

Bernhard Kuster

List of Publications by Year in descending order

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Version: 2024-02-01

254
papers

36,500
citations

5891

81
h-index

3647

180
g-index

274
all docs

274
docs citations

274
times ranked

42954
citing authors

#	ARTICLE	IF	CITATIONS
1	High sensitivity glycomics in biomedicine. <i>Mass Spectrometry Reviews</i> , 2022, 41, 1014-1039.	2.8	9
2	ProteomicsDB: toward a FAIR open-source resource for life-science research. <i>Nucleic Acids Research</i> , 2022, 50, D1541-D1552.	6.5	35
3	A novel Cereblon E3 ligase modulator with antitumor activity in gastrointestinal cancer. <i>Bioorganic Chemistry</i> , 2022, 119, 105505.	2.0	13
4	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.	2.4	16
5	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
6	Linking post-translational modifications and protein turnover by site-resolved protein turnover profiling. <i>Nature Communications</i> , 2022, 13, 165.	5.8	33
7	Plant Proteome Dynamics. <i>Annual Review of Plant Biology</i> , 2022, 73, 67-92.	8.6	22
8	Posttranslational modification of the RHO of plants protein RACB by phosphorylation and cross-kingdom conserved ubiquitination. <i>PLoS ONE</i> , 2022, 17, e0258924.	1.1	4
9	High temporal resolution proteome and phosphoproteome profiling of stem cell-derived hepatocyte development. <i>Cell Reports</i> , 2022, 38, 110604.	2.9	8
10	Epigenetic drug screening defines a PRMT5 inhibitor-sensitive pancreatic cancer subtype. <i>JCI Insight</i> , 2022, 7, .	2.3	6
11	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.	2.5	9
12	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
13	Prosit-TMT: Deep Learning Boosts Identification of TMT-Labeled Peptides. <i>Analytical Chemistry</i> , 2022, 94, 7181-7190.	3.2	8
14	Target deconvolution of HDAC pharmacopoeia reveals MBLAC2 as common off-target. <i>Nature Chemical Biology</i> , 2022, 18, 812-820.	3.9	36
15	Novel, highly potent PROTACs targeting AURORA-A kinase. <i>Current Research in Chemical Biology</i> , 2022, 2, 100032.	1.4	9
16	Mass spectrometry-based draft of the mouse proteome. <i>Nature Methods</i> , 2022, 19, 803-811.	9.0	19
17	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.	2.6	3
18	Defining the carrier proteome limit for single-cell proteomics. <i>Nature Methods</i> , 2021, 18, 76-83.	9.0	142

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19	Robust Microflow LC-MS/MS for Proteome Analysis: 38â€“000 Runs and Counting. <i>Analytical Chemistry</i> , 2021, 93, 3686-3690.	3.2	36
20	SARSâ€“CoVâ€“2 infection remodels the host protein thermal stability landscape. <i>Molecular Systems Biology</i> , 2021, 17, e10188.	3.2	17
21	Chemical Phosphoproteomics Sheds New Light on the Targets and Modes of Action of AKT Inhibitors. <i>ACS Chemical Biology</i> , 2021, 16, 631-641.	1.6	21
22	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
23	Multilevel proteomics reveals host perturbations by SARS-CoV-2 and SARS-CoV. <i>Nature</i> , 2021, 594, 246-252.	13.7	475
24	Systematic analysis of migration factors by MigExpress identifies essential cell migration control genes in nonâ€“small cell lung cancer. <i>Molecular Oncology</i> , 2021, 15, 1797-1817.	2.1	9
25	Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. <i>Journal of Proteome Research</i> , 2021, 20, 3388-3394.	1.8	22
26	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
27	Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics. <i>Nature Communications</i> , 2021, 12, 3346.	5.8	90
28	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
29	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.	9.0	198
30	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.	3.2	25
31	Cytomegalovirus subverts macrophage identity. <i>Cell</i> , 2021, 184, 3774-3793.e25.	13.5	34
32	Stress-primed secretory autophagy promotes extracellular BDNF maturation by enhancing MMP9 secretion. <i>Nature Communications</i> , 2021, 12, 4643.	5.8	50
33	Degradation of CCNK/CDK12 is a druggable vulnerability of colorectal cancer. <i>Cell Reports</i> , 2021, 36, 109394.	2.9	41
34	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
35	PLK1â€“dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBVâ€“infected mice. <i>EMBO Reports</i> , 2021, 22, e53007.	2.0	5
36	Mutations and variants of ONECUT1 in diabetes. <i>Nature Medicine</i> , 2021, 27, 1928-1940.	15.2	24

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37	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.	1.8	12
38	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020, 48, D1153-D1163.	6.5	126
39	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
40	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
41	PROTAC-mediated degradation reveals a non-catalytic function of AURORA-A kinase. <i>Nature Chemical Biology</i> , 2020, 16, 1179-1188.	3.9	73
42	Proteome activity landscapes of tumor cell lines determine drug responses. <i>Nature Communications</i> , 2020, 11, 3639.	5.8	47
43	Radiosensitization by Kinase Inhibition Revealed by Phosphoproteomic Analysis of Pancreatic Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1649-1663.	2.5	7
44	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PP1 and PP2A. <i>Nature Communications</i> , 2020, 11, 3583.	5.8	38
45	PTPN2 Deficiency Enhances Programmed T Cell Expansion and Survival Capacity of Activated T Cells. <i>Cell Reports</i> , 2020, 32, 107957.	2.9	28
46	Proteomic and transcriptomic profiling of aerial organ development in <i>Arabidopsis</i> . <i>Scientific Data</i> , 2020, 7, 334.	2.4	20
47	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.	2.6	8
48	Mass-spectrometry-based draft of the <i>Arabidopsis</i> proteome. <i>Nature</i> , 2020, 579, 409-414.	13.7	328
49	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.	1.8	11
50	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
51	Proteomic and Metabolite Profiling Reveals Profound Structural and Metabolic Reorganization of Adipocyte Mitochondria in Obesity. <i>Obesity</i> , 2020, 28, 590-600.	1.5	10
52	Combined proteomics/miRNomics of dendritic cell immunotherapy-treated glioblastoma patients as a screening for survival-associated factors. <i>Npj Vaccines</i> , 2020, 5, 5.	2.9	19
53	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
54	Generating high quality libraries for DIA MS with empirically corrected peptide predictions. <i>Nature Communications</i> , 2020, 11, 1548.	5.8	148

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55	Meltome atlas—thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.	9.0	152
56	Loss of the Fanconi anemia-associated protein NIPA causes bone marrow failure. <i>Journal of Clinical Investigation</i> , 2020, 130, 2827-2844.	3.9	8
57	Identification of molecular targets for the targeted treatment of gastric cancer using dasatinib. <i>Oncotarget</i> , 2020, 11, 535-549.	0.8	29
58	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.	2.5	27
59	Rebuilding core abscisic acid signaling pathways of <i>Arabidopsis</i> in yeast. <i>EMBO Journal</i> , 2019, 38, e101859.	3.5	25
60	Functional expression of electrogenic sodium bicarbonate cotransporter 1 (NBCe1) in mouse cortical astrocytes is dependent on S255 and regulated by mTOR. <i>Glia</i> , 2019, 67, 2264-2278.	2.5	9
61	Interactions between Transport Protein Particle (TRAPP) complexes and Rab GTPases in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 100, 279-297.	2.8	27
62	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
63	The formation of a camalexin-biosynthetic metabolon. <i>Plant Cell</i> , 2019, 31, tpc.00403.2019.	3.1	38
64	Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning. <i>Nature Methods</i> , 2019, 16, 509-518.	9.0	539
65	MOGSA: Integrative Single Sample Gene-set Analysis of Multiple Omics Data. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S153-S168.	2.5	59
66	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
67	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.	0.8	15
68	Chemoproteomic Selectivity Profiling of PI3K and PI3K Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2019, 14, 655-664.	1.6	21
69	Quantification and discovery of sequence determinants of protein-mRNA amount in human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8513.	3.2	63
70	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
71	CiRCus: A Framework to Enable Classification of Complex High-Throughput Experiments. <i>Journal of Proteome Research</i> , 2019, 18, 1486-1493.	1.8	3
72	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8503.	3.2	576

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73	The IMiD-Target Cereblon Determines Transmembrane Protein Quality Control Promoting Tumor Metabolism. <i>Blood</i> , 2019, 134, 314-314.	0.6	0
74	Mining the Human Tissue Proteome for Protein Citrullination. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1378-1391.	2.5	93
75	ProteomicsDB. <i>Nucleic Acids Research</i> , 2018, 46, D1271-D1281.	6.5	197
76	Peptide Level Turnover Measurements Enable the Study of Proteoform Dynamics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 974-992.	2.5	98
77	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
78	Sucrose-Induced Proteomic Response and Carbohydrate Utilization of <i>Lactobacillus sakei</i> TMW 1.411 During Dextran Formation. <i>Frontiers in Microbiology</i> , 2018, 9, 2796.	1.5	21
79	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	1.8	47
80	The gut microbiota promotes hepatic fatty acid desaturation and elongation in mice. <i>Nature Communications</i> , 2018, 9, 3760.	5.8	200
81	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.	2.4	22
82	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
83	Adaptive Resistance to EGFR-Targeted Therapy by Calcium Signaling in NSCLC Cells. <i>Molecular Cancer Research</i> , 2018, 16, 1773-1784.	1.5	9
84	NVPa€BHG712: Effects of Regioisomers on the Affinity and Selectivity toward the EPHrin Family. <i>ChemMedChem</i> , 2018, 13, 1629-1633.	1.6	20
85	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
86	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.	2.3	22
87	DENEDDYLASE1 Protein Counters Automodification of Neddylating Enzymes to Maintain NEDD8 Protein Homeostasis in Arabidopsis. <i>Journal of Biological Chemistry</i> , 2017, 292, 3854-3865.	1.6	17
88	Building ProteomeTools based on a complete synthetic human proteome. <i>Nature Methods</i> , 2017, 14, 259-262.	9.0	182
89	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
90	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.	2.4	23

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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	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
93	Hydrophilic Strong Anion Exchange (hSAX) Chromatography Enables Deep Fractionation of Tissue Proteomes. <i>Methods in Molecular Biology</i> , 2017, 1550, 69-82.	0.4	13
94	Optimized Enrichment of Phosphoproteomes by Fe-IMAC Column Chromatography. <i>Methods in Molecular Biology</i> , 2017, 1550, 47-60.	0.4	26
95	Annotation of the Domestic Pig Genome by Quantitative Proteogenomics. <i>Journal of Proteome Research</i> , 2017, 16, 2887-2898.	1.8	25
96	Chemoproteomics-Aided Medicinal Chemistry for the Discovery of EPHA2 Inhibitors. <i>ChemMedChem</i> , 2017, 12, 999-1011.	1.6	23
97	Targeted Diazotransfer Reagents Enable Selective Modification of Proteins with Azides. <i>Bioconjugate Chemistry</i> , 2017, 28, 913-917.	1.8	24
98	Salivary Proteome Patterns Affecting Human Salt Taste Sensitivity. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 9275-9286.	2.4	25
99	σ -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
100	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.	2.2	3
101	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.	1.8	20
102	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
103	Trimodal Mixed Mode Chromatography That Enables Efficient Offline Two-Dimensional Peptide Fractionation for Proteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 8884-8891.	3.2	22
104	<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
105	The target landscape of clinical kinase drugs. <i>Science</i> , 2017, 358, .	6.0	609
106	Pharmacoproteomic characterisation of human colon and rectal cancer. <i>Molecular Systems Biology</i> , 2017, 13, 951.	3.2	44
107	Bacterial Cellulose Shifts Transcriptome and Proteome of Cultured Endothelial Cells Towards Native Differentiation. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1563-1577.	2.5	18
108	Ethylene glycol improves electrospray ionization efficiency in bottom-up proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 1049-1057.	1.9	14

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109	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
110	Persistent inhibition of pore-based cell migration by sub-toxic doses of miuraenamamide, an actin filament stabilizer. <i>Scientific Reports</i> , 2017, 7, 16407.	1.6	9
111	Preferential microRNA targeting revealed by in vivo competitive binding and differential Argonaute immunoprecipitation. <i>Nucleic Acids Research</i> , 2017, 45, 10218-10228.	6.5	19
112	Wilhelm et al. reply. <i>Nature</i> , 2017, 547, E23-E23.	13.7	7
113	Two serines in the distal C-terminus of the human γ 1-adrenoceptor determine γ -arrestin2 recruitment. <i>PLoS ONE</i> , 2017, 12, e0176450.	1.1	5
114	MALDI-TOF and nESI Orbitrap MS/MS identify orthogonal parts of the phosphoproteome. <i>Proteomics</i> , 2016, 16, 1447-1456.	1.3	13
115	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
116	K + Efflux-Independent NLRP3 Inflammasome Activation by Small Molecules Targeting Mitochondria. <i>Immunity</i> , 2016, 45, 761-773.	6.6	364
117	Expression and Purification of EPHA2 Tyrosine Kinase Domain for Crystallographic and NMR Studies. <i>ChemBioChem</i> , 2016, 17, 2257-2263.	1.3	5
118	Identification of Highly Potent Protein Kinase-Related Kinase-1 Inhibitors by Virtual Screening, Binding Free Energy Rescoring, and in-vitro Testing. <i>ChemMedChem</i> , 2016, 11, 2084-2094.	1.6	10
119	Tofacitinib and analogs as inhibitors of the histone kinase PRK1 (PKN1). <i>Future Medicinal Chemistry</i> , 2016, 8, 1537-1551.	1.1	10
120	Cell cycle-regulated <i>PLEIADE</i> / <i>AtMAP65</i> links membrane and microtubule dynamics during plant cytokinesis. <i>Plant Journal</i> , 2016, 88, 531-541.	2.8	29
121	Chemical Proteomics and Structural Biology Define EPHA2 Inhibition by Clinical Kinase Drugs. <i>ACS Chemical Biology</i> , 2016, 11, 3400-3411.	1.6	42
122	A bead-based western for high-throughput cellular signal transduction analyses. <i>Nature Communications</i> , 2016, 7, 12852.	5.8	84
123	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.	1.8	18
124	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
125	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
126	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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127	Towards Understanding Male Infertility After Spinal Cord Injury Using Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1424-1434.	2.5	26
128	Dimension reduction techniques for the integrative analysis of multi-omics data. <i>Briefings in Bioinformatics</i> , 2016, 17, 628-641.	3.2	280
129	moCluster: Identifying Joint Patterns Across Multiple Omics Data Sets. <i>Journal of Proteome Research</i> , 2016, 15, 755-765.	1.8	88
130	ERN1 and ALPK1 inhibit differentiation of bi-potential tumor-initiating cells in human breast cancer. <i>Oncotarget</i> , 2016, 7, 83278-83293.	0.8	19
131	Inhibitor-based affinity probes for the investigation of JAK signaling pathways. <i>Proteomics</i> , 2015, 15, 3066-3074.	1.3	10
132	Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. <i>Cell Reports</i> , 2015, 12, 183-189.	2.9	22
133	Optimized Chemical Proteomics Assay for Kinase Inhibitor Profiling. <i>Journal of Proteome Research</i> , 2015, 14, 1574-1586.	1.8	104
134	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
135	<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
136	Novel Flp pilus biogenesis-dependent natural transformation. <i>Frontiers in Microbiology</i> , 2015, 6, 84.	1.5	33
137	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
138	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
139	DENEDYLASE1 Deconjugates NEDD8 from Non-Cullin Protein Substrates in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2015, 27, 741-753.	3.1	24
140	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
141	Evaluation of Kinase Activity Profiling Using Chemical Proteomics. <i>ACS Chemical Biology</i> , 2015, 10, 2743-2752.	1.6	32
142	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.	1.3	8
143	Molecular mechanisms behind the antimicrobial activity of hop iso- α -acids in <i>Lactobacillus brevis</i> . <i>Food Microbiology</i> , 2015, 46, 553-563.	2.1	30
144	Mitotic arrest and slippage induced by pharmacological inhibition of Polo-like kinase 1. <i>Molecular Oncology</i> , 2015, 9, 140-154.	2.1	47

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145	Quantitative chemical proteomics reveals a Plk1 inhibitor-compromised cell death pathway in human cells. <i>Cell Research</i> , 2014, 24, 1141-1145.	5.7	19
146	Ion Mobility Tandem Mass Spectrometry Enhances Performance of Bottom-up Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3709-3715.	2.5	98
147	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
148	Probing SH2-domains using Inhibitor Affinity Purification (IAP). <i>Proteome Science</i> , 2014, 12, 41.	0.7	10
149	High-fat diet alters gut microbiota physiology in mice. <i>ISME Journal</i> , 2014, 8, 295-308.	4.4	583
150	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
151	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014, 509, 582-587.	13.7	1,697
152	A hydrodynamically optimized nano-electrospray ionization source and vacuum interface. <i>Analyst</i> , 2014, 139, 1856.	1.7	45
153	Investigating RET RTK Signaling Pathways Using an IAP-Based Activity-Profiling Approach. <i>Journal of Proteome Research</i> , 2014, 13, 3628-3634.	1.8	2
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