth analysis of <i>Bacillus subtilis</i> proteome identifies new ORFs and traces the evolutionary history of modified proteins. Scientific Reports, 2018, 8, 17246.	1.6	22
117	Tackling destructive proteolysis of unconventionally secreted heterologous proteins in <i>Ustilago maydis</i> . Journal of Biotechnology, 2018, 284, 37-51.	1.9	21
118	Analysis of the <i>Plasmodium falciparum</i> proteasome using Blue Native PAGE and label-free quantitative mass spectrometry. Amino Acids, 2012, 43, 1119-1129.	1.2	20
119	Shotgun proteomics of bacterial pathogens: advances, challenges and clinical implications. Expert Review of Proteomics, 2016, 13, 139-156.	1.3	20
120	Alterations in the CO ₂ availability induce alterations in the phosphoproteome of the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. New Phytologist, 2021, 231, 1123-1137.	3.5	20
121	On the Mechanism and Origin of Isoleucyl-tRNA Synthetase Editing against Norvaline. Journal of Molecular Biology, 2019, 431, 1284-1297.	2.0	20
122	Import of extracellular ATP in yeast and man modulates AMPK and TORC1 signalling. Journal of Cell Science, 2019, 132, .	1.2	19
123	Global analysis of bacterial membrane proteins and their modifications. International Journal of Medical Microbiology, 2015, 305, 203-208.	1.5	18
124	Construction and assessment of individualized proteogenomic databases for large-scale analysis of nonsynonymous single nucleotide variants. Proteomics, 2014, 14, 2699-2708.	1.3	17
125	Staphylococcal Enterotoxins Dose-Dependently Modulate the Generation of Myeloid-Derived Suppressor Cells. Frontiers in Cellular and Infection Microbiology, 2018, 8, 321.	1.8	17
126	APEX2-mediated proximity labeling resolves protein networks in <i>Saccharomyces cerevisiae</i> cells. FEBS Journal, 2020, 287, 325-344.	2.2	17

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127	TOR complex 2 localises to the cytokinetic actomyosin ring and controls the fidelity of cytokinesis. <i>Journal of Cell Science</i> , 2016, 129, 2613-24.	1.2	16
128	The BIR2/BIR3-Associated Phospholipase D β 1 Negatively Regulates Plant Immunity. <i>Plant Physiology</i> , 2020, 183, 371-384.	2.3	14
129	Impact of the serum- and glucocorticoid-inducible kinase 1 on platelet dense granule biogenesis and secretion. <i>Journal of Thrombosis and Haemostasis</i> , 2015, 13, 1325-1334.	1.9	13
130	Tyrosine 601 of <i>Bacillus subtilis</i> DnaK Undergoes Phosphorylation and Is Crucial for Chaperone Activity and Heat Shock Survival. <i>Frontiers in Microbiology</i> , 2016, 7, 533.	1.5	13
131	An Interaction Network of RNA-Binding Proteins Involved in <i>Drosophila</i> Oogenesis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1485-1502.	2.5	13
132	The Tyrosine-Autokinase UbK Is Required for Proper Cell Growth and Cell Morphology of <i>Streptococcus pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1942.	1.5	12
133	Parallel reaction monitoring on a Q Exactive mass spectrometer increases reproducibility of phosphopeptide detection in bacterial phosphoproteomics measurements. <i>Journal of Proteomics</i> , 2018, 189, 60-66.	1.2	11
134	Identification and Functional Characterization of Phosphorylation Sites of the Human Papillomavirus 31 E8 ^{E2} Protein. <i>Journal of Virology</i> , 2018, 92, .	1.5	11
135	Efficient reduction of synthetic mRNA induced immune activation by simultaneous delivery of B18R encoding mRNA. <i>Journal of Biological Engineering</i> , 2019, 13, 40.	2.0	11
136	Comparative Transcriptional Profiling of Motor Neuron Disorder-Associated Genes in Various Human Cell Culture Models. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 544043.	1.8	11
137	Phosphoproteome Study of <i>Escherichia coli</i> Devoid of Ser/Thr Kinase YeaG During the Metabolic Shift From Glucose to Malate. <i>Frontiers in Microbiology</i> , 2021, 12, 657562.	1.5	11
138	Toward Quantitative Proteomics of Organ Substructures: Implications for Renal Physiology. <i>Seminars in Nephrology</i> , 2010, 30, 487-499.	0.6	10
139	Regulation of mitochondrial cargo-selective autophagy by posttranslational modifications. <i>Journal of Biological Chemistry</i> , 2021, 297, 101339.	1.6	10
140	Temporal Analysis of Protein Ubiquitylation and Phosphorylation During Parkin-Dependent Mitophagy. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100191.	2.5	10
141	Nic1 Inactivation Enables Stable Isotope Labeling with ¹³ C ⁶ ¹⁵ N ⁴ -Arginine in <i>Schizosaccharomyces pombe</i> . <i>Molecular and Cellular Proteomics</i> , 2015, 14, 243-250.	2.5	9
142	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) Technology in Fission Yeast. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.top079814.	0.2	9
143	The integral spliceosomal component CWC15 is required for development in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2020, 10, 13336.	1.6	9
144	Phosphorylation of the Human Full-Length Protein Kinase C β 1. <i>Journal of Proteome Research</i> , 2008, 7, 2928-2935.	1.8	8

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145	Bi-allelic loss-of-function variants in BCAS3 cause a syndromic neurodevelopmental disorder. <i>American Journal of Human Genetics</i> , 2021, 108, 1069-1082.	2.6	8
146	S/T Phosphorylation of DLL1 Is Required for Full Ligand Activity <i>In Vitro</i> but Dispensable for DLL1 Function <i>In Vivo</i> during Embryonic Patterning and Marginal Zone B Cell Development. <i>Molecular and Cellular Biology</i> , 2014, 34, 1221-1233.	1.1	7
147	Proteogenomics Reveals Perturbed Signaling Networks in Malignant Melanoma Cells Resistant to BRAF Inhibition. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100163.	2.5	7
148	Proteomic analysis of SRF associated transcription complexes identified TFII-I as modulator of SRF function in neurons. <i>European Journal of Cell Biology</i> , 2016, 95, 42-56.	1.6	6
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