

Bernhard Kuster

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6747225/publications.pdf>

Version: 2024-02-01

254
papers

36,500
citations

5896

81
h-index

3650

180
g-index

274
all docs

274
docs citations

274
times ranked

42954
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional organization of the yeast proteome by systematic analysis of protein complexes. Nature, 2002, 415, 141-147.	27.8	4,509
2	Proteome survey reveals modularity of the yeast cell machinery. Nature, 2006, 440, 631-636.	27.8	2,347
3	Mass-spectrometry-based draft of the human proteome. Nature, 2014, 509, 582-587.	27.8	1,697
4	Quantitative mass spectrometry in proteomics: a critical review. Analytical and Bioanalytical Chemistry, 2007, 389, 1017-1031.	3.7	1,448
5	Quantitative chemical proteomics reveals mechanisms of action of clinical ABL kinase inhibitors. Nature Biotechnology, 2007, 25, 1035-1044.	17.5	979
6	A physical and functional map of the human TNF- α /NF- κ B signal transduction pathway. Nature Cell Biology, 2004, 6, 97-105.	10.3	970
7	Tracking cancer drugs in living cells by thermal profiling of the proteome. Science, 2014, 346, 1255-784.	12.6	812
8	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. Analytical and Bioanalytical Chemistry, 2012, 404, 939-965.	3.7	695
9	Computational prediction of proteotypic peptides for quantitative proteomics. Nature Biotechnology, 2007, 25, 125-131.	17.5	653
10	The target landscape of clinical kinase drugs. Science, 2017, 358, .	12.6	609
11	High-fat diet alters gut microbiota physiology in mice. ISME Journal, 2014, 8, 295-308.	9.8	583
12	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. Molecular Systems Biology, 2019, 15, e8503.	7.2	576
13	Cell-cycle-regulated association of RAD50/MRE11/NBS1 with TRF2 and human telomeres. Nature Genetics, 2000, 25, 347-352.	21.4	560
14	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. Nucleic Acids Research, 2003, 31, 3625-3630.	14.5	555
15	Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning. Nature Methods, 2019, 16, 509-518.	19.0	539
16	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. Nature, 2021, 594, 246-252.	27.8	475
17	90S Pre-Ribosomes Include the 35S Pre-rRNA, the U3 snoRNP, and 40S Subunit Processing Factors but Predominantly Lack 60S Synthesis Factors. Molecular Cell, 2002, 10, 105-115.	9.7	427
18	Proteomics: a pragmatic perspective. Nature Biotechnology, 2010, 28, 695-709.	17.5	374

#	ARTICLE	IF	CITATIONS
19	Sequencing of N-Linked Oligosaccharides Directly from Protein Gels: In-Gel Deglycosylation Followed by Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry and Normal-Phase High-Performance Liquid Chromatography. <i>Analytical Biochemistry</i> , 1997, 250, 82-101.	2.4	371
20	K + Efflux-Independent NLRP3 Inflammasome Activation by Small Molecules Targeting Mitochondria. <i>Immunity</i> , 2016, 45, 761-773.	14.3	364
21	A Scalable Approach for Protein False Discovery Rate Estimation in Large Proteomic Data Sets. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2394-2404.	3.8	350
22	ERCC1/XPF Removes the 3' Overhang from Uncapped Telomeres and Represses Formation of Telomeric DNA-Containing Double Minute Chromosomes. <i>Molecular Cell</i> , 2003, 12, 1489-1498.	9.7	349
23	Requirement of ATM-Dependent Monoubiquitylation of Histone H2B for Timely Repair of DNA Double-Strand Breaks. <i>Molecular Cell</i> , 2011, 41, 529-542.	9.7	347
24	Scoring proteomes with proteotypic peptide probes. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 577-583.	37.0	344
25	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020, 579, 409-414.	27.8	328
26	Phospho.ELM: a database of experimentally verified phosphorylation sites in eukaryotic proteins. <i>BMC Bioinformatics</i> , 2004, 5, 79.	2.6	317
27	Detection of Tyrosine Phosphorylated Peptides by Precursor Ion Scanning Quadrupole TOF Mass Spectrometry in Positive Ion Mode. <i>Analytical Chemistry</i> , 2001, 73, 1440-1448.	6.5	306
28	Dimension reduction techniques for the integrative analysis of multi-omics data. <i>Briefings in Bioinformatics</i> , 2016, 17, 628-641.	6.5	280
29	Global Proteome Analysis of the NCI-60 Cell Line Panel. <i>Cell Reports</i> , 2013, 4, 609-620.	6.4	276
30	Confident Phosphorylation Site Localization Using the Mascot Delta Score. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S12.	3.8	247
31	<i>Enterococcus faecalis</i> Metalloprotease Compromises Epithelial Barrier and Contributes to Intestinal Inflammation. <i>Gastroenterology</i> , 2011, 141, 959-971.	1.3	246
32	TMT Labeling for the Masses: A Robust and Cost-efficient, In-solution Labeling Approach. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1468-1478.	3.8	245
33	Measuring and Managing Ratio Compression for Accurate iTRAQ/TMT Quantification. <i>Journal of Proteome Research</i> , 2013, 12, 3586-3598.	3.7	238
34	A multivariate approach to the integration of multi-omics datasets. <i>BMC Bioinformatics</i> , 2014, 15, 162.	2.6	238
35	A Proteome-wide Approach Identifies Sumoylated Substrate Proteins in Yeast. <i>Journal of Biological Chemistry</i> , 2004, 279, 41346-41351.	3.4	236
36	Robust and Sensitive iTRAQ Quantification on an LTQ Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1702-1713.	3.8	219

#	ARTICLE	IF	CITATIONS
37	Robust, reproducible and quantitative analysis of thousands of proteomes by micro-flow LC-MS/MS. Nature Communications, 2020, 11, 157.	12.8	218
38	Sorafenib promotes graft-versus-leukemia activity in mice and humans through IL-15 production in FLT3-ITD-mutant leukemia cells. Nature Medicine, 2018, 24, 282-291.	30.7	216
39	Composition of N-linked carbohydrates from ovalbumin and co-purified glycoproteins. Journal of the American Society for Mass Spectrometry, 2000, 11, 564-571.	2.8	213
40	Profiling Core Proteomes of Human Cell Lines by One-dimensional PAGE and Liquid Chromatography-Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2003, 2, 1297-1305.	3.8	210
41	DMSO enhances electrospray response, boosting sensitivity of proteomic experiments. Nature Methods, 2013, 10, 989-991.	19.0	209
42	Auxin efflux by PIN-FORMED proteins is activated by two different protein kinases, D6 PROTEIN KINASE and PINOID. ELife, 2014, 3, .	6.0	205
43	The Inflammasome Drives GSDMD-Independent Secondary Pyroptosis and IL-1 Release in the Absence of Caspase-1 Protease Activity. Cell Reports, 2017, 21, 3846-3859.	6.4	202
44	Affinity purification-mass spectrometry. FEBS Journal, 2003, 270, 570-578.	0.2	200
45	The gut microbiota promotes hepatic fatty acid desaturation and elongation in mice. Nature Communications, 2018, 9, 3760.	12.8	200
46	The emerging landscape of single-molecule protein sequencing technologies. Nature Methods, 2021, 18, 604-617.	19.0	198
47	ProteomicsDB. Nucleic Acids Research, 2018, 46, D1271-D1281.	14.5	197
48	A Transmembrane Tight Junction Protein Selectively Expressed on Endothelial Cells and Platelets. Journal of Biological Chemistry, 2002, 277, 16294-16303.	3.4	196
49	Lactocepin Secreted By Lactobacillus Exerts Anti-Inflammatory Effects By Selectively Degrading Proinflammatory Chemokines. Cell Host and Microbe, 2012, 11, 387-396.	11.0	196
50	Functional analysis of the human CDC5L complex and identification of its components by mass spectrometry. EMBO Journal, 2000, 19, 6569-6581.	7.8	183
51	Building ProteomeTools based on a complete synthetic human proteome. Nature Methods, 2017, 14, 259-262.	19.0	182
52	Tyrosine Phosphorylation Mapping of the Epidermal Growth Factor Receptor Signaling Pathway. Journal of Biological Chemistry, 2002, 277, 1031-1039.	3.4	175
53	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. Nature Biotechnology, 2013, 31, 557-564.	17.5	164
54	Comprehensive Proteomic Analysis of Human Par Protein Complexes Reveals an Interconnected Protein Network. Journal of Biological Chemistry, 2004, 279, 12804-12811.	3.4	162

#	ARTICLE	IF	CITATIONS
55	Clec12a Is an Inhibitory Receptor for Uric Acid Crystals that Regulates Inflammation in Response to Cell Death. <i>Immunity</i> , 2014, 40, 389-399.	14.3	158
56	Mass Spectrometry-Based Proteomics in Preclinical Drug Discovery. <i>Chemistry and Biology</i> , 2012, 19, 72-84.	6.0	156
57	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155
58	18O-Labeling of N-Glycosylation Sites To Improve the Identification of Gel-Separated Glycoproteins Using Peptide Mass Mapping and Database Searching. <i>Analytical Chemistry</i> , 1999, 71, 1431-1440.	6.5	154
59	Meltome atlasâ€™ thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.	19.0	152
60	Proteome Wide Purification and Identification of <i>O</i>-GlcNAc-Modified Proteins Using Click Chemistry and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2013, 12, 927-936.	3.7	151
61	Generating high quality libraries for DIA MS with empirically corrected peptide predictions. <i>Nature Communications</i> , 2020, 11, 1548.	12.8	148
62	Immunomodulatory drugs disrupt the cereblonâ€™CD147â€™MCT1 axis to exert antitumor activity and teratogenicity. <i>Nature Medicine</i> , 2016, 22, 735-743.	30.7	145
63	Oligosaccharide sequencing technology. <i>Nature</i> , 1997, 388, 205-207.	27.8	144
64	Defining the carrier proteome limit for single-cell proteomics. <i>Nature Methods</i> , 2021, 18, 76-83.	19.0	142
65	Quadrupole time-of-flight versus triple-quadrupole mass spectrometry for the determination of phosphopeptides by precursor ion scanning. <i>Journal of Mass Spectrometry</i> , 2001, 36, 782-790.	1.6	141
66	A public-private partnership to unlock the untargeted kinome. <i>Nature Chemical Biology</i> , 2013, 9, 3-6.	8.0	141
67	Transgenic Mouse Proteomics Identifies New 14-3-3-associated Proteins Involved in Cytoskeletal Rearrangements and Cell Signaling. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2211-2227.	3.8	130
68	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020, 48, D1153-D1163.	14.5	126
69	Unconventional tethering of Ulp1 to the transport channel of the nuclear pore complex by karyopherins. <i>Nature Cell Biology</i> , 2003, 5, 21-27.	10.3	125
70	Mass spectrometry allows direct identification of proteins in large genomes. <i>Proteomics</i> , 2001, 1, 641-650.	2.2	124
71	<i>De novo</i> discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. <i>Journal of Pathology</i> , 2015, 235, 3-13.	4.5	116
72	Comprehensive and Reproducible Phosphopeptide Enrichment Using Iron Immobilized Metal Ion Affinity Chromatography (Fe-IMAC) Columns. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 205-215.	3.8	111

#	ARTICLE	IF	CITATIONS
73	Carbonyl-Reactive Tandem Mass Tags for the Proteome-Wide Quantification of N-Linked Glycans. <i>Analytical Chemistry</i> , 2012, 84, 3716-3724.	6.5	110
74	Glycosylation of Natural Human Neutrophil Gelatinase B and Neutrophil Gelatinase B-Associated Lipocalin. <i>Biochemistry</i> , 1999, 38, 13937-13950.	2.5	108
75	Optimized Chemical Proteomics Assay for Kinase Inhibitor Profiling. <i>Journal of Proteome Research</i> , 2015, 14, 1574-1586.	3.7	104
76	Glycosylation analysis of gel-separated proteins. <i>Proteomics</i> , 2001, 1, 350-361.	2.2	101
77	Identifying proteins and post-translational modifications by mass spectrometry. <i>Current Opinion in Structural Biology</i> , 1998, 8, 393-400.	5.7	98
78	Ion Mobility Tandem Mass Spectrometry Enhances Performance of Bottom-up Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3709-3715.	3.8	98
79	Peptide Level Turnover Measurements Enable the Study of Proteoform Dynamics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 974-992.	3.8	98
80	Plant Cytokinesis Is Orchestrated by the Sequential Action of the TRAPP II and Exocyst Tethering Complexes. <i>Developmental Cell</i> , 2014, 29, 607-620.	7.0	97
81	Mining the Human Tissue Proteome for Protein Citrullination. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1378-1391.	3.8	93
82	MALDI imaging mass spectrometry reveals COX7A2, TAGLN2 and S100-A10 as novel prognostic markers in Barrett's adenocarcinoma. <i>Journal of Proteomics</i> , 2012, 75, 4693-4704.	2.4	90
83	Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics. <i>Nature Communications</i> , 2021, 12, 3346.	12.8	90
84	moCluster: Identifying Joint Patterns Across Multiple Omics Data Sets. <i>Journal of Proteome Research</i> , 2016, 15, 755-765.	3.7	88
85	Comparison of fragmentation modes for the structural determination of complex oligosaccharides ionized by matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1995, 9, 1556-1561.	1.5	87
86	<i>N</i>-Heterocyclic carbenes on close-packed coinage metal surfaces: bis-carbene metal adatom bonding scheme of monolayer films on Au, Ag and Cu. <i>Chemical Science</i> , 2017, 8, 8301-8308.	7.4	87
87	A New Variant of the $\hat{1}^3$ Subunit of Renal Na,K-ATPase. <i>Journal of Biological Chemistry</i> , 2000, 275, 18441-18446.	3.4	84
88	A bead-based western for high-throughput cellular signal transduction analyses. <i>Nature Communications</i> , 2016, 7, 12852.	12.8	84
89	Systematic Identification of the HSP90 Regulated Proteome. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.016675.	3.8	82
90	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2016, 11, 1245-1254.	3.4	82

#	ARTICLE	IF	CITATIONS
91	Lapatinib Resistance in Breast Cancer Cells Is Accompanied by Phosphorylation-Mediated Reprogramming of Glycolysis. <i>Cancer Research</i> , 2017, 77, 1842-1853.	0.9	79
92	ProteomeTools: Systematic Characterization of 21 Post-translational Protein Modifications by Liquid Chromatography Tandem Mass Spectrometry (LC-MS/MS) Using Synthetic Peptides. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1850-1863.	3.8	78
93	Repurposing human kinase inhibitors to create an antibiotic active against drug-resistant <i>Staphylococcus aureus</i> , persisters and biofilms. <i>Nature Chemistry</i> , 2020, 12, 145-158.	13.6	78
94	Data, Reagents, Assays and Merits of Proteomics for SARS-CoV-2 Research and Testing. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1503-1522.	3.8	78
95	SCFFbxo9 and CK2 direct the cellular response to growth factor withdrawal via Tel2/Tti1 degradation and promote survival in multiple myeloma. <i>Nature Cell Biology</i> , 2013, 15, 72-81.	10.3	76
96	PROTAC-mediated degradation reveals a non-catalytic function of AURORA-A kinase. <i>Nature Chemical Biology</i> , 2020, 16, 1179-1188.	8.0	73
97	Clinical response to chemotherapy in oesophageal adenocarcinoma patients is linked to defects in mitochondria. <i>Journal of Pathology</i> , 2013, 230, 410-419.	4.5	71
98	<i>Arabidopsis</i> SH3P2 is an ubiquitin-binding protein that functions together with ESCRT-I and the deubiquitylating enzyme AMSH3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7197-E7204.	7.1	71
99	Challenges in Clinical Metaproteomics Highlighted by the Analysis of Acute Leukemia Patients with Gut Colonization by Multidrug-Resistant <i>Enterobacteriaceae</i> . <i>Proteomes</i> , 2019, 7, 2.	3.5	71
100	Rapid Approach for Sequencing Neutral Oligosaccharides by Exoglycosidase Digestion and Matrix-assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry. , 1996, 31, 1131-1140.		69
101	Comprehensive Identification of Proteins from MALDI Imaging. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2901-2910.	3.8	69
102	Quantitative Chemical Proteomics Reveals New Potential Drug Targets in Head and Neck Cancer. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011635.	3.8	65
103	Structural determination of N-linked carbohydrates by matrix-assisted laser desorption/ionization-mass spectrometry following enzymatic release within sodium dodecyl sulphate-polyacrylamide electrophoresis gels: Application to species-specific glycosylation of β 1-acid glycoprotein. <i>Electrophoresis</i> , 1998, 19, 1950-1959.	2.4	63
104	Phosphotyrosine mediated protein interactions of the discoidin domain receptor 1. <i>Journal of Proteomics</i> , 2012, 75, 3465-3477.	2.4	63
105	Quantification and discovery of sequence determinants of protein-mRNA amount in human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8513.	7.2	63
106	MOGSA: Integrative Single Sample Gene-set Analysis of Multiple Omics Data. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S153-S168.	3.8	59
107	Discovery of O-GlcNAc-modified Proteins in Published Large-scale Proteome Data. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 843-850.	3.8	58
108	A Simple and Effective Cleavable Linker for Chemical Proteomics Applications. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 237-244.	3.8	58

#	ARTICLE	IF	CITATIONS
109	PROCAL: A Set of 40 Peptide Standards for Retention Time Indexing, Column Performance Monitoring, and Collision Energy Calibration. <i>Proteomics</i> , 2017, 17, 1700263.	2.2	58
110	Femtomol sensitivity post-digest ¹⁸ O labeling for relative quantification of differential protein complex composition. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 869-876.	1.5	55
111	Gas-liquid mass transfer in rotating solid foam reactors. <i>Chemical Engineering Science</i> , 2010, 65, 472-479.	3.8	55
112	Optimized Plk1 PBD Inhibitors Based on Poloxin Induce Mitotic Arrest and Apoptosis in Tumor Cells. <i>ACS Chemical Biology</i> , 2015, 10, 2570-2579.	3.4	53
113	Modeling plasticity and dysplasia of pancreatic ductal organoids derived from human pluripotent stem cells. <i>Cell Stem Cell</i> , 2021, 28, 1105-1124.e19.	11.1	53
114	MALDI Imaging Mass Spectrometry for In Situ Proteomic Analysis of Preneoplastic Lesions in Pancreatic Cancer. <i>PLoS ONE</i> , 2012, 7, e39424.	2.5	52
115	Disruption of the PRKCD-FBXO25-HAX-1 axis attenuates the apoptotic response and drives lymphomagenesis. <i>Nature Medicine</i> , 2014, 20, 1401-1409.	30.7	50
116	Stress-primed secretory autophagy promotes extracellular BDNF maturation by enhancing MMP9 secretion. <i>Nature Communications</i> , 2021, 12, 4643.	12.8	50
117	Oxidative stress modulates theophylline effects on steroid responsiveness. <i>Biochemical and Biophysical Research Communications</i> , 2008, 377, 797-802.	2.1	49
118	Comparing Immobilized Kinase Inhibitors and Covalent ATP Probes for Proteomic Profiling of Kinase Expression and Drug Selectivity. <i>Journal of Proteome Research</i> , 2013, 12, 1723-1731.	3.7	48
119	Chemical Proteomics Uncovers EPHA2 as a Mechanism of Acquired Resistance to Small Molecule EGFR Kinase Inhibition. <i>Journal of Proteome Research</i> , 2015, 14, 2617-2625.	3.7	48
120	Mitotic arrest and slippage induced by pharmacological inhibition of Polo-like kinase 1. <i>Molecular Oncology</i> , 2015, 9, 140-154.	4.6	47
121	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
122	Proteome activity landscapes of tumor cell lines determine drug responses. <i>Nature Communications</i> , 2020, 11, 3639.	12.8	47
123	A hydrodynamically optimized nano-electrospray ionization source and vacuum interface. <i>Analyst</i> , 2014, 139, 1856.	3.5	45
124	Effect of the Reducing-terminal Substituents on the High Energy Collision-induced Dissociation Matrix-assisted Laser Desorption/Ionization Mass Spectra of Oligosaccharides. , 1996, 10, 1645-1651.		44
125	Pharmacoproteomic characterisation of human colon and rectal cancer. <i>Molecular Systems Biology</i> , 2017, 13, 951.	7.2	44
126	Label-free quantitative proteome analysis of the surface-bound salivary pellicle. <i>Colloids and Surfaces B: Biointerfaces</i> , 2017, 152, 68-76.	5.0	43

#	ARTICLE	IF	CITATIONS
127	High pH Reversed-Phase Micro-Columns for Simple, Sensitive, and Efficient Fractionation of Proteome and (TMT labeled) Phosphoproteome Digests. <i>Methods in Molecular Biology</i> , 2017, 1550, 83-98.	0.9	43
128	PROTEOFORMER 2.0: Further Developments in the Ribosome Profiling-assisted Proteogenomic Hunt for New Proteoforms. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S126-S140.	3.8	43
129	Co-immunoprecipitation-based identification of putative <scp>BAX INHIBITOR</scp>-interacting proteins involved in cell death regulation and plant-powdery mildew interactions. <i>Molecular Plant Pathology</i> , 2013, 14, 791-802.	4.2	42
130	Translatomics combined with transcriptomics and proteomics reveals novel functional, recently evolved orphan genes in <i>Escherichia coli</i> O157:H7 (EHEC). <i>BMC Genomics</i> , 2016, 17, 133.	2.8	42
131	Chemical Proteomics and Structural Biology Define EPHA2 Inhibition by Clinical Kinase Drugs. <i>ACS Chemical Biology</i> , 2016, 11, 3400-3411.	3.4	42
132	Selective multi-kinase inhibition sensitizes mesenchymal pancreatic cancer to immune checkpoint blockade by remodeling the tumor microenvironment. <i>Nature Cancer</i> , 2022, 3, 318-336.	13.2	42
133	Perspectives in the glycosciences-matrix-assisted laser desorption/ionization (MALDI) mass spectrometry of carbohydrates. <i>Glycoconjugate Journal</i> , 1998, 15, 333-338.	2.7	41
134	Degradation of CCNK/CDK12 is a druggable vulnerability of colorectal cancer. <i>Cell Reports</i> , 2021, 36, 109394.	6.4	41
135	The IMiD target CRBN determines HSP90 activity toward transmembrane proteins essential in multiple myeloma. <i>Molecular Cell</i> , 2021, 81, 1170-1186.e10.	9.7	39
136	The formation of a camalexin-biosynthetic metabolon. <i>Plant Cell</i> , 2019, 31, tpc.00403.2019.	6.6	38
137	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PP1 and PP2A. <i>Nature Communications</i> , 2020, 11, 3583.	12.8	38
138	Design, Synthesis, and Evaluation of WD-Repeat-Containing Protein 5 (WDR5) Degradors. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 10682-10710.	6.4	38
139	Robust Microflow LC-MS/MS for Proteome Analysis: 38,000 Runs and Counting. <i>Analytical Chemistry</i> , 2021, 93, 3686-3690.	6.5	36
140	Target deconvolution of HDAC pharmacopoeia reveals MBLAC2 as common off-target. <i>Nature Chemical Biology</i> , 2022, 18, 812-820.	8.0	36
141	ProteomicsDB: toward a FAIR open-source resource for life-science research. <i>Nucleic Acids Research</i> , 2022, 50, D1541-D1552.	14.5	35
142	Localized Inhibition of Protein Phosphatase 1 by NUA1 Promotes Spliceosome Activity and Reveals a MYC-Sensitive Feedback Control of Transcription. <i>Molecular Cell</i> , 2020, 77, 1322-1339.e11.	9.7	34
143	Cytomegalovirus subverts macrophage identity. <i>Cell</i> , 2021, 184, 3774-3793.e25.	28.9	34
144	Novel Flp pilus biogenesis-dependent natural transformation. <i>Frontiers in Microbiology</i> , 2015, 6, 84.	3.5	33

#	ARTICLE	IF	CITATIONS
145	Linking post-translational modifications and protein turnover by site-resolved protein turnover profiling. <i>Nature Communications</i> , 2022, 13, 165.	12.8	33
146	Evaluation of Kinase Activity Profiling Using Chemical Proteomics. <i>ACS Chemical Biology</i> , 2015, 10, 2743-2752.	3.4	32
147	Protease signaling through protease activated receptor 1 mediate nerve activation by mucosal supernatants from irritable bowel syndrome but not from ulcerative colitis patients. <i>PLoS ONE</i> , 2018, 13, e0193943.	2.5	32
148	Characterization of a Chemical Affinity Probe Targeting Akt Kinases. <i>Journal of Proteome Research</i> , 2013, 12, 3792-3800.	3.7	31
149	Reduced mitochondrial mass and function add to age-related susceptibility toward diet-induced fatty liver in C57BL/6J mice. <i>Physiological Reports</i> , 2016, 4, e12988.	1.7	31
150	Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100076.	3.8	31
151	Covalent Cross-links between the \hat{F}^3 Subunit (FXVD2) and \hat{F}^1 and \hat{F}^2 Subunits of Na,K-ATPase. <i>Journal of Biological Chemistry</i> , 2005, 280, 18291-18301.	3.4	30
152	Molecular mechanisms behind the antimicrobial activity of hop iso- \hat{F}^1 -acids in <i>Lactobacillus brevis</i> . <i>Food Microbiology</i> , 2015, 46, 553-563.	4.2	30
153	Loss of UCP1 function augments recruitment of futile lipid cycling for thermogenesis in murine brown fat. <i>Molecular Metabolism</i> , 2022, 61, 101499.	6.5	30
154	Cell cycle-regulated $\langle \text{sc} \rangle \text{PLEIADE} \langle / \text{sc} \rangle / \text{At} \langle \text{sc} \rangle \text{MAP} \langle / \text{sc} \rangle 65 \hat{\epsilon} 3$ links membrane and microtubule dynamics during plant cytokinesis. <i>Plant Journal</i> , 2016, 88, 531-541.	5.7	29
155	Identification of molecular targets for the targeted treatment of gastric cancer using dasatinib. <i>Oncotarget</i> , 2020, 11, 535-549.	1.8	29
156	PTPN2 Deficiency Enhances Programmed T Cell Expansion and Survival Capacity of Activated T Cells. <i>Cell Reports</i> , 2020, 32, 107957.	6.4	28
157	Quantitative mass spectrometry in proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 937-938.	3.7	27
158	Software Tools for MS-Based Quantitative Proteomics: A Brief Overview. <i>Methods in Molecular Biology</i> , 2012, 893, 489-499.	0.9	27
159	Proteomics Is Not an Island: Multi-omics Integration Is the Key to Understanding Biological Systems. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S1-S4.	3.8	27
160	Interactions between Transport Protein Particle (TRAPP) complexes and Rab $\langle \text{sc} \rangle \text{GTP} \langle / \text{sc} \rangle$ ases in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 100, 279-297.	5.7	27
161	Towards Understanding Male Infertility After Spinal Cord Injury Using Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1424-1434.	3.8	26
162	Optimized Enrichment of Phosphoproteomes by Fe-IMAC Column Chromatography. <i>Methods in Molecular Biology</i> , 2017, 1550, 47-60.	0.9	26

#	ARTICLE	IF	CITATIONS
163	Annotation of the Domestic Pig Genome by Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2017, 16, 2887-2898.	3.7	25
164	Salivary Proteome Patterns Affecting Human Salt Taste Sensitivity. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 9275-9286.	5.2	25
165	Rebuilding core abscisic acid signaling pathways of <i>Arabidopsis</i> in yeast. <i>EMBO Journal</i> , 2019, 38, e101859.	7.8	25
166	Identification of 7â€‘000â€‘9â€‘000 Proteins from Cell Lines and Tissues by Single-Shot Microflow LCâ€‘MS/MS. <i>Analytical Chemistry</i> , 2021, 93, 8687-8692.	6.5	25
167	Oligosaccharides of recombinant mouse gelatinase B variants. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1998, 1425, 587-598.	2.4	24
168	DENEDDYLASE1 Deconjugates NEDD8 from Non-Cullin Protein Substrates in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2015, 27, 741-753.	6.6	24
169	Targeted Diazotransfer Reagents Enable Selective Modification of Proteins with Azides. <i>Bioconjugate Chemistry</i> , 2017, 28, 913-917.	3.6	24
170	Mutations and variants of ONECUT1 in diabetes. <i>Nature Medicine</i> , 2021, 27, 1928-1940.	30.7	24
171	A Novel Two-Stage Tandem Mass Spectrometry Approach and Scoring Scheme for the Identification of O-GlcNAc Modified Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 931-942.	2.8	23
172	Phosphorylation site localization in peptides by MALDI MS/MS and the Mascot Delta Score. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 402, 249-260.	3.7	23
173	Effect of Astringent Stimuli on Salivary Protein Interactions Elucidated by Complementary Proteomics Approaches. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 2147-2154.	5.2	23
174	Chemoproteomicsâ€‘Aided Medicinal Chemistry for the Discovery of EPHA2 Inhibitors. <i>ChemMedChem</i> , 2017, 12, 999-1011.	3.2	23
175	Infection-induced rapid cell death in plants: a means of efficient pathogen defense. <i>Canadian Journal of Botany</i> , 1995, 73, 426-434.	1.1	22
176	Identification of oligosaccharides by matrix-assisted laser desorption ionization and electrospray MS. <i>Biochemical Society Transactions</i> , 1996, 24, 905-912.	3.4	22
177	Bacterial production and functional characterization of the Fab fragment of the murine IgG1/Â monoclonal antibody cmHsp70.1, a reagent for tumour diagnostics. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 161-168.	2.1	22
178	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. <i>Cell Reports</i> , 2015, 12, 183-189.	6.4	22
179	Trimodal Mixed Mode Chromatography That Enables Efficient Offline Two-Dimensional Peptide Fractionation for Proteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 8884-8891.	6.5	22
180	Dynamic Proteome Alteration and Functional Modulation of Human Saliva Induced by Dietary Chemosensory Stimuli. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 5621-5634.	5.2	22

#	ARTICLE	IF	CITATIONS
181	Increased Pancreatic Protease Activity in Response to Antibiotics Impairs Gut Barrier and Triggers Colitis. Cellular and Molecular Gastroenterology and Hepatology, 2018, 6, 370-388.e3.	4.5	22
182	Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. Journal of Proteome Research, 2021, 20, 3388-3394.	3.7	22
183	Plant Proteome Dynamics. Annual Review of Plant Biology, 2022, 73, 67-92.	18.7	22
184	Sucrose-Induced Proteomic Response and Carbohydrate Utilization of Lactobacillus sakei TMW 1.411 During Dextran Formation. Frontiers in Microbiology, 2018, 9, 2796.	3.5	21
185	Chemoproteomic Selectivity Profiling of PIKK and PI3K Kinase Inhibitors. ACS Chemical Biology, 2019, 14, 655-664.	3.4	21
186	Chemical Phosphoproteomics Sheds New Light on the Targets and Modes of Action of AKT Inhibitors. ACS Chemical Biology, 2021, 16, 631-641.	3.4	21
187	Discovery of O-GlcNAc-6-phosphate Modified Proteins in Large-scale Phosphoproteomics Data. Molecular and Cellular Proteomics, 2012, 11, 1063-1069.	3.8	20
188	Quantitative Proteomics for the Comprehensive Analysis of Stress Responses of <i>Lactobacillus paracasei</i> subsp. <i>paracasei</i> F19. Journal of Proteome Research, 2017, 16, 3816-3829.	3.7	20
189	NVPâ€œBHG712: Effects of Regioisomers on the Affinity and Selectivity toward the EPHrin Family. ChemMedChem, 2018, 13, 1629-1633.	3.2	20
190	Proteomic and transcriptomic profiling of aerial organ development in Arabidopsis. Scientific Data, 2020, 7, 334.	5.3	20
191	Quantitative chemical proteomics reveals a Plk1 inhibitor-compromised cell death pathway in human cells. Cell Research, 2014, 24, 1141-1145.	12.0	19
192	New Affinity Probe Targeting VEGF Receptors for Kinase Inhibitor Selectivity Profiling by Chemical Proteomics. Journal of Proteome Research, 2014, 13, 2445-2452.	3.7	19
193	Preferential microRNA targeting revealed by in vivo competitive binding and differential Argonaute immunoprecipitation. Nucleic Acids Research, 2017, 45, 10218-10228.	14.5	19
194	Combined proteomics/miRNomics of dendritic cell immunotherapy-treated glioblastoma patients as a screening for survival-associated factors. Npj Vaccines, 2020, 5, 5.	6.0	19
195	ERN1 and ALPK1 inhibit differentiation of bi-potential tumor-initiating cells in human breast cancer. Oncotarget, 2016, 7, 83278-83293.	1.8	19
196	Mass spectrometry-based draft of the mouse proteome. Nature Methods, 2022, 19, 803-811.	19.0	19
197	ML3 Is a NEDD8- and Ubiquitin-Modified Protein. Plant Physiology, 2013, 163, 135-149.	4.8	18
198	Phosphoproteome Profiling Reveals Molecular Mechanisms of Growth-Factor-Mediated Kinase Inhibitor Resistance in EGFR-Overexpressing Cancer Cells. Journal of Proteome Research, 2016, 15, 4490-4504.	3.7	18

#	ARTICLE	IF	CITATIONS
199	Bacterial Cellulose Shifts Transcriptome and Proteome of Cultured Endothelial Cells Towards Native Differentiation. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1563-1577.	3.8	18
200	Partially glucose-capped oligosaccharides are found on the hemoglobins of the deep-sea tube worm <i>Riftia pachyptila</i> . <i>Glycobiology</i> , 1998, 8, 663-673.	2.5	17
201	DENEDDYLASE1 Protein Counters Automodification of Neddylating Enzymes to Maintain NEDD8 Protein Homeostasis in Arabidopsis. <i>Journal of Biological Chemistry</i> , 2017, 292, 3854-3865.	3.4	17
202	SARS-CoV-2 infection remodels the host protein thermal stability landscape. <i>Molecular Systems Biology</i> , 2021, 17, e10188.	7.2	17
203	Proteomic profiling in cerebral amyloid angiopathy reveals an overlap with CADASIL highlighting accumulation of HTRA1 and its substrates. <i>Acta Neuropathologica Communications</i> , 2022, 10, 6.	5.2	16
204	Detection of plasmid-mediated colistin resistance, <i>mcr-1</i> gene, in <i>Escherichia coli</i> isolated from high-risk patients with acute leukemia in Spain. <i>Journal of Infection and Chemotherapy</i> , 2019, 25, 605-609.	1.7	15
205	An improved two-step calibration method for matrix-assisted laser desorption/ionization time-of-flight mass spectra for proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 1892-1895.	1.5	14
206	Ethylene glycol improves electrospray ionization efficiency in bottom-up proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 1049-1057.	3.7	14
207	MALDI-TOF and nESI Orbitrap MS/MS identify orthogonal parts of the phosphoproteome. <i>Proteomics</i> , 2016, 16, 1447-1456.	2.2	13
208	Hydrophilic Strong Anion Exchange (hSAX) Chromatography Enables Deep Fractionation of Tissue Proteomes. <i>Methods in Molecular Biology</i> , 2017, 1550, 69-82.	0.9	13
209	A novel Cereblon E3 ligase modulator with antitumor activity in gastrointestinal cancer. <i>Bioorganic Chemistry</i> , 2022, 119, 105505.	4.1	13
210	Comprehensive proteome analysis in <i>Cenococcum geophilum</i> Fr. as a tool to discover drought-related proteins. <i>Journal of Proteomics</i> , 2012, 75, 3707-3719.	2.4	12
211	Phosphoramidates as Novel Activity-Based Probes for Serine Proteases. <i>ChemBioChem</i> , 2014, 15, 1106-1110.	2.6	12
212	Evaluation of Disposable Trap Column nanoLC-FAIMS-MS/MS for the Proteomic Analysis of FFPE Tissue. <i>Journal of Proteome Research</i> , 2021, 20, 5402-5411.	3.7	12
213	MScDB: A Mass Spectrometry-centric Protein Sequence Database for Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 2386-2398.	3.7	11
214	A new chemical probe for quantitative proteomic profiling of fibroblast growth factor receptor and its inhibitors. <i>Journal of Proteomics</i> , 2014, 96, 44-55.	2.4	11
215	Reduced mitochondrial resilience enables non-canonical induction of apoptosis after TNF receptor signaling in virus-infected hepatocytes. <i>Journal of Hepatology</i> , 2020, 73, 1347-1359.	3.7	11
216	Probing SH2-domains using Inhibitor Affinity Purification (IAP). <i>Proteome Science</i> , 2014, 12, 41.	1.7	10

#	ARTICLE	IF	CITATIONS
217	Inhibitor-based affinity probes for the investigation of JAK signaling pathways. <i>Proteomics</i> , 2015, 15, 3066-3074.	2.2	10
218	Identification of Highly Potent Protein Kinase-Related Kinase Inhibitors by Virtual Screening, Binding Free Energy Rescoring, and in-vitro Testing. <i>ChemMedChem</i> , 2016, 11, 2084-2094.	3.2	10
219	Tofacitinib and analogs as inhibitors of the histone kinase PRK1 (PKN1). <i>Future Medicinal Chemistry</i> , 2016, 8, 1537-1551.	2.3	10
220	Proteomic and Metabolite Profiling Reveals Profound Structural and Metabolic Reorganization of Adipocyte Mitochondria in Obesity. <i>Obesity</i> , 2020, 28, 590-600.	3.0	10
221	Ultra-high intra-spectrum mass accuracy enables unambiguous identification of fragment reporter ions in isobaric multiplexed quantitative proteomics. <i>Proteomics</i> , 2012, 12, 1328-1332.	2.2	9
222	Characterization of a high field Orbitrap mass spectrometer for proteome analysis. <i>Proteomics</i> , 2013, 13, 2552-2562.	2.2	9
223	Persistent inhibition of pore-based cell migration by sub-toxic doses of miuraenamamide, an actin filament stabilizer. <i>Scientific Reports</i> , 2017, 7, 16407.	3.3	9
224	Adaptive Resistance to EGFR-Targeted Therapy by Calcium Signaling in NSCLC Cells. <i>Molecular Cancer Research</i> , 2018, 16, 1773-1784.	3.4	9
225	Functional expression of electrogenic sodium bicarbonate cotransporter 1 (NBCe1) in mouse cortical astrocytes is dependent on S255-257 and regulated by mTOR. <i>Glia</i> , 2019, 67, 2264-2278.	4.9	9
226	Systematic analysis of migration factors by MigExpress identifies essential cell migration control genes in non-small cell lung cancer. <i>Molecular Oncology</i> , 2021, 15, 1797-1817.	4.6	9
227	High sensitivity glycomics in biomedicine. <i>Mass Spectrometry Reviews</i> , 2022, 41, 1014-1039.	5.4	9
228	SIMSI-Transfer: Software-Assisted Reduction of Missing Values in Phosphoproteomic and Proteomic Isobaric Labeling Data Using Tandem Mass Spectrum Clustering. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100238.	3.8	9
229	Novel, highly potent PROTACs targeting AURORA-A kinase. <i>Current Research in Chemical Biology</i> , 2022, 2, 100032.	2.9	9
230	Quantitative proteome profiling of human myoma and myometrium tissue reveals kinase expression signatures with potential for therapeutic intervention. <i>Proteomics</i> , 2015, 15, 356-364.	2.2	8
231	A series of novel aryl-methanone derivatives as inhibitors of FMS-like tyrosine kinase 3 (FLT3) in FLT3-ITD-positive acute myeloid leukemia. <i>European Journal of Medicinal Chemistry</i> , 2020, 193, 112232.	5.5	8
232	Loss of the Fanconi anemia-associated protein NIPA causes bone marrow failure. <i>Journal of Clinical Investigation</i> , 2020, 130, 2827-2844.	8.2	8
233	High temporal resolution proteome and phosphoproteome profiling of stem cell-derived hepatocyte development. <i>Cell Reports</i> , 2022, 38, 110604.	6.4	8
234	Prosit-TMT: Deep Learning Boosts Identification of TMT-Labeled Peptides. <i>Analytical Chemistry</i> , 2022, 94, 7181-7190.	6.5	8

#	ARTICLE	IF	CITATIONS
235	Radiosensitization by Kinase Inhibition Revealed by Phosphoproteomic Analysis of Pancreatic Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1649-1663.	3.8	7
236	Wilhelm et al. reply. <i>Nature</i> , 2017, 547, E23-E23.	27.8	7
237	Isolation and Structure Determination of a New Iridal from <i>Iris sibirica</i> . <i>Journal of Natural Products</i> , 1995, 58, 299-301.	3.0	6
238	Epigenetic drug screening defines a PRMT5 inhibitor-sensitive pancreatic cancer subtype. <i>JCI Insight</i> , 2022, 7, .	5.0	6
239	Expression and Purification of EPHA2 Tyrosine Kinase Domain for Crystallographic and NMR Studies. <i>ChemBioChem</i> , 2016, 17, 2257-2263.	2.6	5
240	Two serines in the distal C-terminus of the human β 1-adrenoceptor determine β -arrestin2 recruitment. <i>PLoS ONE</i> , 2017, 12, e0176450.	2.5	5
241	PLK1-dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBV-infected mice. <i>EMBO Reports</i> , 2021, 22, e53007.	4.5	5
242	Characterisation of tissue-specific oligosaccharides from rat brain and kidney membrane preparations enriched in Na ⁺ ,K ⁺ -ATPase. <i>Glycoconjugate Journal</i> , 1999, 16, 437-456.	2.7	4
243	Posttranslational modification of the RHO of plants protein RACB by phosphorylation and cross-kingdom conserved ubiquitination. <i>PLoS ONE</i> , 2022, 17, e0258924.	2.5	4
244	Requirement of ATM-Dependent Monoubiquitylation of Histone H2B for Timely Repair of DNA Double-Strand Breaks. <i>Molecular Cell</i> , 2011, 42, 137.	9.7	3
245	PAS-cal: a Generic Recombinant Peptide Calibration Standard for Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 1489-1497.	2.8	3
246	PAS-cal: A repetitive peptide sequence calibration standard for MALDI mass spectrometry. <i>Proteomics</i> , 2014, 14, 2427-2431.	2.2	3
247	Target and identify: triazene linker helps identify azidation sites of labelled proteins via click and cleave strategy. <i>Chemical Communications</i> , 2017, 53, 11929-11932.	4.1	3
248	CiRCus: A Framework to Enable Classification of Complex High-Throughput Experiments. <i>Journal of Proteome Research</i> , 2019, 18, 1486-1493.	3.7	3
249	Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry of N-Linked Carbohydrates and Related Compounds. , 2000, , 403-437.		3
250	Development of hetero-triaryls as a new chemotype for subtype-selective and potent Sirt5 inhibition. <i>European Journal of Medicinal Chemistry</i> , 2022, 240, 114594.	5.5	3
251	Investigating RET RTK Signaling Pathways Using an IAP-Based Activity-Profiling Approach. <i>Journal of Proteome Research</i> , 2014, 13, 3628-3634.	3.7	2
252	Affinity Purification of Proteins Binding to Kinase Inhibitors Immobilized on Self-Assembling Monolayers. <i>Methods in Molecular Biology</i> , 2012, 795, 149-160.	0.9	0

#	ARTICLE	IF	CITATIONS
253	Deciphering The Molecular Impact Of Myc Overexpression On B Cell Receptor Signaling and Its Implications For Burkitt Lymphoma Treatment. Blood, 2013, 122, 3018-3018.	1.4	0
254	The IMiD-Target Cereblon Determines Transmembrane Protein Quality Control Promoting Tumor Metabolism. Blood, 2019, 134, 314-314.	1.4	0