

Bernhard Kuster

List of Publications by Citations

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258
papers

27,972
citations

76
h-index

165
g-index

274
ext. papers

33,021
ext. citations

11.4
avg, IF

6.71
L-index

#	Paper	IF	Citations
258	Functional organization of the yeast proteome by systematic analysis of protein complexes. <i>Nature</i> , 2002 , 415, 141-7	50.4	4018
257	Proteome survey reveals modularity of the yeast cell machinery. <i>Nature</i> , 2006 , 440, 631-6	50.4	2096
256	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014 , 509, 582-7	50.4	1332
255	Quantitative mass spectrometry in proteomics: a critical review. <i>Analytical and Bioanalytical Chemistry</i> , 2007 , 389, 1017-31	4.4	1252
254	Quantitative chemical proteomics reveals mechanisms of action of clinical ABL kinase inhibitors. <i>Nature Biotechnology</i> , 2007 , 25, 1035-44	44.5	864
253	A physical and functional map of the human TNF-alpha/NF-kappa B signal transduction pathway. <i>Nature Cell Biology</i> , 2004 , 6, 97-105	23.4	847
252	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. <i>Analytical and Bioanalytical Chemistry</i> , 2012 , 404, 939-65	4.4	585
251	Computational prediction of proteotypic peptides for quantitative proteomics. <i>Nature Biotechnology</i> , 2007 , 25, 125-31	44.5	582
250	Tracking cancer drugs in living cells by thermal profiling of the proteome. <i>Science</i> , 2014 , 346, 1255784	33.3	526
249	Cell-cycle-regulated association of RAD50/MRE11/NBS1 with TRF2 and human telomeres. <i>Nature Genetics</i> , 2000 , 25, 347-52	36.3	509
248	ELM server: A new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003 , 31, 3625-30	20.1	491
247	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, 105-15	17.6	395
246	High-fat diet alters gut microbiota physiology in mice. <i>ISME Journal</i> , 2014 , 8, 295-308	11.9	393
245	The target landscape of clinical kinase drugs. <i>Science</i> , 2017 , 358,	33.3	389
244	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	3.1	350
243	Proteomics: a pragmatic perspective. <i>Nature Biotechnology</i> , 2010 , 28, 695-709	44.5	325
242	ERCC1/XPF removes the 3S overhang from uncapped telomeres and represses formation of telomeric DNA-containing double minute chromosomes. <i>Molecular Cell</i> , 2003 , 12, 1489-98	17.6	319

241	Scoring proteomes with proteotypic peptide probes. <i>Nature Reviews Molecular Cell Biology</i> , 2005 , 6, 577-587	4.7	310
240	Requirement of ATM-dependent monoubiquitylation of histone H2B for timely repair of DNA double-strand breaks. <i>Molecular Cell</i> , 2011 , 41, 529-42	17.6	288
239	Detection of tyrosine phosphorylated peptides by precursor ion scanning quadrupole TOF mass spectrometry in positive ion mode. <i>Analytical Chemistry</i> , 2001 , 73, 1440-8	7.8	286
238	Phospho.ELM: a database of experimentally verified phosphorylation sites in eukaryotic proteins. <i>BMC Bioinformatics</i> , 2004 , 5, 79	3.6	282
237	Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning. <i>Nature Methods</i> , 2019 , 16, 509-518	21.6	242
236	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. <i>Molecular Systems Biology</i> , 2019 , 15, e8503	12.2	235
235	Global proteome analysis of the NCI-60 cell line panel. <i>Cell Reports</i> , 2013 , 4, 609-20	10.6	225
234	Confident phosphorylation site localization using the Mascot Delta Score. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.003830	7.6	225
233	K Efflux-Independent NLRP3 Inflammasome Activation by Small Molecules Targeting Mitochondria. <i>Immunity</i> , 2016 , 45, 761-773	32.3	219
232	A proteome-wide approach identifies sumoylated substrate proteins in yeast. <i>Journal of Biological Chemistry</i> , 2004 , 279, 41346-51	5.4	218
231	A Scalable Approach for Protein False Discovery Rate Estimation in Large Proteomic Data Sets. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2394-404	7.6	210
230	Robust and sensitive iTRAQ quantification on an LTQ Orbitrap mass spectrometer. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1702-13	7.6	208
229	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, 1297-305	7.6	196
228	Composition of N-linked carbohydrates from ovalbumin and co-purified glycoproteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2000 , 11, 564-71	3.5	194
227	Dimension reduction techniques for the integrative analysis of multi-omics data. <i>Briefings in Bioinformatics</i> , 2016 , 17, 628-41	13.4	192
226	<i>Enterococcus faecalis</i> metalloprotease compromises epithelial barrier and contributes to intestinal inflammation. <i>Gastroenterology</i> , 2011 , 141, 959-71	13.3	186
225	Measuring and managing ratio compression for accurate iTRAQ/TMT quantification. <i>Journal of Proteome Research</i> , 2013 , 12, 3586-98	5.6	177
224	A transmembrane tight junction protein selectively expressed on endothelial cells and platelets. <i>Journal of Biological Chemistry</i> , 2002 , 277, 16294-303	5.4	172

223	DMSO enhances electrospray response, boosting sensitivity of proteomic experiments. <i>Nature Methods</i> , 2013 , 10, 989-91	21.6	170
222	Tyrosine phosphorylation mapping of the epidermal growth factor receptor signaling pathway. <i>Journal of Biological Chemistry</i> , 2002 , 277, 1031-9	5.4	165
221	A multivariate approach to the integration of multi-omics datasets. <i>BMC Bioinformatics</i> , 2014 , 15, 162	3.6	161
220	Affinity purification-mass spectrometry. Powerful tools for the characterization of protein complexes. <i>FEBS Journal</i> , 2003 , 270, 570-8		159
219	Functional analysis of the human CDC5L complex and identification of its components by mass spectrometry. <i>EMBO Journal</i> , 2000 , 19, 6569-81	13	158
218	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. <i>Nature</i> , 2021 , 594, 246-254	25.4	150
217	Lactocepin secreted by <i>Lactobacillus</i> exerts anti-inflammatory effects by selectively degrading proinflammatory chemokines. <i>Cell Host and Microbe</i> , 2012 , 11, 387-96	23.4	149
216	Comprehensive proteomic analysis of human Par protein complexes reveals an interconnected protein network. <i>Journal of Biological Chemistry</i> , 2004 , 279, 12804-11	5.4	149
215	Auxin efflux by PIN-FORMED proteins is activated by two different protein kinases, D6 PROTEIN KINASE and PINOID. <i>ELife</i> , 2014 , 3,	8.9	146
214	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, 1431-40	7.8	145
213	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020 , 579, 409-414	50.4	144
212	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	50.5	144
211	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	10.6	140
210	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008 , 26, 164-7	44.5	138
209	Oligosaccharide sequencing technology. <i>Nature</i> , 1997 , 388, 205-7	50.4	134
208	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , 2013 , 31, 557-64	44.5	132
207	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, 782-90	2.2	127
206	Building ProteomeTools based on a complete synthetic human proteome. <i>Nature Methods</i> , 2017 , 14, 259-262	21.6	126

205	Mass spectrometry-based proteomics in preclinical drug discovery. <i>Chemistry and Biology</i> , 2012 , 19, 72-84	125
204	Proteome wide purification and identification of O-GlcNAc-modified proteins using click chemistry and mass spectrometry. <i>Journal of Proteome Research</i> , 2013 , 12, 927-36	5.6 123
203	A public-private partnership to unlock the untargeted kinome. <i>Nature Chemical Biology</i> , 2013 , 9, 3-6	11.7 119
202	Clec12a is an inhibitory receptor for uric acid crystals that regulates inflammation in response to cell death. <i>Immunity</i> , 2014 , 40, 389-99	32.3 116
201	Mass spectrometry allows direct identification of proteins in large genomes. <i>Proteomics</i> , 2001 , 1, 641-504.8	115
200	ProteomicsDB. <i>Nucleic Acids Research</i> , 2018 , 46, D1271-D1281	20.1 113
199	Unconventional tethering of Ulp1 to the transport channel of the nuclear pore complex by karyopherins. <i>Nature Cell Biology</i> , 2003 , 5, 21-7	23.4 112
198	Immunomodulatory drugs disrupt the cereblon-CD147-MCT1 axis to exert antitumor activity and teratogenicity. <i>Nature Medicine</i> , 2016 , 22, 735-43	50.5 110
197	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, 2211-27	7.6 110
196	TMT Labeling for the Masses: A Robust and Cost-efficient, In-solution Labeling Approach. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1468-1478	7.6 106
195	Robust, reproducible and quantitative analysis of thousands of proteomes by micro-flow LC-MS/MS. <i>Nature Communications</i> , 2020 , 11, 157	17.4 105
194	Carbonyl-reactive tandem mass tags for the proteome-wide quantification of N-linked glycans. <i>Analytical Chemistry</i> , 2012 , 84, 3716-24	7.8 100
193	The gut microbiota promotes hepatic fatty acid desaturation and elongation in mice. <i>Nature Communications</i> , 2018 , 9, 3760	17.4 97
192	De novo discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. <i>Journal of Pathology</i> , 2015 , 235, 3-13	9.4 95
191	Identifying proteins and post-translational modifications by mass spectrometry. <i>Current Opinion in Structural Biology</i> , 1998 , 8, 393-400	8.1 95
190	Glycosylation analysis of gel-separated proteins. <i>Proteomics</i> , 2001 , 1, 350-61	4.8 92
189	Glycosylation of natural human neutrophil gelatinase B and neutrophil gelatinase B-associated lipocalin. <i>Biochemistry</i> , 1999 , 38, 13937-50	3.2 92
188	Comprehensive and reproducible phosphopeptide enrichment using iron immobilized metal ion affinity chromatography (Fe-IMAC) columns. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 205-15	7.6 88

187	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, 4693-704	3.9	83
186	A new variant of the gamma subunit of renal Na,K-ATPase. Identification by mass spectrometry, antibody binding, and expression in cultured cells. <i>Journal of Biological Chemistry</i> , 2000 , 275, 18441-6	5.4	79
185	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, 1556-61	2.2	79
184	Plant cytokinesis is orchestrated by the sequential action of the TRAPP II and exocyst tethering complexes. <i>Developmental Cell</i> , 2014 , 29, 607-620	10.2	76
183	Optimized chemical proteomics assay for kinase inhibitor profiling. <i>Journal of Proteome Research</i> , 2015 , 14, 1574-86	5.6	76
182	Ion mobility tandem mass spectrometry enhances performance of bottom-up proteomics. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3709-15	7.6	76
181	Systematic identification of the HSP90 candidate regulated proteome. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.016675	7.6	72
180	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020 , 48, D1153-D1163	20.1	67
179	Rapid approach for sequencing neutral oligosaccharides by exoglycosidase digestion and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Journal of Mass Spectrometry</i> , 1996 , 31, 1131-40	2.2	66
178	Comprehensive identification of proteins from MALDI imaging. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2901-10	7.6	64
177	Clinical response to chemotherapy in oesophageal adenocarcinoma patients is linked to defects in mitochondria. <i>Journal of Pathology</i> , 2013 , 230, 410-9	9.4	62
176	Lapatinib Resistance in Breast Cancer Cells Is Accompanied by Phosphorylation-Mediated Reprogramming of Glycolysis. <i>Cancer Research</i> , 2017 , 77, 1842-1853	10.1	60
175	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	23.4	60
174	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021 , 18, 604-617	21.6	60
173	Peptide Level Turnover Measurements Enable the Study of Proteoform Dynamics. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 974-992	7.6	59
172	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2016 , 11, 1245-54	4.9	58
171	Quantitative chemical proteomics reveals new potential drug targets in head and neck cancer. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.011635	7.6	57
170	A bead-based western for high-throughput cellular signal transduction analyses. <i>Nature Communications</i> , 2016 , 7, 12852	17.4	56

169	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 alpha1-acid glycoprotein. <i>Electrophoresis</i> , 1998 , 19, 1950-9	3.6	56
168	-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	9.4	55
167	Meltome atlas-thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020 , 17, 495-503	21.6	53
166	Phosphotyrosine mediated protein interactions of the discoidin domain receptor 1. <i>Journal of Proteomics</i> , 2012 , 75, 3465-77	3.9	53
165	Data, Reagents, Assays and Merits of Proteomics for SARS-CoV-2 Research and Testing. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1503-1522	7.6	52
164	Femtomol sensitivity post-digest (18)O labeling for relative quantification of differential protein complex composition. <i>Rapid Communications in Mass Spectrometry</i> , 2004 , 18, 869-76	2.2	52
163	Mining the Human Tissue Proteome for Protein Citrullination. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1378-1391	7.6	51
162	Gas-liquid mass transfer in rotating solid foam reactors. <i>Chemical Engineering Science</i> , 2010 , 65, 472-479	4.4	51
161	Defining the carrier proteome limit for single-cell proteomics. <i>Nature Methods</i> , 2021 , 18, 76-83	21.6	51
160	Generating high quality libraries for DIA MS with empirically corrected peptide predictions. <i>Nature Communications</i> , 2020 , 11, 1548	17.4	50
159	moCluster: Identifying Joint Patterns Across Multiple Omics Data Sets. <i>Journal of Proteome Research</i> , 2016 , 15, 755-65	5.6	48
158	Discovery of O-GlcNAc-modified proteins in published large-scale proteome data. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 843-50	7.6	48
157	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	7.6	47
156	MALDI imaging mass spectrometry for in situ proteomic analysis of preneoplastic lesions in pancreatic cancer. <i>PLoS ONE</i> , 2012 , 7, e39424	3.7	46
155	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, 1723-31	5.6	44
154	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	11.5	44
153	Oxidative stress modulates theophylline effects on steroid responsiveness. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 377, 797-802	3.4	44
152	A simple and effective cleavable linker for chemical proteomics applications. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 237-44	7.6	43

151	Mitotic arrest and slippage induced by pharmacological inhibition of Polo-like kinase 1. <i>Molecular Oncology</i> , 2015 , 9, 140-54	7.9	41
150	Optimized Plk1 PBD Inhibitors Based on Poloxin Induce Mitotic Arrest and Apoptosis in Tumor Cells. <i>ACS Chemical Biology</i> , 2015 , 10, 2570-9	4.9	38
149	Effect of the reducing-terminal substituents on the high energy collision-induced dissociation matrix-assisted laser desorption/ionization mass spectra of oligosaccharides. <i>Rapid Communications in Mass Spectrometry</i> , 1996 , 10, 1645-51	2.2	38
148	Disruption of the PRKCD-FBXO25-HAX-1 axis attenuates the apoptotic response and drives lymphomagenesis. <i>Nature Medicine</i> , 2014 , 20, 1401-9	50.5	36
147	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	17.6	36
146	Chemical Proteomics Uncovers EPHA2 as a Mechanism of Acquired Resistance to Small Molecule EGFR Kinase Inhibition. <i>Journal of Proteome Research</i> , 2015 , 14, 2617-25	5.6	35
145	Label-free quantitative proteome analysis of the surface-bound salivary pellicle. <i>Colloids and Surfaces B: Biointerfaces</i> , 2017 , 152, 68-76	6	34
144	PROCAL: A Set of 40 Peptide Standards for Retention Time Indexing, Column Performance Monitoring, and Collision Energy Calibration. <i>Proteomics</i> , 2017 , 17, 1700263	4.8	34
143	Perspectives in the glycosciences--matrix-assisted laser desorption/ionization (MALDI) mass spectrometry of carbohydrates. <i>Glycoconjugate Journal</i> , 1998 , 15, 333-8	3	34
142	Quantification and discovery of sequence determinants of protein-per-mRNA amount in human tissues. <i>Molecular Systems Biology</i> , 2019 , 15, e8513	12.2	33
141	A hydrodynamically optimized nano-electrospray ionization source and vacuum interface. <i>Analyst, The</i> , 2014 , 139, 1856-67	5	33
140	PROTAC-mediated degradation reveals a non-catalytic function of AURORA-A kinase. <i>Nature Chemical Biology</i> , 2020 , 16, 1179-1188	11.7	31
139	Chemical Proteomics and Structural Biology Define EPHA2 Inhibition by Clinical Kinase Drugs. <i>ACS Chemical Biology</i> , 2016 , 11, 3400-3411	4.9	29
138	Pharmacoproteomic characterisation of human colon and rectal cancer. <i>Molecular Systems Biology</i> , 2017 , 13, 951	12.2	28
137	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	7.6	27
136	Evaluation of Kinase Activity Profiling Using Chemical Proteomics. <i>ACS Chemical Biology</i> , 2015 , 10, 2743-52	4.2	27
135	Covalent cross-links between the gamma subunit (FXD2) and alpha and beta subunits of Na,K-ATPase: modeling the alpha-gamma interaction. <i>Journal of Biological Chemistry</i> , 2005 , 280, 18291-304	5.4	27
134	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	1.4	26

133	Challenges in Clinical Metaproteomics Highlighted by the Analysis of Acute Leukemia Patients with Gut Colonization by Multidrug-Resistant Enterobacteriaceae. <i>Proteomes</i> , 2019 , 7,	4.6	26
132	Novel Flp pilus biogenesis-dependent natural transformation. <i>Frontiers in Microbiology</i> , 2015 , 6, 84	5.7	26
131	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	5.7	26
130	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 4051-4069	5.6	26
129	Molecular mechanisms behind the antimicrobial activity of hop iso- α -acids in <i>Lactobacillus brevis</i> . <i>Food Microbiology</i> , 2015 , 46, 553-563	6	25
128	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	4.5	25
127	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	3.7	24
126	Characterization of a chemical affinity probe targeting Akt kinases. <i>Journal of Proteome Research</i> , 2013 , 12, 3792-800	5.6	24
125	Software tools for MS-based quantitative proteomics: a brief overview. <i>Methods in Molecular Biology</i> , 2012 , 893, 489-99	1.4	24
124	Modeling plasticity and dysplasia of pancreatic ductal organoids derived from human pluripotent stem cells. <i>Cell Stem Cell</i> , 2021 , 28, 1105-1124.e19	18	23
123	Annotation of the Domestic Pig Genome by Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2017 , 16, 2887-2898	5.6	22
122	MOGSA: Integrative Single Sample Gene-set Analysis of Multiple Omics Data. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, S153-S168	7.6	22
121	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	2.6	22
120	Towards Understanding Male Infertility After Spinal Cord Injury Using Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1424-34	7.6	22
119	Phosphorylation site localization in peptides by MALDI MS/MS and the Mascot Delta Score. <i>Analytical and Bioanalytical Chemistry</i> , 2012 , 402, 249-60	4.4	22
118	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, 931-42	3.5	22
117	DENEDDYLASE1 deconjugates NEDD8 from non-cullin protein substrates in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2015 , 27, 741-53	11.6	21
116	Cell cycle-regulated PLEIADE/AtMAP65-3 links membrane and microtubule dynamics during plant cytokinesis. <i>Plant Journal</i> , 2016 , 88, 531-541	6.9	21

115	Targeted Diazotransfer Reagents Enable Selective Modification of Proteins with Azides. <i>Bioconjugate Chemistry</i> , 2017 , 28, 913-917	6.3	20
114	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	17.6	20
113	Trimodal Mixed Mode Chromatography That Enables Efficient Offline Two-Dimensional Peptide Fractionation for Proteome Analysis. <i>Analytical Chemistry</i> , 2017 , 89, 8884-8891	7.8	20
112	Oligosaccharides of recombinant mouse gelatinase B variants. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1998 , 1425, 587-98	4	20
111	The Formation of a Camalexin Biosynthetic Metabolon. <i>Plant Cell</i> , 2019 , 31, 2697-2710	11.6	19
110	Bacterial production and functional characterization of the Fab fragment of the murine IgG1/lambda monoclonal antibody cmHsp70.1, a reagent for tumour diagnostics. <i>Protein Engineering, Design and Selection</i> , 2010 , 23, 161-8	1.9	19
109	Identification of oligosaccharides by matrix-assisted laser desorption ionization and electrospray MS. <i>Biochemical Society Transactions</i> , 1996 , 24, 905-12	5.1	19
108	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	5.7	18
107	Discovery of O-GlcNAc-6-phosphate modified proteins in large-scale phosphoproteomics data. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1063-9	7.6	18
106	The IMiD target CRBN determines HSP90 activity toward transmembrane proteins essential in multiple myeloma. <i>Molecular Cell</i> , 2021 , 81, 1170-1186.e10	17.6	18
105	New affinity probe targeting VEGF receptors for kinase inhibitor selectivity profiling by chemical proteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 2445-52	5.6	17
104	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. <i>Cell Reports</i> , 2015 , 12, 183-9	10.6	17
103	Infection-induced rapid cell death in plants: a means of efficient pathogen defense. <i>Canadian Journal of Botany</i> , 1995 , 73, 426-434		17
102	DENEDDYLASE1 Protein Counters Automodification of Neddylating Enzymes to Maintain NEDD8 Protein Homeostasis in. <i>Journal of Biological Chemistry</i> , 2017 , 292, 3854-3865	5.4	16
101	Optimized Enrichment of Phosphoproteomes by Fe-IMAC Column Chromatography. <i>Methods in Molecular Biology</i> , 2017 , 1550, 47-60	1.4	16
100	Quantitative chemical proteomics reveals a Plk1 inhibitor-compromised cell death pathway in human cells. <i>Cell Research</i> , 2014 , 24, 1141-5	24.7	16
99	Partially glucose-capped oligosaccharides are found on the hemoglobins of the deep-sea tube worm <i>Riftia pachyptila</i> . <i>Glycobiology</i> , 1998 , 8, 663-73	5.8	16
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