

# Boris Macek

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2972505/publications.pdf>

Version: 2024-02-01

172  
papers

16,654  
citations

25034

57  
h-index

16650

123  
g-index

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.	28.9	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.	3.8	1,395
3	Higher-energy C-trap dissociation for peptide modification analysis. <i>Nature Methods</i> , 2007, 4, 709-712.	19.0	844
4	SHARPIN forms a linear ubiquitin ligase complex regulating NF- $\kappa$ B activity and apoptosis. <i>Nature</i> , 2011, 471, 637-641.	27.8	655
5	Metabolic priming by a secreted fungal effector. <i>Nature</i> , 2011, 478, 395-398.	27.8	509
6	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007, 8, R250.	9.6	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.	3.8	385
8	Global and Site-Specific Quantitative Phosphoproteomics: Principles and Applications. <i>Annual Review of Pharmacology and Toxicology</i> , 2009, 49, 199-221.	9.4	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.	3.8	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.	3.8	251
11	C-Mannosylation and O-Fucosylation of the Thrombospondin Type 1 Module. <i>Journal of Biological Chemistry</i> , 2001, 276, 6485-6498.	3.4	228
12	Protein post-translational modifications in bacteria. <i>Nature Reviews Microbiology</i> , 2019, 17, 651-664.	28.6	223
13	Fast-Forward Genetics Identifies Plant CPL Phosphatases as Regulators of miRNA Processing Factor HYL1. <i>Cell</i> , 2012, 151, 859-870.	28.9	219
14	Initial Quantitative Proteomic Map of 28 Mouse Tissues Using the SILAC Mouse. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1709-1722.	3.8	204
15	MapZ marks the division sites and positions FtsZ rings in <i>Streptococcus pneumoniae</i> . <i>Nature</i> , 2014, 516, 259-262.	27.8	194
16	Proteomic analysis of the acid-soluble organic matrix of the chicken calcified eggshell layer. <i>Proteomics</i> , 2006, 6, 3801-3810.	2.2	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.	3.8	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.	3.5	166

#	ARTICLE	IF	CITATIONS
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.	12.8	156
20	Proteogenomics of <i>Pristionchus pacificus</i> reveals distinct proteome structure of nematode models. <i>Genome Research</i> , 2010, 20, 837-846.	5.5	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.	8.2	153
22	The Ser/Thr/Tyr phosphoproteome of <i>Lactococcus lactis</i> IL1403 reveals multiply phosphorylated proteins. <i>Proteomics</i> , 2008, 8, 3486-3493.	2.2	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.	3.8	141
24	The neuropeptide complement of the marine annelid <i>Platynereis dumerilii</i> . <i>BMC Genomics</i> , 2013, 14, 906.	2.8	139
25	Solid Tumor Proteome and Phosphoproteome Analysis by High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2008, 7, 5314-5326.	3.7	132
26	Bacterial single-stranded DNA-binding proteins are phosphorylated on tyrosine. <i>Nucleic Acids Research</i> , 2006, 34, 1588-1596.	14.5	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.	3.5	118
28	IAPs regulate the plasticity of cell migration by directly targeting Rac1 for degradation. <i>EMBO Journal</i> , 2012, 31, 14-28.	7.8	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.	3.7	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.	3.7	108
31	Protein Kinase CK1 $\hat{I}$ ± Regulates Erythrocyte Survival. <i>Cellular Physiology and Biochemistry</i> , 2012, 29, 171-180.	1.6	108
32	Multi-omics discovery of exome-derived neoantigens in hepatocellular carcinoma. <i>Genome Medicine</i> , 2019, 11, 28.	8.2	107
33	C-Mannosylation and O-Fucosylation of Thrombospondin Type 1 Repeats. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 11-18.	3.8	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.	3.6	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.	2.9	105
36	Dimerization and direct membrane interaction of Nup53 contribute to nuclear pore complex assembly. <i>EMBO Journal</i> , 2012, 31, 4072-4084.	7.8	104

#	ARTICLE	IF	CITATIONS
37	Phosphoproteins of the chicken eggshell calcified layer. <i>Proteomics</i> , 2007, 7, 106-115.	2.2	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.	3.8	91
39	PLEKHM1 Regulates Salmonella-Containing Vacuole Biogenesis and Infection. <i>Cell Host and Microbe</i> , 2015, 17, 58-71.	11.0	89
40	Impact of phosphoproteomics on studies of bacterial physiology. <i>FEMS Microbiology Reviews</i> , 2012, 36, 877-892.	8.6	86
41	Toll-like receptor 2 activation depends on lipopeptide shedding by bacterial surfactants. <i>Nature Communications</i> , 2016, 7, 12304.	12.8	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.	2.5	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.	3.7	83
44	Mouse urinary peptides provide a molecular basis for genotype discrimination by nasal sensory neurons. <i>Nature Communications</i> , 2013, 4, 1616.	12.8	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.	3.8	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.	3.5	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.	3.8	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, .	4.5	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.	12.8	72
50	Cytosolic Hsp70 and Hsp40 chaperones enable the biogenesis of mitochondrial $\beta$ -barrel proteins. <i>Journal of Cell Biology</i> , 2018, 217, 3091-3108.	5.2	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.	3.8	71
52	MAPU: Max-Planck Unified database of organellar, cellular, tissue and body fluid proteomes. <i>Nucleic Acids Research</i> , 2007, 35, D771-D779.	14.5	69
53	Cross-phosphorylation of bacterial serine/threonine and tyrosine protein kinases on key regulatory residues. <i>Frontiers in Microbiology</i> , 2014, 5, 495.	3.5	69
54	NetPhosBac — A predictor for Ser/Thr phosphorylation sites in bacterial proteins. <i>Proteomics</i> , 2009, 9, 116-125.	2.2	67

#	ARTICLE	IF	CITATIONS
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.	5.1	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.	3.5	67
57	Structural and Functional Characterization of the Bacterial Type III Secretion Export Apparatus. <i>PLoS Pathogens</i> , 2016, 12, e1006071.	4.7	66
58	Bone morphogenetic protein (BMP)1-3 enhances bone repair. <i>Biochemical and Biophysical Research Communications</i> , 2011, 408, 25-31.	2.1	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.	2.5	60
60	The cytosolic cochaperone Sti1 is relevant for mitochondrial biogenesis and morphology. <i>FEBS Journal</i> , 2016, 283, 3338-3352.	4.7	60
61	Internally tagged ubiquitin: a tool to identify linear polyubiquitin-modified proteins by mass spectrometry. <i>Nature Methods</i> , 2017, 14, 504-512.	19.0	59
62	The Signal Transduction Protein PII Controls Ammonium, Nitrate and Urea Uptake in Cyanobacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 1428.	3.5	59
63	DRP1 interacts directly with BAX to induce its activation and apoptosis. <i>EMBO Journal</i> , 2022, 41, e108587.	7.8	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.	3.8	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.	7.1	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.	6.1	55
67	Cell-selective labeling using amino acid precursors for proteomic studies of multicellular environments. <i>Nature Methods</i> , 2013, 10, 768-773.	19.0	55
68	Siteâ€specific analysis of bacterial phosphoproteomes. <i>Proteomics</i> , 2011, 11, 3002-3011.	2.2	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.	5.6	54
70	High Accuracy Mass Spectrometry in Large-Scale Analysis of Protein Phosphorylation. <i>Methods in Molecular Biology</i> , 2009, 492, 131-142.	0.9	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, .	3.6	52
72	The novel P<sub>II</sub>-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, .	7.1	52

#	ARTICLE	IF	CITATIONS
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.	2.3	49
74	The phosphoproteome and its physiological dynamics in <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2014, 304, 121-132.	3.6	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.	3.5	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.	6.6	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.	3.8	47
78	Interaction of NCOR/SMRT Repressor Complexes with Papillomavirus E8 <sup>E2C</sup> Proteins Inhibits Viral Replication. <i>PLoS Pathogens</i> , 2016, 12, e1005556.	4.7	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.	6.1	44
80	Extending SILAC to Proteomics of Plant Cell Lines. <i>Plant Cell</i> , 2011, 23, 1701-1705.	6.6	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.	1.5	41
82	TORC1 and TORC2 converge to regulate the SAGA coactivator in response to nutrient availability. <i>EMBO Reports</i> , 2017, 18, 2197-2218.	4.5	39
83	The translational regulator FMRP controls lipid and glucose metabolism in mice and humans. <i>Molecular Metabolism</i> , 2019, 21, 22-35.	6.5	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.	3.7	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.	12.8	36
87	A bacterial effector counteracts host autophagy by promoting degradation of an autophagy component. <i>EMBO Journal</i> , 2022, 41, .	7.8	36
88	Proteome-wide measurement of non-canonical bacterial mistranslation by quantitative mass spectrometry of protein modifications. <i>Scientific Reports</i> , 2016, 6, 28631.	3.3	34
89	Structural studies on protein O-fucosylation by electron capture dissociation. <i>International Journal of Mass Spectrometry</i> , 2004, 234, 11-21.	1.5	32
90	Arabidopsis RNA processing factor SERRATE regulates the transcription of intronless genes. <i>ELife</i> , 2018, 7, .	6.0	32

#	ARTICLE	IF	CITATIONS
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.	3.5	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.	1.9	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.	3.8	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.	7.1	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.	3.7	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.	3.0	28
97	A Trimeric Lipoprotein Assists in Trimeric Autotransporter Biogenesis in Enterobacteria. <i>Journal of Biological Chemistry</i> , 2014, 289, 7388-7398.	3.4	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.	0.7	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.	3.5	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.	2.0	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.	7.8	26
102	Proteomic analysis of Rac1 signaling regulation by guanine nucleotide exchange factors. <i>Cell Cycle</i> , 2016, 15, 1961-1974.	2.6	26
103	Identifying components required for OMP biogenesis as novel targets for anti-infective drugs. <i>Virulence</i> , 2017, 8, 1170-1188.	4.4	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.	6.6	26
105	Phosphoproteome dynamics mediate revival of bacterial spores. <i>BMC Biology</i> , 2015, 13, 76.	3.8	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.	2.5	25
107	Serine-Threonine Kinases Encoded by Split <i>hipA</i> Homologs Inhibit Tryptophanyl-tRNA Synthetase. <i>MBio</i> , 2019, 10, .	4.1	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.	3.8	25

#	ARTICLE	IF	CITATIONS
109	Discovery of a small protein factor involved in the coordinated degradation of phycobilisomes in cyanobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	25
110	Stable Isotope Labeling by Amino Acids Applied to Bacterial Cell Culture. <i>Methods in Molecular Biology</i> , 2014, 1188, 9-22.	0.9	25
111	Activation of <i>Bacillus subtilis</i> Ugd by the BY-Kinase PtkA Proceeds via Phosphorylation of Its Residue Tyrosine 70. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009, 17, 83-89.	1.0	23
112	GIT1 Phosphorylation on Serine 46 by PKD3 Regulates Paxillin Trafficking and Cellular Protrusive Activity. <i>Journal of Biological Chemistry</i> , 2012, 287, 34604-34613.	3.4	23
113	Ubiquitin-dependent regulation of Cdc42 by XIAP. <i>Cell Death and Disease</i> , 2017, 8, e2900-e2900.	6.3	23
114	<i>Staphylococcus aureus</i> Lpl protein triggers human host cell invasion via activation of Hsp90 receptor. <i>Cellular Microbiology</i> , 2020, 22, e13111.	2.1	23
115	Phosphorylation of Ser 402 impedes phosphatase activity of slingshot 1. <i>EMBO Reports</i> , 2011, 12, 527-533.	4.5	22
116	In-depth analysis of <i>Bacillus subtilis</i> proteome identifies new ORFs and traces the evolutionary history of modified proteins. <i>Scientific Reports</i> , 2018, 8, 17246.	3.3	22
117	Tackling destructive proteolysis of unconventionally secreted heterologous proteins in <i>Ustilago maydis</i> . <i>Journal of Biotechnology</i> , 2018, 284, 37-51.	3.8	21
118	Analysis of the <i>Plasmodium falciparum</i> proteasome using Blue Native PAGE and label-free quantitative mass spectrometry. <i>Amino Acids</i> , 2012, 43, 1119-1129.	2.7	20
119	Shotgun proteomics of bacterial pathogens: advances, challenges and clinical implications. <i>Expert Review of Proteomics</i> , 2016, 13, 139-156.	3.0	20
120	Alterations in the CO <sub>2</sub> availability induce alterations in the phosphoproteome of the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>New Phytologist</i> , 2021, 231, 1123-1137.	7.3	20
121	On the Mechanism and Origin of Isoleucyl-tRNA Synthetase Editing against Norvaline. <i>Journal of Molecular Biology</i> , 2019, 431, 1284-1297.	4.2	20
122	Import of extracellular ATP in yeast and man modulates AMPK and TORC1 signalling. <i>Journal of Cell Science</i> , 2019, 132, .	2.0	19
123	Global analysis of bacterial membrane proteins and their modifications. <i>International Journal of Medical Microbiology</i> , 2015, 305, 203-208.	3.6	18
124	Construction and assessment of individualized proteogenomic databases for large-scale analysis of nonsynonymous single nucleotide variants. <i>Proteomics</i> , 2014, 14, 2699-2708.	2.2	17
125	Staphylococcal Enterotoxins Dose-Dependently Modulate the Generation of Myeloid-Derived Suppressor Cells. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 321.	3.9	17
126	APEX2-mediated proximity labeling resolves protein networks in <i>Saccharomyces cerevisiae</i> cells. <i>FEBS Journal</i> , 2020, 287, 325-344.	4.7	17



#	ARTICLE	IF	CITATIONS
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.	2.0	16
128	The BIR2/BIR3-Associated Phospholipase D $\beta$ 1 Negatively Regulates Plant Immunity. <i>Plant Physiology</i> , 2020, 183, 371-384.	4.8	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.	3.8	13
130	Tyrosine 601 of Bacillus subtilis DnaK Undergoes Phosphorylation and Is Crucial for Chaperone Activity and Heat Shock Survival. <i>Frontiers in Microbiology</i> , 2016, 7, 533.	3.5	13
131	An Interaction Network of RNA-Binding Proteins Involved in Drosophila Oogenesis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1485-1502.	3.8	13
132	The Tyrosine-Autokinase UbK Is Required for Proper Cell Growth and Cell Morphology of Streptococcus pneumoniae. <i>Frontiers in Microbiology</i> , 2019, 10, 1942.	3.5	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.	2.4	11
134	Identification and Functional Characterization of Phosphorylation Sites of the Human Papillomavirus 31 E8 <sup>E2</sup> Protein. <i>Journal of Virology</i> , 2018, 92, .	3.4	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.	4.7	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.	3.7	11
137	Phosphoproteome Study of Escherichia coli Devoid of Ser/Thr Kinase YeaG During the Metabolic Shift From Glucose to Malate. <i>Frontiers in Microbiology</i> , 2021, 12, 657562.	3.5	11
138	Toward Quantitative Proteomics of Organ Substructures: Implications for Renal Physiology. <i>Seminars in Nephrology</i> , 2010, 30, 487-499.	1.6	10
139	Regulation of mitochondrial cargo-selective autophagy by posttranslational modifications. <i>Journal of Biological Chemistry</i> , 2021, 297, 101339.	3.4	10
140	Temporal Analysis of Protein Ubiquitylation and Phosphorylation During Parkin-Dependent Mitophagy. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100191.	3.8	10
141	Nic1 Inactivation Enables Stable Isotope Labeling with <sup>13</sup> C <sup>6</sup> <sup>15</sup> N <sup>4</sup> -Arginine in Schizosaccharomyces pombe. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 243-250.	3.8	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.	0.3	9
143	The integral spliceosomal component CWC15 is required for development in Arabidopsis. <i>Scientific Reports</i> , 2020, 10, 13336.	3.3	9
144	Phosphorylation of the Human Full-Length Protein Kinase C $\beta$ 1. <i>Journal of Proteome Research</i> , 2008, 7, 2928-2935.	3.7	8

#	ARTICLE	IF	CITATIONS
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.	6.2	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.	2.3	7
147	Proteogenomics Reveals Perturbed Signaling Networks in Malignant Melanoma Cells Resistant to BRAF Inhibition. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100163.	3.8	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.	3.6	6
149	Ste12/Fab1 phosphatidylinositol-3-phosphate 5-kinase is required for nitrogen-regulated mitotic commitment and cell size control. <i>PLoS ONE</i> , 2017, 12, e0172740.	2.5	6
150	Proteome and phosphoproteome analysis of commensally induced dendritic cell maturation states. <i>Journal of Proteomics</i> , 2018, 180, 11-24.	2.4	6
151	An integrated workflow for enhanced taxonomic and functional coverage of the mouse fecal metaproteome. <i>Gut Microbes</i> , 2021, 13, 1994836.	9.8	6
152	Urine release of systemically administered bone morphogenetic protein hybrid molecule. <i>Journal of Nephrology</i> , 2007, 20, 311-9.	2.0	6
153	Construction, Growth, and Harvesting of Fission Yeast Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) Strains. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot091678.	0.3	5
154	Proteome Response of a Metabolically Flexible Anoxygenic Phototroph to Fe(II) Oxidation. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	5
155	A Nanobody-Based Toolset to Monitor and Modify the Mitochondrial GTPase Miro1. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 835302.	3.5	5
156	A TOR (target of rapamycin) and nutritional phosphoproteome of fission yeast reveals novel targets in networks conserved in humans. <i>Open Biology</i> , 2021, 11, 200405.	3.6	4
157	Proteome Dynamics during Antibiotic Persistence and Resuscitation. <i>MSystems</i> , 2021, 6, e0054921.	3.8	4
158	Conserved Salt Bridges Facilitate Assembly of the Helical Core Export Apparatus of a <i>Salmonella enterica</i> Type III Secretion System. <i>Journal of Molecular Biology</i> , 2021, 433, 167175.	4.2	4
159	Resources for Assignment of Phosphorylation Sites on Peptides and Proteins. <i>Methods in Molecular Biology</i> , 2016, 1355, 293-306.	0.9	4
160	Detecting Posttranslational Modifications of Bacterial SSB Proteins. , 2012, 922, 205-218.		3
161	Carpal Tunnel Syndrome Is Associated With High Fibrinogen and Fibrinogen Deposits. <i>Neurosurgery</i> , 2014, 75, 276-285.	1.1	3
162	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)-Based Quantitative Proteomics and Phosphoproteomics in Fission Yeast. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot091686.	0.3	3

#	ARTICLE	IF	CITATIONS
163	Putative link between Polo-like kinases (PLKs) and Toll-like receptor (TLR) signaling in transformed and primary human immune cells. <i>Scientific Reports</i> , 2019, 9, 13168.	3.3	3
164	Profiling of time-dependent human plasma protein adsorption on non-coated and heparin-coated oxygenator membranes. , 2022, 139, 213014.		3
165	The RNA-Binding Protein Scp160p Facilitates Aggregation of Many Endogenous Q/N-Rich Proteins. <i>Cell Reports</i> , 2018, 24, 20-26.	6.4	2
166	<i>Bacillus subtilis</i> single-stranded DNA-binding protein SsbA is phosphorylated at threonine 38 by the serine/threonine kinase YabT. <i>Periodicum Biologorum</i> , 2017, 118, .	0.1	2
167	Proteasomal turnover of the RhoGAP tumor suppressor DLC1 is regulated by HECTD1 and USP7. <i>Scientific Reports</i> , 2022, 12, 5036.	3.3	2
168	Phosphopeptide Enrichment from Bacterial Samples Utilizing Titanium Oxide Affinity Chromatography. <i>Methods in Molecular Biology</i> , 2018, 1841, 231-247.	0.9	1
169	Individualized Proteogenomics Reveals the Mutational Landscape of Melanoma Patients in Response to Immunotherapy. <i>Cancers</i> , 2021, 13, 5411.	3.7	1
170	Chapter 9. LC-MS for the Identification of Post-Translational Modifications of Proteins. <i>RSC Chromatography Monographs</i> , 2011, , 123-132.	0.1	0
171	The polarity protein Scribble positions DLC3 at adherens junctions to regulate Rho signaling. <i>Development (Cambridge)</i> , 2016, 143, e1.2-e1.2.	2.5	0
172	RNA Interactome Identification via RNA-BiOLD in Mouse Embryonic Fibroblasts. <i>Bio-protocol</i> , 2020, 10, e3476.	0.4	0