Ruedi Aebersold

List of Publications by Year
in descending order

293 papers	63,878 citations	1457 107 h-index	959 238 g-index
338 all docs	338 docs citations	338 times ranked	63522 citing authors

#	Article	IF	Citations
1	Mass spectrometry-based proteomics. Nature, 2003, 422, 198-207.	13.7	6,282
2	Empirical Statistical Model To Estimate the Accuracy of Peptide Identifications Made by MS/MS and Database Search. Analytical Chemistry, 2002, 74, 5383-5392.	3.2	4,503
3	Targeted Data Extraction of the MS/MS Spectra Generated by Data-independent Acquisition: A New Concept for Consistent and Accurate Proteome Analysis. Molecular and Cellular Proteomics, 2012, 11, O111.016717.	2.5	2,285
4	On the Dependency of Cellular Protein Levels on mRNA Abundance. Cell, 2016, 165, 535-550.	13.5	2,216
5	Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network. Science, 2001, 292, 929-934.	6.0	1,921
6	Checkpoint blockade cancer immunotherapy targets tumour-specific mutant antigens. Nature, 2014, 515, 577-581.	13.7	1,705
7	Mass-spectrometric exploration of proteome structure and function. Nature, 2016, 537, 347-355.	13.7	1,573
8	The CRAPome: a contaminant repository for affinity purification–mass spectrometry data. Nature Methods, 2013, 10, 730-736.	9.0	1,353
9	Selected reaction monitoring for quantitative proteomics: a tutorial. Molecular Systems Biology, 2008, 4, 222.	3.2	1,215
10	Selected reaction monitoring–based proteomics: workflows, potential, pitfalls and future directions. Nature Methods, 2012, 9, 555-566.	9.0	1,177
11	Quantitative profiling of differentiation-induced microsomal proteins using isotope-coded affinity tags and mass spectrometry. Nature Biotechnology, 2001, 19, 946-951.	9.4	913
12	NAD $^+$ repletion improves mitochondrial and stem cell function and enhances life span in mice. Science, 2016, 352, 1436-1443.	6.0	907
13	Interpretation of Shotgun Proteomic Data. Molecular and Cellular Proteomics, 2005, 4, 1419-1440.	2.5	904
14	The PeptideAtlas project. Nucleic Acids Research, 2006, 34, D655-D658.	6.5	733
15	A common open representation of mass spectrometry data and its application to proteomics research. Nature Biotechnology, 2004, 22, 1459-1466.	9.4	724
16	A guided tour of the Trans–Proteomic Pipeline. Proteomics, 2010, 10, 1150-1159.	1.3	710
17	Data‐independent acquisition‐based SWATH ‐ MS for quantitative proteomics: a tutorial. Molecular Systems Biology, 2018, 14, e8126.	3.2	701
18	The minimum information about a proteomics experiment (MIAPE). Nature Biotechnology, 2007, 25, 887-893.	9.4	694

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19	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. Nature Biotechnology, 2014, 32, 219-223.	9.4	692
20	The quantitative proteome of a human cell line. Molecular Systems Biology, 2011, 7, 549.	3.2	691
21	The quantitative and condition-dependent Escherichia coli proteome. Nature Biotechnology, 2016, 34, 104-110.	9.4	655
22	Options and considerations when selecting a quantitative proteomics strategy. Nature Biotechnology, 2010, 28, 710-721.	9.4	581
23	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	3.9	580
24	Reproducible isolation of distinct, overlapping segments of the phosphoproteome. Nature Methods, 2007, 4, 231-237.	9.0	555
25	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. Nature Methods, 2016, 13, 741-748.	9.0	537
26	Quantitative Analysis of Fission Yeast Transcriptomes and Proteomes in Proliferating and Quiescent Cells. Cell, 2012, 151, 671-683.	13.5	513
27	iProphet: Multi-level Integrative Analysis of Shotgun Proteomic Data Improves Peptide and Protein Identification Rates and Error Estimates. Molecular and Cellular Proteomics, 2011, 10, M111.007690.	2.5	490
28	Development and validation of a spectral library searching method for peptide identification from MS/MS. Proteomics, 2007, 7, 655-667.	1.3	487
29	mProphet: automated data processing and statistical validation for large-scale SRM experiments. Nature Methods, 2011, 8, 430-435.	9.0	481
30	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. Nature Communications, 2017, 8, 291.	5.8	423
31	Molecular architecture of the 26S proteasome holocomplex determined by an integrative approach. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1380-1387.	3.3	422
32	Probing Native Protein Structures by Chemical Cross-linking, Mass Spectrometry, and Bioinformatics. Molecular and Cellular Proteomics, 2010, 9, 1634-1649.	2.5	407
33	Proteome-wide cellular protein concentrations of the human pathogen Leptospira interrogans. Nature, 2009, 460, 762-765.	13.7	402
34	diaPASEF: parallel accumulation–serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	9.0	387
35	Identification of cross-linked peptides from large sequence databases. Nature Methods, 2008, 5, 315-318.	9.0	379
36	A repository of assays to quantify 10,000 human proteins by SWATH-MS. Scientific Data, 2014, 1, 140031.	2.4	370

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37	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. Nature Medicine, 2015, 21, 407-413.	15.2	358
38	Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. Science, 2012, 337, 1348-1352.	6.0	357
39	A Mass Spectrometric-Derived Cell Surface Protein Atlas. PLoS ONE, 2015, 10, e0121314.	1.1	356
40	The study of macromolecular complexes by quantitative proteomics. Nature Genetics, 2003, 33, 349-355.	9.4	350
41	The complete structure of the 55 S mammalian mitochondrial ribosome. Science, 2015, 348, 303-308.	6.0	344
42	Crosslinking and Mass Spectrometry: An Integrated Technology to Understand the Structure and Function of Molecular Machines. Trends in Biochemical Sciences, 2016, 41, 20-32.	3.7	330
43	A multicenter study benchmarks software tools for label-free proteome quantification. Nature Biotechnology, 2016, 34, 1130-1136.	9.4	321
44	Crucial HSP70 co-chaperone complex unlocks metazoan protein disaggregation. Nature, 2015, 524, 247-251.	13.7	320
45	Building high-quality assay libraries for targeted analysis of SWATH MS data. Nature Protocols, 2015, 10, 426-441.	5.5	319
46	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. Nature, 2013, 494, 266-270.	13.7	307
47	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. Nature Methods, 2013, 10, 1246-1253.	9.0	302
48	Quantitative variability of 342 plasma proteins in a human twin population. Molecular Systems Biology, 2015, 11, 786.	3.2	300
49	Large-Scale Quantitative Assessment of Different In-Solution Protein Digestion Protocols Reveals Superior Cleavage Efficiency of Tandem Lys-C/Trypsin Proteolysis over Trypsin Digestion. Journal of Proteome Research, 2012, 11, 5145-5156.	1.8	298
50	Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. Cell, 2016, 166, 766-778.	13.5	295
51	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	2.5	294
52	Genome-wide Mapping of Transcriptional Start Sites Defines an Extensive Leaderless Transcriptome in Mycobacterium tuberculosis. Cell Reports, 2013, 5, 1121-1131.	2.9	283
53	Protein Identification False Discovery Rates for Very Large Proteomics Data Sets Generated by Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2009, 8, 2405-2417.	2.5	282
54	Architecture and conformational switch mechanism of the ryanodine receptor. Nature, 2015, 517, 39-43.	13.7	282

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55	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. Nature Biotechnology, 2012, 30, 221-223.	9.4	281
56	Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation. Rapid Communications in Mass Spectrometry, 2001, 15, 1214-1221.	0.7	277
57	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. Science Signaling, 2010, 3, rs4.	1.6	277
58	Mapping differential interactomes by affinity purification coupled with data-independent mass spectrometry acquisition. Nature Methods, 2013, 10, 1239-1245.	9.0	277
59	Early Steps in Autophagy Depend on Direct Phosphorylation of Atg9 by the Atg1 Kinase. Molecular Cell, 2014, 53, 471-483.	4.5	274
60	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. Nature Methods, 2012, 9, 901-903.	9.0	273
61	Quantification of mRNA and protein and integration with protein turnover in a bacterium. Molecular Systems Biology, 2011, 7, 511.	3.2	267
62	Mass Spectrometry Applied to Bottom-Up Proteomics: Entering the High-Throughput Era for Hypothesis Testing. Annual Review of Analytical Chemistry, 2016, 9, 449-472.	2.8	266
63	Expanding the Chemical Cross-Linking Toolbox by the Use of Multiple Proteases and Enrichment by Size Exclusion Chromatography. Molecular and Cellular Proteomics, 2012, 11, M111.014126.	2.5	264
64	The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. Structure, 2012, 20, 814-825.	1.6	261
65	Systems proteomics of liver mitochondria function. Science, 2016, 352, aad0189.	6.0	257
66	Building consensus spectral libraries for peptide identification in proteomics. Nature Methods, 2008, 5, 873-875.	9.0	255
67	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. Nature Biotechnology, 2019, 37, 314-322.	9.4	254
68	An integrated workflow for charting the human interaction proteome: insights into the PP2A system. Molecular Systems Biology, 2009, 5, 237.	3.2	253
69	ATM-Dependent and -Independent Dynamics of the Nuclear Phosphoproteome After DNA Damage. Science Signaling, 2010, 3, rs3.	1.6	245
70	Lysine-specific chemical cross-linking of protein complexes and identification of cross-linking sites using LC-MS/MS and the xQuest/xProphet software pipeline. Nature Protocols, 2014, 9, 120-137.	5.5	244
71	A High-Density Map for Navigating the Human Polycomb Complexome. Cell Reports, 2016, 17, 583-595.	2.9	234
72	The complete structure of the large subunit of the mammalian mitochondrial ribosome. Nature, 2014, 515, 283-286.	13.7	231

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73	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. Cell Host and Microbe, 2015, 18, 96-108.	5.1	229
74	TRIM24 Is an Oncogenic Transcriptional Activator in Prostate Cancer. Cancer Cell, 2016, 29, 846-858.	7.7	228
75	Multilayered Genetic and Omics Dissection of Mitochondrial Activity in a Mouse Reference Population. Cell, 2014, 158, 1415-1430.	13.5	222
76	Chemical cross-linking/mass spectrometry targeting acidic residues in proteins and protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9455-9460.	3.3	213
77	Architecture of the large subunit of the mammalian mitochondrial ribosome. Nature, 2014, 505, 515-519.	13.7	207
78	Quantitative proteomics: challenges and opportunities in basic and applied research. Nature Protocols, 2017, 12, 1289-1294.	5.5	200
79	Molecular Architecture of the 40Sâ‹¯eIF1â‹¯eIF3 Translation Initiation Complex. Cell, 2014, 158, 1123-1135.	13.5	193
80	Quantitative measurements of <i><scp>N</scp></i>â€‹linked glycoproteins in human plasma by <scp>SWATH</scp>â€‹<scp>MS</scp>. Proteomics, 2013, 13, 1247-1256.	1.3	190
81	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. Nature Methods, 2017, 14, 921-927.	9.0	189
82	Analysis of Major Histocompatibility Complex (MHC) Immunopeptidomes Using Mass Spectrometry*. Molecular and Cellular Proteomics, 2015, 14, 3105-3117.	2.5	188
83	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometryâ€“Based Assays. Clinical Chemistry, 2016, 62, 48-69.	1.5	187
84	The Human Plasma Proteome Draft of 2017: Building on the Human Plasma PeptideAtlas from Mass Spectrometry and Complementary Assays. Journal of Proteome Research, 2017, 16, 4299-4310.	1.8	185
85	Generating and navigating proteome maps using mass spectrometry. Nature Reviews Molecular Cell Biology, 2010, 11, 789-801.	16.1	181
86	The Protein Interaction Landscape of the Human CMGC Kinase Group. Cell Reports, 2013, 3, 1306-1320.	2.9	178
87	Cancer genetics-guided discovery of serum biomarker signatures for diagnosis and prognosis of prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3342-3347.	3.3	175
88	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. Nature Methods, 2016, 13, 777-783.	9.0	173
89	Structures of human PRC2 with its cofactors AEBP2 and JARID2. Science, 2018, 359, 940-944.	6.0	170
90	The Mtb Proteome Library: A Resource of Assays to Quantify the Complete Proteome of Mycobacterium tuberculosis. Cell Host and Microbe, 2013, 13, 602-612.	5.1	165

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91	Glycoproteomic Analysis of Prostate Cancer Tissues by SWATH Mass Spectrometry Discovers N-acylethanolamine Acid Amidase and Protein Tyrosine Kinase 7 as Signatures for Tumor Aggressiveness. Molecular and Cellular Proteomics, 2014, 13, 1753-1768.	2.5	165
92	Insights into autophagosome biogenesis from structural and biochemical analyses of the ATG2A-WIPI4 complex. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9792-E9801.	3.3	159
93	Reproducible and Consistent Quantification of the Saccharomyces cerevisiae Proteome by SWATH-mass spectrometry *. Molecular and Cellular Proteomics, 2015, 14, 739-749.	2.5	158
94	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. Journal of Proteome Research, 2016, 15, 3961-3970.	1.8	158
95	Proteomic and interactomic insights into the molecular basis of cell functional diversity. Nature Reviews Molecular Cell Biology, 2020, 21, 327-340.	16.1	156
96	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	5.8	152
97	A Class of Environmental and Endogenous Toxins Induces BRCA2 Haploinsufficiency and Genome Instability. Cell, 2017, 169, 1105-1118.e15.	13.5	149
98	RNF168 Promotes Noncanonical K27 Ubiquitination to Signal DNA Damage. Cell Reports, 2015, 10, 226-238.	2.9	147
99	An Automated Pipeline for High-Throughput Label-Free Quantitative Proteomics. Journal of Proteome Research, 2013, 12, 1628-1644.	1.8	146
100	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. Molecular and Cellular Proteomics, 2015, 14, 2301-2307.	2.5	146
101	Impact of Alternative Splicing on the Human Proteome. Cell Reports, 2017, 20, 1229-1241.	2.9	145
102	Proteomics meets the scientific method. Nature Methods, 2013, 10, 24-27.	9.0	139
103	JARID2 and AEBP2 regulate PRC2 in the presence of H2AK119ub1 and other histone modifications. Science, 2021, 371, .	6.0	137
104	Standard Guidelines for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2012, 11, 2005-2013.	1.8	135
105	The Structural Basis of Substrate Recognition by the Eukaryotic Chaperonin TRiC/CCT. Cell, 2014, 159, 1042-1055.	13.5	131
106	Inference and quantification of peptidoforms in large sample cohorts by SWATH-MS. Nature Biotechnology, 2017, 35, 781-788.	9.4	122
107	Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. Molecular Cell, 2015, 58, 977-988.	4.5	120
108	Quantitative proteomics analysis of signalosome dynamics in primary T cells identifies the surface receptor CD6 as a Lat adaptor–independent TCR signaling hub. Nature Immunology, 2014, 15, 384-392.	7.0	119

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109	The SysteMHC Atlas project. Nucleic Acids Research, 2018, 46, D1237-D1247.	6.5	119
110	Estimation of Absolute Protein Quantities of Unlabeled Samples by Selected Reaction Monitoring Mass Spectrometry. Molecular and Cellular Proteomics, 2012, 11, M111.013987.	2.5	117
111	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. Nature Communications, 2017, 8, 1212.	5.8	112
112	Statistical protein quantification and significance analysis in label-free LC-MS experiments with complex designs. BMC Bioinformatics, 2012, 13, S6.	1.2	110
113	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. Nature Methods, 2015, 12, 725-731.	9.0	109
114	Complexâ€centric proteome profiling by <scp>SEC</scp> â€•<scp>SWATH</scp> â€•<scp>MS</scp>. Molecular Systems Biology, 2019, 15, e8438.	3.2	109
115	Epigenetic stress responses induce muscle stem-cell ageing by Hoxa9 developmental signals. Nature, 2016, 540, 428-432.	13.7	108
116	An open-source computational and data resource to analyze digital maps of immunopeptidomes. ELife, 2015, 4, .	2.8	107
117	Quantitative Interactomics in Primary T Cells Provides a Rationale for Concomitant PD-1 and BTLA Coinhibitor Blockade in Cancer Immunotherapy. Cell Reports, 2019, 27, 3315-3330.e7.	2.9	106
118	A mass spectrometric journey into protein and proteome research. Journal of the American Society for Mass Spectrometry, 2003, 14, 685-695.	1.2	105
119	The Calcineurin Signaling Network Evolves via Conserved Kinase-Phosphatase Modules that Transcend Substrate Identity. Molecular Cell, 2014, 55, 422-435.	4.5	102
120	The Biology/Disease-driven Human Proteome Project (B/D-HPP): Enabling Protein Research for the Life Sciences Community. Journal of Proteome Research, 2013, 12, 23-27.	1.8	100
121	Highâ€throughput proteomic analysis of <scp>FFPE</scp> tissue samples facilitates tumor stratification. Molecular Oncology, 2019, 13, 2305-2328.	2.1	100
122	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Analytical Chemistry, 2019, 91, 6953-6961.	3.2	100
123	The Chaperonin TRiC/CCT Associates with Prefoldin through a Conserved Electrostatic Interface Essential for Cellular Proteostasis. Cell, 2019, 177, 751-765.e15.	13.5	98
124	Insertion of the Biogenesis Factor Rei1 Probes the Ribosomal Tunnel during 60S Maturation. Cell, 2016, 164, 91-102.	13.5	97
125	Conserved Peptide Fragmentation as a Benchmarking Tool for Mass Spectrometers and a Discriminating Feature for Targeted Proteomics. Molecular and Cellular Proteomics, 2014, 13, 2056-2071.	2.5	96
126	Structural basis of AAUAAA polyadenylation signal recognition by the human CPSF complex. Nature Structural and Molecular Biology, 2018, 25, 135-138.	3.6	96

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127	ChromID identifies the protein interactome at chromatin marks. Nature Biotechnology, 2020, 38, 728-736.	9.4	90
128	A Conserved Mito-Cytosolic Translational Balance Links Two Longevity Pathways. Cell Metabolism, 2020, 31, 549-563.e7.	7.2	87
129	A Case for a Human Immuno-Peptidome Project Consortium. Immunity, 2017, 47, 203-208.	6.6	84
130	From coarse to fine: the absolute <i>Escherichia coli</i> proteome under diverse growth conditions. Molecular Systems Biology, 2021, 17, e9536.	3.2	82
131	Prediction of colorectal cancer diagnosis based onÂcirculating plasma proteins. EMBO Molecular Medicine, 2015, 7, 1166-1178.	3.3	80
132	Identification of a Set of Conserved Eukaryotic Internal Retention Time Standards for Data-independent Acquisition Mass Spectrometry. Molecular and Cellular Proteomics, 2015, 14, 2800-2813.	2.5	76
133	Structure of a human cap-dependent 48S translation pre-initiation complex. Nucleic Acids Research, 2018, 46, 2678-2689.	6.5	76
134	Strategies to enable large-scale proteomics for reproducible research. Nature Communications, 2020, 11, 3793.	5.8	75
135	Kinase Interaction Network Expands Functional and Disease Roles of Human Kinases. Molecular Cell, 2020, 79, 504-520.e9.	4.5	74
136	Target of Rapamycin Complex 2 Regulates Actin Polarization and Endocytosis via Multiple Pathways. Journal of Biological Chemistry, 2015, 290, 14963-14978.	1.6	72
137	Advancing translational research and precision medicine with targeted proteomics. Journal of Proteomics, 2018, 189, 1-10.	1.2	72
138	Breast Cancer Classification Based on Proteotypes Obtained by SWATH Mass Spectrometry. Cell Reports, 2019, 28, 832-843.e7.	2.9	72
139	Structural insights into the assembly and polyA signal recognition mechanism of the human CPSF complex. ELife, 2017, 6, .	2.8	71
140	Epigenetics and Proteomics Join Transcriptomics in the Quest for Tuberculosis Biomarkers. MBio, 2015, 6, e01187-15.	1.8	70
141	The interactome of <scp>KRAB</scp> zinc finger proteins reveals the evolutionary history of their functional diversification. EMBO Journal, 2019, 38, e101220.	3.5	67
142	Antigenic Characterization of the HCMV gH/gL/gO and Pentamer Cell Entry Complexes Reveals Binding Sites for Potently Neutralizing Human Antibodies. PLoS Pathogens, 2015, 11, e1005230.	2.1	65
143	Systematic Analysis of Human Protein Phosphatase Interactions and Dynamics. Cell Systems, 2017, 4, 430-444.e5.	2.9	65
144	Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. Science Signaling, 2015, 8, rs4.	1.6	64

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145	Proteome-wide selected reaction monitoring assays for the human pathogen Streptococcus pyogenes. Nature Communications, 2012, 3, 1301.	5.8	63
146	aLFQ: an R-package for estimating absolute protein quantities from label-free LC-MS/MS proteomics data. Bioinformatics, 2014, 30, 2511-2513.	1.8	63
147	Mass spectrometry–driven phosphoproteomics: patterning the systems biology mosaic. Wiley Interdisciplinary Reviews: Developmental Biology, 2014, 3, 83-112.	5.9	63
148	Phosphoproteomic analyses reveal novel cross–modulation mechanisms between two signaling pathways in yeast. Molecular Systems Biology, 2014, 10, 767.	3.2	58
149	Diagnostics and correction of batch effects in large–scale proteomic studies: a tutorial. Molecular Systems Biology, 2021, 17, e10240.	3.2	57
150	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. Cell Systems, 2020, 10, 133-155.e6.	2.9	57
151	Comparative 'omics analyses differentiate Mycobacterium tuberculosis and Mycobacterium bovis and reveal distinct macrophage responses to infection with the human and bovine tubercle bacilli. Microbial Genomics, 2018, 4, .	1.0	57
152	Identification of <scp>C</scp> dk targets that control cytokinesis. EMBO Journal, 2015, 34, 81-96.	3.5	56
153	Updated Reference Genome Sequence and Annotation of Mycobacterium bovis AF2122/97. Genome Announcements, 2017, 5, .	0.8	55
154	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	1.9	52
155	Huntingtin's spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. ELife, 2016, 5, e11184.	2.8	52
156	Phosphoproteomic analysis identifies proteins involved in transcription-coupled mRNA decay as targets of Snf1 signaling. Science Signaling, 2014, 7, ra64.	1.6	51
157	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. Life Science Alliance, 2018, 1, e201800042.	1.3	51
158	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. Genomics, Proteomics and Bioinformatics, 2020, 18, 104-119.	3.0	51
159	Attenuation of pattern recognition receptor signaling is mediated by a <scp>MAP</scp> kinase kinase kinase. EMBO Reports, 2016, 17, 441-454.	2.0	50
160	Applications and Developments in Targeted Proteomics: From SRM to DIA/SWATH. Proteomics, 2016, 16, 2065-2067.	1.3	50
161	Quantifying and Localizing the Mitochondrial Proteome Across Five Tissues in A Mouse Population. Molecular and Cellular Proteomics, 2018, 17, 1766-1777.	2.5	50
162	Non–invasive prognostic protein biomarker signatures associated with colorectal cancer. EMBO Molecular Medicine, 2015, 7, 1153-1165.	3.3	49

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163	Inferring causal metabolic signals that regulate the dynamic <scp>TORC</scp>1â€dependent transcriptome. Molecular Systems Biology, 2015, 11, 802.	3.2	49
164	Quantitative Proteome Analysis: Methods and Applications. Journal of Infectious Diseases, 2003, 187, S315-S320.	1.9	48
165	Systems-level Proteomics of Two Ubiquitous Leaf Commensals Reveals Complementary Adaptive Traits for Phyllosphere Colonization. Molecular and Cellular Proteomics, 2016, 15, 3256-3269.	2.5	48
166	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. Cell, 2019, 177, 1308-1318.e10.	13.5	48
167	Comprehensive proteome analysis of human skeletal muscle in cachexia and sarcopenia: a pilot study. Journal of Cachexia, Sarcopenia and Muscle, 2017, 8, 567-582.	2.9	47
168	Reproducible quantitative proteotype data matrices for systems biology. Molecular Biology of the Cell, 2015, 26, 3926-3931.	0.9	46
169	A tissue-based draft map of the murine MHC class I immunopeptidome. Scientific Data, 2018, 5, 180157.	2.4	45
170	Minimal sample requirement for highly multiplexed protein quantification in cell lines and tissues by PCT-SWATH mass spectrometry. Proteomics, 2015, 15, 3711-3721.	1.3	44
171	Structural modeling of proteinâ€"RNA complexes using crosslinking of segmentally isotope-labeled RNA and MS/MS. Nature Methods, 2017, 14, 487-490.	9.0	44
172	Sensitive Quantitative Proteomics of Human Hematopoietic Stem and Progenitor Cells by Data-independent Acquisition Mass Spectrometry. Molecular and Cellular Proteomics, 2019, 18, 1454-1467.	2.5	43
173	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. Molecular and Cellular Proteomics, 2014, 13, 1905-1913.	2.5	42
174	Mass spectrometry-based proteomic quest for diabetes biomarkers. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 519-527.	1.1	42
175	A Targeted Mass Spectrometry Strategy for Developing Proteomic Biomarkers: A Case Study of Epithelial Ovarian Cancer. Molecular and Cellular Proteomics, 2019, 18, 1836-1850.	2.5	42
176	Reproducible Tissue Homogenization and Protein Extraction for Quantitative Proteomics Using MicroPestle-Assisted Pressure-Cycling Technology. Journal of Proteome Research, 2016, 15, 1821-1829.	1.8	41
177	Proteome-wide association studies identify biochemical modules associated with a wing-size phenotype in Drosophila melanogaster. Nature Communications, 2016, 7, 12649.	5.8	41
178	Systems proteomics approaches to study bacterial pathogens: application to Mycobacterium tuberculosis. Current Opinion in Microbiology, 2017, 39, 64-72.	2.3	41
179	Molecular basis of AKAP79 regulation by calmodulin. Nature Communications, 2017, 8, 1681.	5.8	41
180	SWATH2stats: An R/Bioconductor Package to Process and Convert Quantitative SWATH-MS Proteomics Data for Downstream Analysis Tools. PLoS ONE, 2016, 11, e0153160.	1.1	40

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181	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. Nature Communications, 2021, 12, 3810.	5.8	40
182	Evolution of organelle-associated protein profiling. Journal of Proteomics, 2009, 72, 4-11.	1.2	39
183	Delayed effects of transcriptional responses in Mycobacterium tuberculosis exposed to nitric oxide suggest other mechanisms involved in survival. Scientific Reports, 2017, 7, 8208.	1.6	39
184	Systematic characterization of panâ€‹cancer mutation clusters. Molecular Systems Biology, 2018, 14, e7974.	3.2	39
185	Arabidopsis proteome and the mass spectral assay library. Scientific Data, 2019, 6, 278.	2.4	39
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