

Bernhard Kuster

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	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	7.3	1
257	Linking post-translational modifications and protein turnover by site-resolved protein turnover profiling.. <i>Nature Communications</i> , 2022 , 13, 165	17.4	3
256	Plant Proteome Dynamics.. <i>Annual Review of Plant Biology</i> , 2022 ,	30.7	2
255	Posttranslational modification of the RHO of plants protein RACB by phosphorylation and cross-kingdom conserved ubiquitination.. <i>PLoS ONE</i> , 2022 , 17, e0258924	3.7	0
254	High temporal resolution proteome and phosphoproteome profiling of stem cell-derived hepatocyte development.. <i>Cell Reports</i> , 2022 , 38, 110604	10.6	0
253	Epigenetic drug screening defines a PRMT5 inhibitor sensitive pancreatic cancer subtype.. <i>JCI Insight</i> , 2022 ,	9.9	1
252	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 , 100238	7.6	3
251	Loss of UCP1 function augments recruitment of futile lipid cycling for thermogenesis in murine brown fat.. <i>Molecular Metabolism</i> , 2022 , 101499	8.8	1
250	Prosit-TMT: Deep Learning Boosts Identification of TMT-Labeled Peptides.. <i>Analytical Chemistry</i> , 2022 ,	7.8	1
249	Novel, highly potent PROTACs targeting AURORA-A kinase. <i>Current Research in Chemical Biology</i> , 2022 , 100032		0
248	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	5.6	1
247	A novel Cereblon E3 ligase modulator with antitumor activity in gastrointestinal cancer. <i>Bioorganic Chemistry</i> , 2021 , 119, 105505	5.1	2
246	ProteomicsDB: toward a FAIR open-source resource for life-science research. <i>Nucleic Acids Research</i> , 2021 ,	20.1	7
245	PLK1-dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBV-infected mice. <i>EMBO Reports</i> , 2021 , 22, e53007	6.5	1
244	Mutations and variants of ONECUT1 in diabetes. <i>Nature Medicine</i> , 2021 , 27, 1928-1940	50.5	6
243	Chemical Phosphoproteomics Sheds New Light on the Targets and Modes of Action of AKT Inhibitors. <i>ACS Chemical Biology</i> , 2021 , 16, 631-641	4.9	5
242	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

241	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. <i>Nature</i> , 2021 , 594, 246-252	5.4	150
240	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	7.9	1
239	Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. <i>Journal of Proteome Research</i> , 2021 , 20, 3388-3394	5.6	6
238	Design, Synthesis, and Evaluation of WD-Repeat-Containing Protein 5 (WDR5) Degradors. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 10682-10710	8.3	9
237	Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics. <i>Nature Communications</i> , 2021 , 12, 3346	17.4	16
236	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
235	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021 , 18, 604-617	21.6	60
234	Identification of 7 000-9 000 Proteins from Cell Lines and Tissues by Single-Shot Microflow LC-MS/MS. <i>Analytical Chemistry</i> , 2021 , 93, 8687-8692	7.8	9
233	Cytomegalovirus subverts macrophage identity. <i>Cell</i> , 2021 , 184, 3774-3793.e25	56.2	1
232	Stress-primed secretory autophagy promotes extracellular BDNF maturation by enhancing MMP9 secretion. <i>Nature Communications</i> , 2021 , 12, 4643	17.4	10
231	Defining the carrier proteome limit for single-cell proteomics. <i>Nature Methods</i> , 2021 , 18, 76-83	21.6	51
230	Robust Microflow LC-MS/MS for Proteome Analysis: 38 000 Runs and Counting. <i>Analytical Chemistry</i> , 2021 , 93, 3686-3690	7.8	16
229	SARS-CoV-2 infection remodels the host protein thermal stability landscape. <i>Molecular Systems Biology</i> , 2021 , 17, e10188	12.2	5
228	Degradation of CCNK/CDK12 is a druggable vulnerability of colorectal cancer. <i>Cell Reports</i> , 2021 , 36, 109394	10.6	9
227	High sensitivity glycomics in biomedicine. <i>Mass Spectrometry Reviews</i> , 2021 , e21730	11	1
226	Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100076	7.6	9
225	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	6.8	5
224	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020 , 579, 409-414	50.4	144

223	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	13.4	6
222	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
221	Proteomic and Metabolite Profiling Reveals Profound Structural and Metabolic Reorganization of Adipocyte Mitochondria in Obesity. <i>Obesity</i> , 2020 , 28, 590-600	8	6
220	Combined proteomics/miRNomics of dendritic cell immunotherapy-treated glioblastoma patients as a screening for survival-associated factors. <i>Npj Vaccines</i> , 2020 , 5, 5	9.5	12
219	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
218	Generating high quality libraries for DIA MS with empirically corrected peptide predictions. <i>Nature Communications</i> , 2020 , 11, 1548	17.4	50
217	Meltome atlas-thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020 , 17, 495-503	21.6	53
216	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020 , 48, D1153-D1163	20.1	67
215	Loss of the Fanconi anemia-associated protein NIPA causes bone marrow failure. <i>Journal of Clinical Investigation</i> , 2020 , 130, 2827-2844	15.9	3
214	Identification of molecular targets for the targeted treatment of gastric cancer using dasatinib. <i>Oncotarget</i> , 2020 , 11, 535-549	3.3	15
213	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
212	Repurposing human kinase inhibitors to create an antibiotic active against drug-resistant <i>Staphylococcus aureus</i> , persists and biofilms. <i>Nature Chemistry</i> , 2020 , 12, 145-158	17.6	36
211	PROTAC-mediated degradation reveals a non-catalytic function of AURORA-A kinase. <i>Nature Chemical Biology</i> , 2020 , 16, 1179-1188	11.7	31
210	Proteome activity landscapes of tumor cell lines determine drug responses. <i>Nature Communications</i> , 2020 , 11, 3639	17.4	16
209	Radiosensitization by Kinase Inhibition Revealed by Phosphoproteomic Analysis of Pancreatic Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1649-1663	7.6	2
208	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PP1 and PP2A. <i>Nature Communications</i> , 2020 , 11, 3583	17.4	7
207	PTPN2 Deficiency Enhances Programmed T Cell Expansion and Survival Capacity of Activated T Cells. <i>Cell Reports</i> , 2020 , 32, 107957	10.6	2
206	Proteomic and transcriptomic profiling of aerial organ development in Arabidopsis. <i>Scientific Data</i> , 2020 , 7, 334	8.2	7

205	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
204	The Formation of a Camalexin Biosynthetic Metabolon. <i>Plant Cell</i> , 2019 , 31, 2697-2710	11.6	19
203	Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning. <i>Nature Methods</i> , 2019 , 16, 509-518	21.6	242
202	MOGSA: Integrative Single Sample Gene-set Analysis of Multiple Omics Data. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, S153-S168	7.6	22
201	Characterization of Drug-Protein Interactions by Chemoproteomics 2019 , 247-263		1
200	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
199	Detection of plasmid-mediated colistin resistance, mcr-1 gene, in Escherichia coli isolated from high-risk patients with acute leukemia in Spain. <i>Journal of Infection and Chemotherapy</i> , 2019 , 25, 605-609 ^{2,2}		12
198	Chemoproteomic Selectivity Profiling of PIKK and PI3K Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2019 , 14, 655-664	4.9	8
197	Quantification and discovery of sequence determinants of protein-per-mRNA amount in 29 human tissues. <i>Molecular Systems Biology</i> , 2019 , 15, e8513	12.2	33
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	CiRCus: A Framework to Enable Classification of Complex High-Throughput Experiments. <i>Journal of Proteome Research</i> , 2019 , 18, 1486-1493	5.6	
194	Rebuilding core abscisic acid signaling pathways of Arabidopsis in yeast. <i>EMBO Journal</i> , 2019 , 38, e101859		15
193	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	9	4
192	Interactions between Transport Protein Particle (TRAPP) complexes and Rab GTPases in Arabidopsis. <i>Plant Journal</i> , 2019 , 100, 279-297	6.9	13
191	The IMiD-Target Cereblon Determines Transmembrane Protein Quality Control Promoting Tumor Metabolism. <i>Blood</i> , 2019 , 134, 314-314	2.2	
190	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. <i>Molecular Systems Biology</i> , 2019 , 15, e8503	12.2	235
189	Kinobeads: A Chemical Proteomic Approach for Kinase Inhibitor Selectivity Profiling and Target Discovery. <i>Methods and Principles in Medicinal Chemistry</i> , 2019 , 97-130	0.4	3
188	Mining the Human Tissue Proteome for Protein Citrullination. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1378-1391	7.6	51

187	ProteomicsDB. <i>Nucleic Acids Research</i> , 2018 , 46, D1271-D1281	20.1	113
186	Peptide Level Turnover Measurements Enable the Study of Proteoform Dynamics. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 974-992	7.6	59
185	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
184	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
183	Increased Pancreatic Protease Activity in Response to Antibiotics Impairs Gut Barrier and Triggers Colitis. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2018 , 6, 370-388.e3	7.9	13
182	Sucrose-Induced Proteomic Response and Carbohydrate Utilization of TMW 1.411 During Dextran Formation. <i>Frontiers in Microbiology</i> , 2018 , 9, 2796	5.7	12
181	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 4051-4066	9.6	26
180	The gut microbiota promotes hepatic fatty acid desaturation and elongation in mice. <i>Nature Communications</i> , 2018 , 9, 3760	17.4	97
179	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	5.7	12
178	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
177	Adaptive Resistance to EGFR-Targeted Therapy by Calcium Signaling in NSCLC Cells. <i>Molecular Cancer Research</i> , 2018 , 16, 1773-1784	6.6	4
176	NVP-BHG712: Effects of Regioisomers on the Affinity and Selectivity toward the Ephrin Family. <i>ChemMedChem</i> , 2018 , 13, 1629-1633	3.7	11
175	DENEDDYLAASE1 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
174	Building ProteomeTools based on a complete synthetic human proteome. <i>Nature Methods</i> , 2017 , 14, 259-262	21.6	126
173	Label-free quantitative proteome analysis of the surface-bound salivary pellicle. <i>Colloids and Surfaces B: Biointerfaces</i> , 2017 , 152, 68-76	6	34
172	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
171	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
170	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

169	Hydrophilic Strong Anion Exchange (hSAX) Chromatography Enables Deep Fractionation of Tissue Proteomes. <i>Methods in Molecular Biology</i> , 2017 , 1550, 69-82	1.4	13
168	Optimized Enrichment of Phosphoproteomes by Fe-IMAC Column Chromatography. <i>Methods in Molecular Biology</i> , 2017 , 1550, 47-60	1.4	16
167	Annotation of the Domestic Pig Genome by Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2017 , 16, 2887-2898	5.6	22
166	Chemoproteomics-Aided Medicinal Chemistry for the Discovery of EPHA2 Inhibitors. <i>ChemMedChem</i> , 2017 , 12, 999-1011	3.7	15
165	Targeted Diazotransfer Reagents Enable Selective Modification of Proteins with Azides. <i>Bioconjugate Chemistry</i> , 2017 , 28, 913-917	6.3	20
164	Salivary Proteome Patterns Affecting Human Salt Taste Sensitivity. <i>Journal of Agricultural and Food Chemistry</i> , 2017 , 65, 9275-9286	5.7	14
163	-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
162	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	5.8	3
161	Persistent inhibition of pore-based cell migration by sub-toxic doses of miuraenamamide, an actin filament stabilizer. <i>Scientific Reports</i> , 2017 , 7, 16407	4.9	7
160	Preferential microRNA targeting revealed by in vivo competitive binding and differential Argonaute immunoprecipitation. <i>Nucleic Acids Research</i> , 2017 , 45, 10218-10228	20.1	12
159	Quantitative Proteomics for the Comprehensive Analysis of Stress Responses of <i>Lactobacillus paracasei</i> subsp. <i>paracasei</i> F19. <i>Journal of Proteome Research</i> , 2017 , 16, 3816-3829	5.6	11
158	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
157	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
156	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
155	The target landscape of clinical kinase drugs. <i>Science</i> , 2017 , 358,	33.3	389
154	Pharmacoproteomic characterisation of human colon and rectal cancer. <i>Molecular Systems Biology</i> , 2017 , 13, 951	12.2	28
153	Bacterial Cellulose Shifts Transcriptome and Proteome of Cultured Endothelial Cells Towards Native Differentiation. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1563-1577	7.6	15
152	Ethylene glycol improves electrospray ionization efficiency in bottom-up proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2017 , 409, 1049-1057	4.4	11

151	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
150	Two serines in the distal C-terminus of the human β -adrenoceptor determine β arrestin2 recruitment. <i>PLoS ONE</i> , 2017 , 12, e0176450	3.7	5
149	Wilhelm et al. reply. <i>Nature</i> , 2017 , 547, E23	50.4	4
148	Identification of Highly Potent Protein Kinase C-Related Kinase 1 Inhibitors by Virtual Screening, Binding Free Energy Rescoring, and in vitro Testing. <i>ChemMedChem</i> , 2016 , 11, 2084-94	3.7	8
147	Tofacitinib and analogs as inhibitors of the histone kinase PRK1 (PKN1). <i>Future Medicinal Chemistry</i> , 2016 , 8, 1537-51	4.1	6
146	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
145	Chemical Proteomics and Structural Biology Define EPHA2 Inhibition by Clinical Kinase Drugs. <i>ACS Chemical Biology</i> , 2016 , 11, 3400-3411	4.9	29
144	A bead-based western for high-throughput cellular signal transduction analyses. <i>Nature Communications</i> , 2016 , 7, 12852	17.4	56
143	Phosphoproteome Profiling Reveals Molecular Mechanisms of Growth-Factor-Mediated Kinase Inhibitor Resistance in EGFR-Overexpressing Cancer Cells. <i>Journal of Proteome Research</i> , 2016 , 15, 4490-4504	5.6	12
142	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
141	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
140	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2016 , 11, 1245-54	4.9	58
139	Towards Understanding Male Infertility After Spinal Cord Injury Using Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1424-34	7.6	22
138	Dimension reduction techniques for the integrative analysis of multi-omics data. <i>Briefings in Bioinformatics</i> , 2016 , 17, 628-41	13.4	192
137	moCluster: Identifying Joint Patterns Across Multiple Omics Data Sets. <i>Journal of Proteome Research</i> , 2016 , 15, 755-65	5.6	48
136	ERN1 and ALPK1 inhibit differentiation of bi-potential tumor-initiating cells in human breast cancer. <i>Oncotarget</i> , 2016 , 7, 83278-83293	3.3	11
135	MALDI-TOF and nESI Orbitrap MS/MS identify orthogonal parts of the phosphoproteome. <i>Proteomics</i> , 2016 , 16, 1447-56	4.8	9
134	Translatomics combined with transcriptomics and proteomics reveals novel functional, recently evolved orphan genes in Escherichia coli O157:H7 (EHEC). <i>BMC Genomics</i> , 2016 , 17, 133	4.5	25

133	K Efflux-Independent NLRP3 Inflammasome Activation by Small Molecules Targeting Mitochondria. <i>Immunity</i> , 2016 , 45, 761-773	32.3	219
132	Expression and Purification of EPHA2 Tyrosine Kinase Domain for Crystallographic and NMR Studies. <i>ChemBioChem</i> , 2016 , 17, 2257-2263	3.8	2
131	De novo discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. <i>Journal of Pathology</i> , 2015 , 235, 3-13	9.4	95
130	Massenspektrometrie-basierte Proteinforschung. <i>BioSpektrum</i> , 2015 , 21, 32-35	0.1	
129	Novel Flp pilus biogenesis-dependent natural transformation. <i>Frontiers in Microbiology</i> , 2015 , 6, 84	5.7	26
128	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
127	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
126	DENEDDYLEASE1 deconjugates NEDD8 from non-cullin protein substrates in Arabidopsis thaliana. <i>Plant Cell</i> , 2015 , 27, 741-53	11.6	21
125	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
124	Evaluation of Kinase Activity Profiling Using Chemical Proteomics. <i>ACS Chemical Biology</i> , 2015 , 10, 2743-52	4.2	27
123	Quantitative proteome profiling of human myoma and myometrium tissue reveals kinase expression signatures with potential for therapeutic intervention. <i>Proteomics</i> , 2015 , 15, 356-64	4.8	8
122	Molecular mechanisms behind the antimicrobial activity of hop iso-acids in Lactobacillus brevis. <i>Food Microbiology</i> , 2015 , 46, 553-563	6	25
121	Mitotic arrest and slippage induced by pharmacological inhibition of Polo-like kinase 1. <i>Molecular Oncology</i> , 2015 , 9, 140-54	7.9	41
120	Inhibitor-based affinity probes for the investigation of JAK signaling pathways. <i>Proteomics</i> , 2015 , 15, 3066-74	4.8	10
119	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
118	Optimized chemical proteomics assay for kinase inhibitor profiling. <i>Journal of Proteome Research</i> , 2015 , 14, 1574-86	5.6	76
117	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
116	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

115	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014 , 509, 582-7	50.4	1332
114	A hydrodynamically optimized nano-electrospray ionization source and vacuum interface. <i>Analyst, The</i> , 2014 , 139, 1856-67	5	33
113	Investigating RET RTK signaling pathways using an IAP-based activity-profiling approach. <i>Journal of Proteome Research</i> , 2014 , 13, 3628-34	5.6	2
112	PAS-cal: a generic recombinant peptide calibration standard for mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2014 , 25, 1489-97	3.5	1
111	A multivariate approach to the integration of multi-omics datasets. <i>BMC Bioinformatics</i> , 2014 , 15, 162	3.6	161
110	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
109	Tracking cancer drugs in living cells by thermal profiling of the proteome. <i>Science</i> , 2014 , 346, 1255784	33.3	526
108	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	3.9	11
107	Phosphoramidates as novel activity-based probes for serine proteases. <i>ChemBioChem</i> , 2014 , 15, 1106-10	3.8	10
106	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
105	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
104	PAS-cal: A repetitive peptide sequence calibration standard for MALDI mass spectrometry. <i>Proteomics</i> , 2014 , 14, 2427-31	4.8	3
103	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
102	Ion mobility tandem mass spectrometry enhances performance of bottom-up proteomics. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3709-15	7.6	76
101	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
100	Probing SH2-domains using Inhibitor Affinity Purification (IAP). <i>Proteome Science</i> , 2014 , 12, 41	2.6	10
99	High-fat diet alters gut microbiota physiology in mice. <i>ISME Journal</i> , 2014 , 8, 295-308	11.9	393
98	Global proteome analysis of the NCI-60 cell line panel. <i>Cell Reports</i> , 2013 , 4, 609-20	10.6	225

97	Characterization of a high field Orbitrap mass spectrometer for proteome analysis. <i>Proteomics</i> , 2013 , 13, 2552-62	4.8	9
96	DMSO enhances electrospray response, boosting sensitivity of proteomic experiments. <i>Nature Methods</i> , 2013 , 10, 989-91	21.6	170
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7	Generating high-quality libraries for DIA-MS with empirically-corrected peptide predictions	1
6	MOGSA: integrative single sample gene-set analysis of multiple omics data	4
5	Posttranslational modification of the RHO of plants protein RACB by phosphorylation and cross-kingdom conserved ubiquitination	1
4	Universal Spectrum Explorer: A standalone (web-)application for cross-resource spectrum comparison	2
3	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues	1
2	A hetero-oligomeric remorin-receptor complex regulates plant development	1
1	Target deconvolution of HDAC pharmacopoeia highlights MBLAC2 as common off-target	1