

Bernhard Kuster

List of Publications by Year in descending order

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254
papers

36,500
citations

5876

81
h-index

3638

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. <i>Nature</i> , 2002, 415, 141-147.	13.7	4,509
2	Proteome survey reveals modularity of the yeast cell machinery. <i>Nature</i> , 2006, 440, 631-636.	13.7	2,347
3	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014, 509, 582-587.	13.7	1,697
4	Quantitative mass spectrometry in proteomics: a critical review. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 1017-1031.	1.9	1,448
5	Quantitative chemical proteomics reveals mechanisms of action of clinical ABL kinase inhibitors. <i>Nature Biotechnology</i> , 2007, 25, 1035-1044.	9.4	979
6	A physical and functional map of the human TNF- α /NF- κ B signal transduction pathway. <i>Nature Cell Biology</i> , 2004, 6, 97-105.	4.6	970
7	Tracking cancer drugs in living cells by thermal profiling of the proteome. <i>Science</i> , 2014, 346, 1255-784.	6.0	812
8	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 939-965.	1.9	695
9	Computational prediction of proteotypic peptides for quantitative proteomics. <i>Nature Biotechnology</i> , 2007, 25, 125-131.	9.4	653
10	The target landscape of clinical kinase drugs. <i>Science</i> , 2017, 358, .	6.0	609
11	High-fat diet alters gut microbiota physiology in mice. <i>ISME Journal</i> , 2014, 8, 295-308.	4.4	583
12	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8503.	3.2	576
13	Cell-cycle-regulated association of RAD50/MRE11/NBS1 with TRF2 and human telomeres. <i>Nature Genetics</i> , 2000, 25, 347-352.	9.4	560
14	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3625-3630.	6.5	555
15	Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning. <i>Nature Methods</i> , 2019, 16, 509-518.	9.0	539
16	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. <i>Nature</i> , 2021, 594, 246-252.	13.7	475
17	90S Pre-Ribosomes Include the 35S Pre-rRNA, the U3 snoRNP, and 40S Subunit Processing Factors but Predominantly Lack 60S Synthesis Factors. <i>Molecular Cell</i> , 2002, 10, 105-115.	4.5	427
18	Proteomics: a pragmatic perspective. <i>Nature Biotechnology</i> , 2010, 28, 695-709.	9.4	374

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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.	1.1	371
20	K + Efflux-Independent NLRP3 Inflammasome Activation by Small Molecules Targeting Mitochondria. <i>Immunity</i> , 2016, 45, 761-773.	6.6	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.	2.5	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.	4.5	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.	4.5	347
24	Scoring proteomes with proteotypic peptide probes. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 577-583.	16.1	344
25	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020, 579, 409-414.	13.7	328
26	Phospho.ELM: a database of experimentally verified phosphorylation sites in eukaryotic proteins. <i>BMC Bioinformatics</i> , 2004, 5, 79.	1.2	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.	3.2	306
28	Dimension reduction techniques for the integrative analysis of multi-omics data. <i>Briefings in Bioinformatics</i> , 2016, 17, 628-641.	3.2	280
29	Global Proteome Analysis of the NCI-60 Cell Line Panel. <i>Cell Reports</i> , 2013, 4, 609-620.	2.9	276
30	Confident Phosphorylation Site Localization Using the Mascot Delta Score. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S12.	2.5	247
31	Enterococcus faecalis Metalloprotease Compromises Epithelial Barrier and Contributes to Intestinal Inflammation. <i>Gastroenterology</i> , 2011, 141, 959-971.	0.6	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.	2.5	245
33	Measuring and Managing Ratio Compression for Accurate iTRAQ/TMT Quantification. <i>Journal of Proteome Research</i> , 2013, 12, 3586-3598.	1.8	238
34	A multivariate approach to the integration of multi-omics datasets. <i>BMC Bioinformatics</i> , 2014, 15, 162.	1.2	238
35	A Proteome-wide Approach Identifies Sumoylated Substrate Proteins in Yeast. <i>Journal of Biological Chemistry</i> , 2004, 279, 41346-41351.	1.6	236
36	Robust and Sensitive iTRAQ Quantification on an LTQ Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1702-1713.	2.5	219

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37	Robust, reproducible and quantitative analysis of thousands of proteomes by micro-flow LC-MS/MS. <i>Nature Communications</i> , 2020, 11, 157.	5.8	218
38	Sorafenib promotes graft-versus-leukemia activity in mice and humans through IL-15 production in FLT3-ITD-mutant leukemia cells. <i>Nature Medicine</i> , 2018, 24, 282-291.	15.2	216
39	Composition of N-linked carbohydrates from ovalbumin and co-purified glycoproteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2000, 11, 564-571.	1.2	213
40	Profiling Core Proteomes of Human Cell Lines by One-dimensional PAGE and Liquid Chromatography-Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 1297-1305.	2.5	210
41	DMSO enhances electrospray response, boosting sensitivity of proteomic experiments. <i>Nature Methods</i> , 2013, 10, 989-991.	9.0	209
42	Auxin efflux by PIN-FORMED proteins is activated by two different protein kinases, D6 PROTEIN KINASE and PINOID. <i>ELife</i> , 2014, 3, .	2.8	205
43	The Inflammasome Drives GSDMD-Independent Secondary Pyroptosis and IL-1 Release in the Absence of Caspase-1 Protease Activity. <i>Cell Reports</i> , 2017, 21, 3846-3859.	2.9	202
44	Affinity purification-mass spectrometry. <i>FEBS Journal</i> , 2003, 270, 570-578.	0.2	200
45	The gut microbiota promotes hepatic fatty acid desaturation and elongation in mice. <i>Nature Communications</i> , 2018, 9, 3760.	5.8	200
46	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.	9.0	198
47	ProteomicsDB. <i>Nucleic Acids Research</i> , 2018, 46, D1271-D1281.	6.5	197
48	A Transmembrane Tight Junction Protein Selectively Expressed on Endothelial Cells and Platelets. <i>Journal of Biological Chemistry</i> , 2002, 277, 16294-16303.	1.6	196
49	Lactocepin Secreted By <i>Lactobacillus</i> Exerts Anti-Inflammatory Effects By Selectively Degrading Proinflammatory Chemokines. <i>Cell Host and Microbe</i> , 2012, 11, 387-396.	5.1	196
50	Functional analysis of the human CDC5L complex and identification of its components by mass spectrometry. <i>EMBO Journal</i> , 2000, 19, 6569-6581.	3.5	183
51	Building ProteomeTools based on a complete synthetic human proteome. <i>Nature Methods</i> , 2017, 14, 259-262.	9.0	182
52	Tyrosine Phosphorylation Mapping of the Epidermal Growth Factor Receptor Signaling Pathway. <i>Journal of Biological Chemistry</i> , 2002, 277, 1031-1039.	1.6	175
53	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , 2013, 31, 557-564.	9.4	164
54	Comprehensive Proteomic Analysis of Human Par Protein Complexes Reveals an Interconnected Protein Network. <i>Journal of Biological Chemistry</i> , 2004, 279, 12804-12811.	1.6	162

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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.	6.6	158
56	Mass Spectrometry-Based Proteomics in Preclinical Drug Discovery. <i>Chemistry and Biology</i> , 2012, 19, 72-84.	6.2	156
57	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	9.4	155
58	¹⁸ O-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.	3.2	154
59	Meltome atlas [™] thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.	9.0	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.	1.8	151
61	Generating high quality libraries for DIA MS with empirically corrected peptide predictions. <i>Nature Communications</i> , 2020, 11, 1548.	5.8	148
62	Immunomodulatory drugs disrupt the cereblon [®] “CD147 [®] “MCT1 axis to exert antitumor activity and teratogenicity. <i>Nature Medicine</i> , 2016, 22, 735-743.	15.2	145
63	Oligosaccharide sequencing technology. <i>Nature</i> , 1997, 388, 205-207.	13.7	144
64	Defining the carrier proteome limit for single-cell proteomics. <i>Nature Methods</i> , 2021, 18, 76-83.	9.0	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.	0.7	141
66	A public-private partnership to unlock the untargeted kinome. <i>Nature Chemical Biology</i> , 2013, 9, 3-6.	3.9	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.	2.5	130
68	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020, 48, D1153-D1163.	6.5	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.	4.6	125
70	Mass spectrometry allows direct identification of proteins in large genomes. <i>Proteomics</i> , 2001, 1, 641-650.	1.3	124
71	<i>De novo</i> discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. <i>Journal of Pathology</i> , 2015, 235, 3-13.	2.1	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.	2.5	111

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73	Carbonyl-Reactive Tandem Mass Tags for the Proteome-Wide Quantification of N-Linked Glycans. <i>Analytical Chemistry</i> , 2012, 84, 3716-3724.	3.2	110
74	Glycosylation of Natural Human Neutrophil Gelatinase B and Neutrophil Gelatinase B-Associated Lipocalin. <i>Biochemistry</i> , 1999, 38, 13937-13950.	1.2	108
75	Optimized Chemical Proteomics Assay for Kinase Inhibitor Profiling. <i>Journal of Proteome Research</i> , 2015, 14, 1574-1586.	1.8	104
76	Glycosylation analysis of gel-separated proteins. <i>Proteomics</i> , 2001, 1, 350-361.	1.3	101
77	Identifying proteins and post-translational modifications by mass spectrometry. <i>Current Opinion in Structural Biology</i> , 1998, 8, 393-400.	2.6	98
78	Ion Mobility Tandem Mass Spectrometry Enhances Performance of Bottom-up Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3709-3715.	2.5	98
79	Peptide Level Turnover Measurements Enable the Study of Proteoform Dynamics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 974-992.	2.5	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.	3.1	97
81	Mining the Human Tissue Proteome for Protein Citrullination. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1378-1391.	2.5	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.	1.2	90
83	Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics. <i>Nature Communications</i> , 2021, 12, 3346.	5.8	90
84	moCluster: Identifying Joint Patterns Across Multiple Omics Data Sets. <i>Journal of Proteome Research</i> , 2016, 15, 755-765.	1.8	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.	0.7	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.	3.7	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.	1.6	84
88	A bead-based western for high-throughput cellular signal transduction analyses. <i>Nature Communications</i> , 2016, 7, 12852.	5.8	84
89	Systematic Identification of the HSP90 Regulated Proteome. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.016675.	2.5	82
90	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2016, 11, 1245-1254.	1.6	82

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91	Lapatinib Resistance in Breast Cancer Cells Is Accompanied by Phosphorylation-Mediated Reprogramming of Glycolysis. <i>Cancer Research</i> , 2017, 77, 1842-1853.	0.4	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.	2.5	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.	6.6	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.	2.5	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.	4.6	76
96	PROTAC-mediated degradation reveals a non-catalytic function of AURORA-A kinase. <i>Nature Chemical Biology</i> , 2020, 16, 1179-1188.	3.9	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.	2.1	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.	3.3	71
99	Challenges in Clinical Metaproteomics Highlighted by the Analysis of Acute Leukemia Patients with Gut Colonization by Multidrug-Resistant Enterobacteriaceae. <i>Proteomes</i> , 2019, 7, 2.	1.7	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.	2.5	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.	2.5	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.	1.3	63
104	Phosphotyrosine mediated protein interactions of the discoidin domain receptor 1. <i>Journal of Proteomics</i> , 2012, 75, 3465-3477.	1.2	63
105	Quantification and discovery of sequence determinants of protein mRNA amount in human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8513.	3.2	63
106	MOGSA: Integrative Single Sample Gene-set Analysis of Multiple Omics Data. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S153-S168.	2.5	59
107	Discovery of O-GlcNAc-modified Proteins in Published Large-scale Proteome Data. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 843-850.	2.5	58
108	A Simple and Effective Cleavable Linker for Chemical Proteomics Applications. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 237-244.	2.5	58

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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.	1.3	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.	0.7	55
111	Gas-liquid mass transfer in rotating solid foam reactors. <i>Chemical Engineering Science</i> , 2010, 65, 472-479.	1.9	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.	1.6	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.	5.2	53
114	MALDI Imaging Mass Spectrometry for In Situ Proteomic Analysis of Preneoplastic Lesions in Pancreatic Cancer. <i>PLoS ONE</i> , 2012, 7, e39424.	1.1	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.	15.2	50
116	Stress-primed secretory autophagy promotes extracellular BDNF maturation by enhancing MMP9 secretion. <i>Nature Communications</i> , 2021, 12, 4643.	5.8	50
117	Oxidative stress modulates theophylline effects on steroid responsiveness. <i>Biochemical and Biophysical Research Communications</i> , 2008, 377, 797-802.	1.0	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.	1.8	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.	1.8	48
120	Mitotic arrest and slippage induced by pharmacological inhibition of Polo-like kinase 1. <i>Molecular Oncology</i> , 2015, 9, 140-154.	2.1	47
121	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	1.8	47
122	Proteome activity landscapes of tumor cell lines determine drug responses. <i>Nature Communications</i> , 2020, 11, 3639.	5.8	47
123	A hydrodynamically optimized nano-electrospray ionization source and vacuum interface. <i>Analyst</i> , 2014, 139, 1856.	1.7	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.	3.2	44
126	Label-free quantitative proteome analysis of the surface-bound salivary pellicle. <i>Colloids and Surfaces B: Biointerfaces</i> , 2017, 152, 68-76.	2.5	43

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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.	0.4	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.	2.5	43
129	Co-immunoprecipitation-based identification of putative BAX INHIBITOR-1 interacting proteins involved in cell death regulation and plant-powdery mildew interactions. <i>Molecular Plant Pathology</i> , 2013, 14, 791-802.	2.0	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.	1.2	42
131	Chemical Proteomics and Structural Biology Define EPHA2 Inhibition by Clinical Kinase Drugs. <i>ACS Chemical Biology</i> , 2016, 11, 3400-3411.	1.6	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.	5.7	42
133	Perspectives in the glycosciences-matrix-assisted laser desorption/ionization (MALDI) mass spectrometry of carbohydrates. <i>Glycoconjugate Journal</i> , 1998, 15, 333-338.	1.4	41
134	Degradation of CCNK/CDK12 is a druggable vulnerability of colorectal cancer. <i>Cell Reports</i> , 2021, 36, 109394.	2.9	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.	4.5	39
136	The formation of a camalexin-biosynthetic metabolon. <i>Plant Cell</i> , 2019, 31, tpc.00403.2019.	3.1	38
137	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PPI and PP2A. <i>Nature Communications</i> , 2020, 11, 3583.	5.8	38
138	Design, Synthesis, and Evaluation of WD-Repeat-Containing Protein 5 (WDR5) Degraders. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 10682-10710.	2.9	38
139	Robust Microflow LC-MS/MS for Proteome Analysis: 38,000 Runs and Counting. <i>Analytical Chemistry</i> , 2021, 93, 3686-3690.	3.2	36
140	Target deconvolution of HDAC pharmacopoeia reveals MBLAC2 as common off-target. <i>Nature Chemical Biology</i> , 2022, 18, 812-820.	3.9	36
141	ProteomicsDB: toward a FAIR open-source resource for life-science research. <i>Nucleic Acids Research</i> , 2022, 50, D1541-D1552.	6.5	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.	4.5	34
143	Cytomegalovirus subverts macrophage identity. <i>Cell</i> , 2021, 184, 3774-3793.e25.	13.5	34
144	Novel Flp pilus biogenesis-dependent natural transformation. <i>Frontiers in Microbiology</i> , 2015, 6, 84.	1.5	33

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145	Linking post-translational modifications and protein turnover by site-resolved protein turnover profiling. <i>Nature Communications</i> , 2022, 13, 165.	5.8	33
146	Evaluation of Kinase Activity Profiling Using Chemical Proteomics. <i>ACS Chemical Biology</i> , 2015, 10, 2743-2752.	1.6	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.	1.1	32
148	Characterization of a Chemical Affinity Probe Targeting Akt Kinases. <i>Journal of Proteome Research</i> , 2013, 12, 3792-3800.	1.8	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.	0.7	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.	2.5	31
151	Covalent Cross-links between the \hat{I}^3 Subunit (FXVD2) and \hat{I}^1 and \hat{I}^2 Subunits of Na,K-ATPase. <i>Journal of Biological Chemistry</i> , 2005, 280, 18291-18301.	1.6	30
152	Molecular mechanisms behind the antimicrobial activity of hop iso- \hat{I}^1 -acids in <i>Lactobacillus brevis</i> . <i>Food Microbiology</i> , 2015, 46, 553-563.	2.1	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.	3.0	30
154	Cell cycle-regulated <i>PLEIADE</i> / <i>AtMAP</i> links membrane and microtubule dynamics during plant cytokinesis. <i>Plant Journal</i> , 2016, 88, 531-541.	2.8	29
155	Identification of molecular targets for the targeted treatment of gastric cancer using dasatinib. <i>Oncotarget</i> , 2020, 11, 535-549.	0.8	29
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