

Ruedi Aebersold

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306
papers

48,708
citations

101
h-index

219
g-index

338
ext. papers

58,164
ext. citations

15.3
avg, IF

7.83
L-index

#	Paper	IF	Citations
306	Mass spectrometry-based proteomics. <i>Nature</i> , 2003 , 422, 198-207	50.4	5480
305	Empirical statistical model to estimate the accuracy of peptide identifications made by MS/MS and database search. <i>Analytical Chemistry</i> , 2002 , 74, 5383-92	7.8	3930
304	Targeted data extraction of the MS/MS spectra generated by data-independent acquisition: a new concept for consistent and accurate proteome analysis. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, O114:0167-77	7.6	1713
303	Integrated genomic and proteomic analyses of a systematically perturbed metabolic network. <i>Science</i> , 2001 , 292, 929-34	33.3	1691
302	Checkpoint blockade cancer immunotherapy targets tumour-specific mutant antigens. <i>Nature</i> , 2014 , 515, 577-81	50.4	1331
301	On the Dependency of Cellular Protein Levels on mRNA Abundance. <i>Cell</i> , 2016 , 165, 535-50	56.2	1235
300	Selected reaction monitoring for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , 2008 , 4, 222	12.2	1081
299	Mass-spectrometric exploration of proteome structure and function. <i>Nature</i> , 2016 , 537, 347-55	50.4	1070
298	Selected reaction monitoring-based proteomics: workflows, potential, pitfalls and future directions. <i>Nature Methods</i> , 2012 , 9, 555-66	21.6	997
297	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2013 , 10, 730-6	21.6	894
296	Quantitative profiling of differentiation-induced microsomal proteins using isotope-coded affinity tags and mass spectrometry. <i>Nature Biotechnology</i> , 2001 , 19, 946-51	44.5	828
295	Interpretation of shotgun proteomic data: the protein inference problem. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1419-40	7.6	756
294	NAD ⁺ repletion improves mitochondrial and stem cell function and enhances life span in mice. <i>Science</i> , 2016 , 352, 1436-43	33.3	645
293	A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004 , 22, 1459-66	44.5	632
292	A guided tour of the Trans-Proteomic Pipeline. <i>Proteomics</i> , 2010 , 10, 1150-9	4.8	590
291	The PeptideAtlas project. <i>Nucleic Acids Research</i> , 2006 , 34, D655-8	20.1	590
290	The quantitative proteome of a human cell line. <i>Molecular Systems Biology</i> , 2011 , 7, 549	12.2	586

289	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007 , 25, 887-925	44.5	583
288	Reproducible isolation of distinct, overlapping segments of the phosphoproteome. <i>Nature Methods</i> , 2007 , 4, 231-7	21.6	524
287	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , 2014 , 32, 219-23	44.5	508
286	Options and considerations when selecting a quantitative proteomics strategy. <i>Nature Biotechnology</i> , 2010 , 28, 710-21	44.5	501
285	The quantitative and condition-dependent Escherichia coli proteome. <i>Nature Biotechnology</i> , 2016 , 34, 104-10	44.5	422
284	Development and validation of a spectral library searching method for peptide identification from MS/MS. <i>Proteomics</i> , 2007 , 7, 655-67	4.8	405
283	iProphet: multi-level integrative analysis of shotgun proteomic data improves peptide and protein identification rates and error estimates. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.007690	7.6	397
282	Data-independent acquisition-based SWATH-MS for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , 2018 , 14, e8126	12.2	389
281	Quantitative analysis of fission yeast transcriptomes and proteomes in proliferating and quiescent cells. <i>Cell</i> , 2012 , 151, 671-83	56.2	388
280	Molecular architecture of the 26S proteasome holocomplex determined by an integrative approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 1380-7	11.5	380
279	Probing native protein structures by chemical cross-linking, mass spectrometry, and bioinformatics. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1634-49	7.6	367
278	mProphet: automated data processing and statistical validation for large-scale SRM experiments. <i>Nature Methods</i> , 2011 , 8, 430-5	21.6	357
277	Proteome-wide cellular protein concentrations of the human pathogen <i>Leptospira interrogans</i> . <i>Nature</i> , 2009 , 460, 762-5	50.4	349
276	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016 , 13, 741-8	21.6	337
275	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
274	Structural probing of a protein phosphatase 2A network by chemical cross-linking and mass spectrometry. <i>Science</i> , 2012 , 337, 1348-52	33.3	323
273	Identification of cross-linked peptides from large sequence databases. <i>Nature Methods</i> , 2008 , 5, 315-8	21.6	323
272	The study of macromolecular complexes by quantitative proteomics. <i>Nature Genetics</i> , 2003 , 33, 349-55	36.3	319

271	Ribosome. The complete structure of the 55S mammalian mitochondrial ribosome. <i>Science</i> , 2015 , 348, 303-8	33.3	275
270	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014 , 1, 1400318.2		266
269	Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation. <i>Rapid Communications in Mass Spectrometry</i> , 2001 , 15, 1214-21	2.2	258
268	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017 , 8, 291	17.4	252
267	Crosslinking and Mass Spectrometry: An Integrated Technology to Understand the Structure and Function of Molecular Machines. <i>Trends in Biochemical Sciences</i> , 2016 , 41, 20-32	10.3	251
266	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. <i>Nature Medicine</i> , 2015 , 21, 407-13	50.5	250
265	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 2013 , 494, 266-70	50.4	250
264	Protein identification false discovery rates for very large proteomics data sets generated by tandem mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 2405-17	7.6	250
263	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. <i>Nature Methods</i> , 2013 , 10, 1246-53	21.6	249
262	The human proteome project: current state and future direction. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.009993	7.6	249
261	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , 2012 , 30, 221-3	44.5	244
260	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016 , 166, 766-778	56.2	236
259	Architecture and conformational switch mechanism of the ryanodine receptor. <i>Nature</i> , 2015 , 517, 39-43	50.4	230
258	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015 , 10, 426-41	18.8	229
257	Phosphoproteomic analysis reveals interconnected system-wide responses to perturbations of kinases and phosphatases in yeast. <i>Science Signaling</i> , 2010 , 3, rs4	8.8	229
256	Large-scale quantitative assessment of different in-solution protein digestion protocols reveals superior cleavage efficiency of tandem Lys-C/trypsin proteolysis over trypsin digestion. <i>Journal of Proteome Research</i> , 2012 , 11, 5145-56	5.6	227
255	Early steps in autophagy depend on direct phosphorylation of Atg9 by the Atg1 kinase. <i>Molecular Cell</i> , 2014 , 53, 471-83	17.6	225
254	Crucial HSP70 co-chaperone complex unlocks metazoan protein disaggregation. <i>Nature</i> , 2015 , 524, 247-51	50.4	224

253	Quantitative variability of 342 plasma proteins in a human twin population. <i>Molecular Systems Biology</i> , 2015 , 11, 786	12.2	222
252	False discovery rate estimation for cross-linked peptides identified by mass spectrometry. <i>Nature Methods</i> , 2012 , 9, 901-3	21.6	219
251	An integrated workflow for charting the human interaction proteome: insights into the PP2A system. <i>Molecular Systems Biology</i> , 2009 , 5, 237	12.2	218
250	The molecular architecture of the eukaryotic chaperonin TRiC/CCT. <i>Structure</i> , 2012 , 20, 814-25	5.2	216
249	Building consensus spectral libraries for peptide identification in proteomics. <i>Nature Methods</i> , 2008 , 5, 873-5	21.6	214
248	Expanding the chemical cross-linking toolbox by the use of multiple proteases and enrichment by size exclusion chromatography. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.014126	7.6	213
247	ATM-dependent and -independent dynamics of the nuclear phosphoproteome after DNA damage. <i>Science Signaling</i> , 2010 , 3, rs3	8.8	212
246	Mapping differential interactomes by affinity purification coupled with data-independent mass spectrometry acquisition. <i>Nature Methods</i> , 2013 , 10, 1239-45	21.6	207
245	Quantification of mRNA and protein and integration with protein turnover in a bacterium. <i>Molecular Systems Biology</i> , 2011 , 7, 511	12.2	207
244	Genome-wide mapping of transcriptional start sites defines an extensive leaderless transcriptome in <i>Mycobacterium tuberculosis</i> . <i>Cell Reports</i> , 2013 , 5, 1121-31	10.6	206
243	Mass Spectrometry Applied to Bottom-Up Proteomics: Entering the High-Throughput Era for Hypothesis Testing. <i>Annual Review of Analytical Chemistry</i> , 2016 , 9, 449-72	12.5	202
242	A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , 2016 , 34, 1130-1136	44.5	202
241	A mass spectrometric-derived cell surface protein atlas. <i>PLoS ONE</i> , 2015 , 10, e0121314	3.7	199
240	The complete structure of the large subunit of the mammalian mitochondrial ribosome. <i>Nature</i> , 2014 , 515, 283-6	50.4	195
239	Systems proteomics of liver mitochondria function. <i>Science</i> , 2016 , 352, aad0189	33.3	193
238	Lysine-specific chemical cross-linking of protein complexes and identification of cross-linking sites using LC-MS/MS and the xQuest/xProphet software pipeline. <i>Nature Protocols</i> , 2014 , 9, 120-37	18.8	179
237	Quantitative measurements of N-linked glycoproteins in human plasma by SWATH-MS. <i>Proteomics</i> , 2013 , 13, 1247-56	4.8	171
236	Architecture of the large subunit of the mammalian mitochondrial ribosome. <i>Nature</i> , 2014 , 505, 515-9	50.4	164

235	Multilayered genetic and omics dissection of mitochondrial activity in a mouse reference population. <i>Cell</i> , 2014 , 158, 1415-1430	56.2	161
234	TRIM24 Is an Oncogenic Transcriptional Activator in Prostate Cancer. <i>Cancer Cell</i> , 2016 , 29, 846-858	24.3	160
233	Chemical cross-linking/mass spectrometry targeting acidic residues in proteins and protein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 9455-60	11.5	158
232	Molecular architecture of the 40S/eIF1/eIF3 translation initiation complex. <i>Cell</i> , 2014 , 158, 1123-1135	56.2	157
231	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. <i>Cell Host and Microbe</i> , 2015 , 18, 96-108	23.4	155
230	Cancer genetics-guided discovery of serum biomarker signatures for diagnosis and prognosis of prostate cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 3342-7	11.5	153
229	A High-Density Map for Navigating the Human Polycomb Complexome. <i>Cell Reports</i> , 2016 , 17, 583-595	10.6	147
228	Analysis of Major Histocompatibility Complex (MHC) Immunopeptidomes Using Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 3105-17	7.6	143
227	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. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1753-68	7.6	143
226	The Mtb proteome library: a resource of assays to quantify the complete proteome of Mycobacterium tuberculosis. <i>Cell Host and Microbe</i> , 2013 , 13, 602-612	23.4	139
225	Generating and navigating proteome maps using mass spectrometry. <i>Nature Reviews Molecular Cell Biology</i> , 2010 , 11, 789-801	48.7	139
224	Reproducible and consistent quantification of the Saccharomyces cerevisiae proteome by SWATH-mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 739-49	7.6	136
223	The protein interaction landscape of the human CMGC kinase group. <i>Cell Reports</i> , 2013 , 3, 1306-20	10.6	136
222	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry-Based Assays. <i>Clinical Chemistry</i> , 2016 , 62, 48-69	5.5	135
221	Quantitative proteomics: challenges and opportunities in basic and applied research. <i>Nature Protocols</i> , 2017 , 12, 1289-1294	18.8	133
220	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016 , 15, 3961-3970	5.6	130
219	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. <i>Nature Methods</i> , 2017 , 14, 921-927	21.6	129
218	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. <i>Nature Biotechnology</i> , 2019 , 37, 314-322	44.5	129

217	Proteomics meets the scientific method. <i>Nature Methods</i> , 2013 , 10, 24-7	21.6	123
216	An automated pipeline for high-throughput label-free quantitative proteomics. <i>Journal of Proteome Research</i> , 2013 , 12, 1628-44	5.6	123
215	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , 2016 , 13, 777-83	21.6	122
214	Standard guidelines for the chromosome-centric human proteome project. <i>Journal of Proteome Research</i> , 2012 , 11, 2005-13	5.6	121
213	The Human Plasma Proteome Draft of 2017: Building on the Human Plasma PeptideAtlas from Mass Spectrometry and Complementary Assays. <i>Journal of Proteome Research</i> , 2017 , 16, 4299-4310	5.6	119
212	RNF168 promotes noncanonical K27 ubiquitination to signal DNA damage. <i>Cell Reports</i> , 2015 , 10, 226-38	10.6	119
211	Structures of human PRC2 with its cofactors AEBP2 and JARID2. <i>Science</i> , 2018 , 359, 940-944	33.3	109
210	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2301-7	7.6	104
209	Estimation of absolute protein quantities of unlabeled samples by selected reaction monitoring mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.013987	7.6	103
208	Insights into autophagosome biogenesis from structural and biochemical analyses of the ATG2A-WIPI4 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E9792-E9801	11.5	103
207	Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. <i>Molecular Cell</i> , 2015 , 58, 977-88	17.6	101
206	The structural basis of substrate recognition by the eukaryotic chaperonin TRiC/CCT. <i>Cell</i> , 2014 , 159, 1042-1055	56.2	98
205	A Class of Environmental and Endogenous Toxins Induces BRCA2 Haploinsufficiency and Genome Instability. <i>Cell</i> , 2017 , 169, 1105-1118.e15	56.2	93
204	Statistical protein quantification and significance analysis in label-free LC-MS experiments with complex designs. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 16, S6	3.6	93
203	Quantitative proteomics analysis of signalosome dynamics in primary T cells identifies the surface receptor CD6 as a Lat adaptor-independent TCR signaling hub. <i>Nature Immunology</i> , 2014 , 15, 384-392	19.1	92
202	A mass spectrometric journey into protein and proteome research. <i>Journal of the American Society for Mass Spectrometry</i> , 2003 , 14, 685-95	3.5	91
201	The SystemMHC Atlas project. <i>Nucleic Acids Research</i> , 2018 , 46, D1237-D1247	20.1	87
200	The biology/disease-driven human proteome project (B/D-HPP): enabling protein research for the life sciences community. <i>Journal of Proteome Research</i> , 2013 , 12, 23-7	5.6	87

199	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015 , 12, 725-31	21.6	86
198	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017 , 35, 781-788	44.5	85
197	diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020 , 17, 1229-1236	21.6	85
196	Epigenetic stress responses induce muscle stem-cell ageing by Hoxa9 developmental signals. <i>Nature</i> , 2016 , 540, 428-432	50.4	79
195	Insertion of the Biogenesis Factor Rei1 Probes the Ribosomal Tunnel during 60S Maturation. <i>Cell</i> , 2016 , 164, 91-102	56.2	75
194	Impact of Alternative Splicing on the Human Proteome. <i>Cell Reports</i> , 2017 , 20, 1229-1241	10.6	74
193	The calcineurin signaling network evolves via conserved kinase-phosphatase modules that transcend substrate identity. <i>Molecular Cell</i> , 2014 , 55, 422-435	17.6	70
192	Proteomic and interactomic insights into the molecular basis of cell functional diversity. <i>Nature Reviews Molecular Cell Biology</i> , 2020 , 21, 327-340	48.7	68
191	Prediction of colorectal cancer diagnosis based on circulating plasma proteins. <i>EMBO Molecular Medicine</i> , 2015 , 7, 1166-78	12	68
190	An open-source computational and data resource to analyze digital maps of immunopeptidomes. <i>ELife</i> , 2015 , 4,	8.9	68
189	Conserved peptide fragmentation as a benchmarking tool for mass spectrometers and a discriminating feature for targeted proteomics. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2056-71	7.6	65
188	Proteome-wide selected reaction monitoring assays for the human pathogen <i>Streptococcus pyogenes</i> . <i>Nature Communications</i> , 2012 , 3, 1301	17.4	62
187	Complex-centric proteome profiling by SEC-SWATH-MS. <i>Molecular Systems Biology</i> , 2019 , 15, e8438	12.2	61
186	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. <i>Nature Communications</i> , 2017 , 8, 1212	17.4	59
185	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020 , 11, 5301	17.4	59
184	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019 , 91, 6953-6961	7.8	57
183	Structural basis of AAUAAA polyadenylation signal recognition by the human CPSF complex. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 135-138	17.6	57
182	Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. <i>Science Signaling</i> , 2015 , 8, rs4	8.8	56

181	Mass spectrometry-driven phosphoproteomics: patterning the systems biology mosaic. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2014 , 3, 83-112	5.9	56
180	Target of Rapamycin Complex 2 Regulates Actin Polarization and Endocytosis via Multiple Pathways. <i>Journal of Biological Chemistry</i> , 2015 , 290, 14963-78	5.4	55
179	Antigenic Characterization of the HCMV gH/gL/gO and Pentamer Cell Entry Complexes Reveals Binding Sites for Potently Neutralizing Human Antibodies. <i>PLoS Pathogens</i> , 2015 , 11, e1005230	7.6	54
178	Structural insights into the assembly and polyA signal recognition mechanism of the human CPSF complex. <i>ELife</i> , 2017 , 6,	8.9	52
177	Identification of a Set of Conserved Eukaryotic Internal Retention Time Standards for Data-independent Acquisition Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2800-13	7.6	51
176	Epigenetics and Proteomics Join Transcriptomics in the Quest for Tuberculosis Biomarkers. <i>MBio</i> , 2015 , 6, e01187-15	7.8	48
175	aLFQ: an R-package for estimating absolute protein quantities from label-free LC-MS/MS proteomics data. <i>Bioinformatics</i> , 2014 , 30, 2511-3	7.2	48
174	Structure of a human cap-dependent 48S translation pre-initiation complex. <i>Nucleic Acids Research</i> , 2018 , 46, 2678-2689	20.1	47
173	Quantitative Interactomics in Primary T Cells Provides a Rationale for Concomitant PD-1 and BTLA Coinhibitor Blockade in Cancer Immunotherapy. <i>Cell Reports</i> , 2019 , 27, 3315-3330.e7	10.6	46
172	A Case for a Human Immuno-Peptidome Project Consortium. <i>Immunity</i> , 2017 , 47, 203-208	32.3	46
171	Systematic Analysis of Human Protein Phosphatase Interactions and Dynamics. <i>Cell Systems</i> , 2017 , 4, 430-444.e5	10.6	44
170	Advancing translational research and precision medicine with targeted proteomics. <i>Journal of Proteomics</i> , 2018 , 189, 1-10	3.9	44
169	Identification of Cdk targets that control cytokinesis. <i>EMBO Journal</i> , 2015 , 34, 81-96	13	43
168	High-throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification. <i>Molecular Oncology</i> , 2019 , 13, 2305-2328	7.9	43
167	Phosphoproteomic analysis identifies proteins involved in transcription-coupled mRNA decay as targets of Snf1 signaling. <i>Science Signaling</i> , 2014 , 7, ra64	8.8	41
166	JARID2 and AEBP2 regulate PRC2 in the presence of H2AK119ub1 and other histone modifications. <i>Science</i> , 2021 , 371,	33.3	41
165	Breast Cancer Classification Based on Proteotypes Obtained by SWATH Mass Spectrometry. <i>Cell Reports</i> , 2019 , 28, 832-843.e7	10.6	40
164	Non-invasive prognostic protein biomarker signatures associated with colorectal cancer. <i>EMBO Molecular Medicine</i> , 2015 , 7, 1153-65	12	40

163	Quantitative proteome analysis: methods and applications. <i>Journal of Infectious Diseases</i> , 2003 , 187 Suppl 2, S315-20	7	40
162	Attenuation of pattern recognition receptor signaling is mediated by a MAP kinase kinase. <i>EMBO Reports</i> , 2016 , 17, 441-54	6.5	39
161	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. <i>Life Science Alliance</i> , 2018 , 1,	5.8	38
160	Quantifying and Localizing the Mitochondrial Proteome Across Five Tissues in A Mouse Population. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1766-1777	7.6	37
159	A Conserved Mito-Cytosolic Translational Balance Links Two Longevity Pathways. <i>Cell Metabolism</i> , 2020 , 31, 549-563.e7	24.6	36
158	Minimal sample requirement for highly multiplexed protein quantification in cell lines and tissues by PCT-SWATH mass spectrometry. <i>Proteomics</i> , 2015 , 15, 3711-21	4.8	36
157	qcML: an exchange format for quality control metrics from mass spectrometry experiments. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1905-13	7.6	36
156	The Chaperonin TRiC/CCT Associates with Prefoldin through a Conserved Electrostatic Interface Essential for Cellular Proteostasis. <i>Cell</i> , 2019 , 177, 751-765.e15	56.2	35
155	Range of protein detection by selected/multiple reaction monitoring mass spectrometry in an unfractionated human cell culture lysate. <i>Proteomics</i> , 2012 , 12, 1185-93	4.8	35
154	Evolution of organelle-associated protein profiling. <i>Journal of Proteomics</i> , 2009 , 72, 4-11	3.9	35
153	Mass spectrometry-based proteomic quest for diabetes biomarkers. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 519-27	4	34
152	Reproducible Tissue Homogenization and Protein Extraction for Quantitative Proteomics Using MicroPestle-Assisted Pressure-Cycling Technology. <i>Journal of Proteome Research</i> , 2016 , 15, 1821-9	5.6	34
151	Reproducible quantitative proteotype data matrices for systems biology. <i>Molecular Biology of the Cell</i> , 2015 , 26, 3926-31	3.5	33
150	The interactome of KRAB zinc finger proteins reveals the evolutionary history of their functional diversification. <i>EMBO Journal</i> , 2019 , 38, e101220	13	33
149	Proteome-wide association studies identify biochemical modules associated with a wing-size phenotype in <i>Drosophila melanogaster</i> . <i>Nature Communications</i> , 2016 , 7, 12649	17.4	32
148	Huntingtin β spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. <i>ELife</i> , 2016 , 5, e11184	8.9	32
147	The Evolving Contribution of Mass Spectrometry to Integrative Structural Biology. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 966-74	3.5	32
146	Updated Reference Genome Sequence and Annotation of AF2122/97. <i>Genome Announcements</i> , 2017 , 5,		31

145	ChromID identifies the protein interactome at chromatin marks. <i>Nature Biotechnology</i> , 2020 , 38, 728-736	4.5	31
144	SWATH2stats: An R/Bioconductor Package to Process and Convert Quantitative SWATH-MS Proteomics Data for Downstream Analysis Tools. <i>PLoS ONE</i> , 2016 , 11, e0153160	3.7	31
143	A Combined Shotgun and Targeted Mass Spectrometry Strategy for Breast Cancer Biomarker Discovery. <i>Journal of Proteome Research</i> , 2015 , 14, 2807-18	5.6	28
142	Chemical cross-linking/mass spectrometry maps the amyloid β peptide binding region on both apolipoprotein E domains. <i>ACS Chemical Biology</i> , 2015 , 10, 1010-6	4.9	28
141	Phosphoproteomic analyses reveal novel cross-modulation mechanisms between two signaling pathways in yeast. <i>Molecular Systems Biology</i> , 2014 , 10, 767	12.2	28
140	Systems-level Proteomics of Two Ubiquitous Leaf Commensals Reveals Complementary Adaptive Traits for Phyllosphere Colonization. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 3256-3269	7.6	28
139	Comprehensive proteome analysis of human skeletal muscle in cachexia and sarcopenia: a pilot study. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2017 , 8, 567-582	10.3	27
138	Delayed effects of transcriptional responses in <i>Mycobacterium tuberculosis</i> exposed to nitric oxide suggest other mechanisms involved in survival. <i>Scientific Reports</i> , 2017 , 7, 8208	4.9	27
137	Structural modeling of protein-RNA complexes using crosslinking of segmentally isotope-labeled RNA and MS/MS. <i>Nature Methods</i> , 2017 , 14, 487-490	21.6	26
136	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. <i>Cell</i> , 2019 , 177, 1308-1318	13.1	26
135	Sensitive Quantitative Proteomics of Human Hematopoietic Stem and Progenitor Cells by Data-independent Acquisition Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1454-1467	7.6	26
134	Inferring causal metabolic signals that regulate the dynamic TORC1-dependent transcriptome. <i>Molecular Systems Biology</i> , 2015 , 11, 802	12.2	26
133	Strategies to enable large-scale proteomics for reproducible research. <i>Nature Communications</i> , 2020 , 11, 3793	17.4	26
132	Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS. <i>Cell Reports</i> , 2018 , 23, 2819-2831.e5	10.6	26
131	Multiplexed Targeted Mass Spectrometry-Based Assays for the Quantification of N-Linked Glycosite-Containing Peptides in Serum. <i>Analytical Chemistry</i> , 2015 , 87, 10830-8	7.8	25
130	Systematic characterization of pan-cancer mutation clusters. <i>Molecular Systems Biology</i> , 2018 , 14, e7974	12.2	25
129	Conformational control and DNA-binding mechanism of the metazoan origin recognition complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E5906-E5915	11.5	25
128	Modulation of the chromatin phosphoproteome by the Haspin protein kinase. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1724-40	7.6	25

127	Comparative Omics analyses differentiate Mycobacterium tuberculosis and Mycobacterium bovis and reveal distinct macrophage responses to infection with the human and bovine tubercle bacilli. <i>Microbial Genomics</i> , 2018 , 4,	4.4	25
126	Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020 , 19, 4735-4746	5.6	25
125	A Targeted Mass Spectrometry Strategy for Developing Proteomic Biomarkers: A Case Study of Epithelial Ovarian Cancer. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1836-1850	7.6	24
124	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. <i>Cell Systems</i> , 2020 , 10, 133-155.e6	10.6	24
123	Arabidopsis proteome and the mass spectral assay library. <i>Scientific Data</i> , 2019 , 6, 278	8.2	24
122	Automated SWATH Data Analysis Using Targeted Extraction of Ion Chromatograms. <i>Methods in Molecular Biology</i> , 2017 , 1550, 289-307	1.4	23
121	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. <i>Cell Reports</i> , 2017 , 18, 3219-3226	10.6	23
120	A tissue-based draft map of the murine MHC class I immunopeptidome. <i>Scientific Data</i> , 2018 , 5, 180157	8.2	23
119	Generation of a zebrafish SWATH-MS spectral library to quantify 10,000 proteins. <i>Scientific Data</i> , 2019 , 6, 190011	8.2	23
118	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 104-119	6.5	23
117	Confident site localization using a simulated phosphopeptide spectral library. <i>Journal of Proteome Research</i> , 2015 , 14, 2348-59	5.6	22
116	Global Metabonomic and Proteomic Analysis of Human Conjunctival Epithelial Cells (IOBA-NHC) in Response to Hyperosmotic Stress. <i>Journal of Proteome Research</i> , 2015 , 14, 3982-95	5.6	22
115	Kinase Interaction Network Expands Functional and Disease Roles of Human Kinases. <i>Molecular Cell</i> , 2020 , 79, 504-520.e9	17.6	22
114	Systems proteomics approaches to study bacterial pathogens: application to Mycobacterium tuberculosis. <i>Current Opinion in Microbiology</i> , 2017 , 39, 64-72	7.9	21
113	Structural and biochemical characterization of the Cop9 signalosome CSN5/CSN6 heterodimer. <i>PLoS ONE</i> , 2014 , 9, e105688	3.7	21
112	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>iScience</i> , 2019 , 21, 664-680	6.1	21
111	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , 2019 , 10, 2524	17.4	20
110	Integrating highly quantitative proteomics and genome-scale metabolic modeling to study pH adaptation in the human pathogen. <i>Npj Systems Biology and Applications</i> , 2016 , 2, 16017	5	20

109	Quantitative proteomics signature profiling based on network contextualization. <i>Biology Direct</i> , 2015 , 10, 71	7.2	20
108	A Candida albicans PeptideAtlas. <i>Journal of Proteomics</i> , 2014 , 97, 62-8	3.9	19
107	Molecular Architecture of Yeast Chromatin Assembly Factor 1. <i>Scientific Reports</i> , 2016 , 6, 26702	4.9	19
106	Identification of Protein Abundance Changes in Hepatocellular Carcinoma Tissues Using PCT-SWATH. <i>Proteomics - Clinical Applications</i> , 2019 , 13, e1700179	3.1	19
105	AP-SWATH Reveals Direct Involvement of VCP/p97 in Integrated Stress Response Signaling Through Facilitating CREP/PPP1R15B Degradation. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1295-1307	7.6	18
104	Highlights of the Biology and Disease-driven Human Proteome Project, 2015-2016. <i>Journal of Proteome Research</i> , 2016 , 15, 3979-3987	5.6	18
103	The GTPase Nog1 co-ordinates the assembly, maturation and quality control of distant ribosomal functional centers. <i>ELife</i> , 2020 , 9,	8.9	18
102	Parallel accumulation Serial fragmentation combined with data-independent acquisition (diaPASEF): Bottom-up proteomics with near optimal ion usage		18
101	Molecular basis of AKAP79 regulation by calmodulin. <i>Nature Communications</i> , 2017 , 8, 1681	17.4	17
100	Complex-centric proteome profiling by SEC-SWATH-MS for the parallel detection of hundreds of protein complexes. <i>Nature Protocols</i> , 2020 , 15, 2341-2386	18.8	17
99	A curated collection of tissue microarray images and clinical outcome data of prostate cancer patients. <i>Scientific Data</i> , 2017 , 4, 170014	8.2	16
98	mzDB: a file format using multiple indexing strategies for the efficient analysis of large LC-MS/MS and SWATH-MS data sets. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 771-81	7.6	16
97	Multi-layered proteomic analyses decode compositional and functional effects of cancer mutations on kinase complexes. <i>Nature Communications</i> , 2020 , 11, 3563	17.4	16
96	Mitochondrial translation and dynamics synergistically extend lifespan in C. elegans through HLH-30. <i>Journal of Cell Biology</i> , 2020 , 219,	7.3	16
95	and Proteome Analysis of Human Immunodeficiency Virus (HIV)-1-infected, Human CD4 T Cells. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, S108-S123	7.6	15
94	Cooperative target mRNA destabilization and translation inhibition by miR-58 microRNA family in C. elegans. <i>Genome Research</i> , 2015 , 25, 1680-91	9.7	15
93	Germ-free and microbiota-associated mice yield small intestinal epithelial organoids with equivalent and robust transcriptome/proteome expression phenotypes. <i>Cellular Microbiology</i> , 2020 , 22, e13191	3.9	15
92	The interdependence of transcript and protein abundance: new data--new complexities. <i>Molecular Systems Biology</i> , 2016 , 12, 856	12.2	15

91	Lipidated apolipoprotein E4 structure and its receptor binding mechanism determined by a combined cross-linking coupled to mass spectrometry and molecular dynamics approach. <i>PLoS Computational Biology</i> , 2018 , 14, e1006165	5	15
90	Mycobacterium tuberculosis in the Proteomics Era. <i>Microbiology Spectrum</i> , 2014 , 2,	8.9	14
89	Phosphoproteomics reveals novel modes of function and inter-relationships among PIKKs in response to genotoxic stress. <i>EMBO Journal</i> , 2021 , 40, e104400	13	14
88	CHAPTER 4:Getting Absolute: Determining Absolute Protein Quantities via Selected Reaction Monitoring Mass Spectrometry. <i>New Developments in Mass Spectrometry</i> , 2014 , 80-109	2.3	14
87	Systems Pharmacology Dissection of Cholesterol Regulation Reveals Determinants of Large Pharmacodynamic Variability between Cell Lines. <i>Cell Systems</i> , 2017 , 5, 604-619.e7	10.6	13
86	Separation of blood microsamples by exploiting sedimentation at the microscale. <i>Scientific Reports</i> , 2018 , 8, 14101	4.9	13
85	CryoEM structures of Arabidopsis DDR complexes involved in RNA-directed DNA methylation. <i>Nature Communications</i> , 2019 , 10, 3916	17.4	12
84	Accelerated Protein Biomarker Discovery from FFPE Tissue Samples Using Single-Shot, Short Gradient Microflow SWATH MS. <i>Journal of Proteome Research</i> , 2020 , 19, 2732-2741	5.6	12
83	Review of Batch Effects Prevention, Diagnostics, and Correction Approaches. <i>Methods in Molecular Biology</i> , 2020 , 2051, 373-387	1.4	12
82	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. <i>Bioinformatics</i> , 2015 , 31, 2415-7	7.2	11
81	Integrative Structural Investigation on the Architecture of Human Importin4_Histone H3/H4_Asf1a Complex and Its Histone H3 Tail Binding. <i>Journal of Molecular Biology</i> , 2018 , 430, 822-841	6.5	11
80	The need for national centers for proteomics. <i>Nature Biotechnology</i> , 2002 , 20, 651	44.5	11
79	Proteomic identification of a marker signature for MAPKi resistance in melanoma. <i>EMBO Journal</i> , 2019 , 38, e95874	13	11
78	Molecular basis for disassembly of an importin:ribosomal protein complex by the escortin Tsr2. <i>Nature Communications</i> , 2018 , 9, 3669	17.4	11
77	Orthogonal Proteomic Platforms and Their Implications for the Stable Classification of High-Grade Serous Ovarian Cancer Subtypes. <i>iScience</i> , 2020 , 23, 101079	6.1	10
76	Fast and Efficient XML Data Access for Next-Generation Mass Spectrometry. <i>PLoS ONE</i> , 2015 , 10, e0125108	3.9	10
75	Contribution of Mass Spectrometry-Based Proteomics to the Understanding of TNF- α Signaling. <i>Journal of Proteome Research</i> , 2017 , 16, 14-33	5.6	9
74	A new class of protein biomarkers based on subcellular distribution: application to a mouse liver cancer model. <i>Scientific Reports</i> , 2019 , 9, 6913	4.9	9

73	Microbial Proteome Profiling and Systems Biology: Applications to Mycobacterium tuberculosis. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 883, 235-54	3.6	9
72	Histone epiproteomic profiling distinguishes oligodendroglioma, IDH-mutant and 1p/19q co-deleted from IDH-mutant astrocytoma and reveals less tri-methylation of H3K27 in oligodendrogliomas. <i>Acta Neuropathologica</i> , 2020 , 139, 211-213	14.3	9
71	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. <i>Cell Systems</i> , 2020 , 11, 589-607.e8	10.6	9
70	From coarse to fine: the absolute Escherichia coli proteome under diverse growth conditions. <i>Molecular Systems Biology</i> , 2021 , 17, e9536	12.2	9
69	Mild Acid Elution and MHC Immunoaffinity Chromatography Reveal Similar Albeit Not Identical Profiles of the HLA Class I Immunopeptidome. <i>Journal of Proteome Research</i> , 2021 , 20, 289-304	5.6	9
68	Proteomics goes parallel. <i>Nature Biotechnology</i> , 2018 , 36, 1051-1053	44.5	9
67	System-Wide Quantitative Proteomics of the Metabolic Syndrome in Mice: Genotypic and Dietary Effects. <i>Journal of Proteome Research</i> , 2017 , 16, 831-841	5.6	8
66	A first dataset toward a standardized community-driven global mapping of the human immunopeptidome. <i>Data in Brief</i> , 2016 , 7, 201-5	1.2	8
65	Targeted protein quantification using sparse reference labeling. <i>Nature Methods</i> , 2014 , 11, 301-4	21.6	8
64	Genotype-phenotype relationships in light of a modular protein interaction landscape. <i>Molecular BioSystems</i> , 2013 , 9, 1064-7		8
63	The structure and symmetry of the radial spoke protein complex in flagella. <i>Journal of Cell Science</i> , 2020 , 133,	5.3	8
62	Diagnostics and correction of batch effects in large-scale proteomic studies: a tutorial. <i>Molecular Systems Biology</i> , 2021 , 17, e10240	12.2	8
61	Application of SWATH Proteomics to Mouse Biology. <i>Current Protocols in Mouse Biology</i> , 2017 , 7, 130-143.1	13.1	7
60	Chemical Genetics of AGC-kinases Reveals Shared Targets of Ypk1, Protein Kinase A and Sch9. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 655-671	7.6	7
59	Systems pharmacology using mass spectrometry identifies critical response nodes in prostate cancer. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 26	5	7
58	The MLL1 trimeric catalytic complex is a dynamic conformational ensemble stabilized by multiple weak interactions. <i>Nucleic Acids Research</i> , 2019 , 47, 9433-9447	20.1	7
57	Progress Identifying and Analyzing the Human Proteome: 2021 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2021 , 20, 5227-5240	5.6	7
56	The Polyglutamine Expansion at the N-Terminal of Huntingtin Protein Modulates the Dynamic Configuration and Phosphorylation of the C-Terminal HEAT Domain. <i>Structure</i> , 2020 , 28, 1035-1050.e8	5.2	7

55	PCprophet: a framework for protein complex prediction and differential analysis using proteomic data. <i>Nature Methods</i> , 2021 , 18, 520-527	21.6	7
54	Convergent network effects along the axis of gene expression during prostate cancer progression. <i>Genome Biology</i> , 2020 , 21, 302	18.3	6
53	The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2021 ,	2.2	6
52	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. <i>Nature Communications</i> , 2021 , 12, 3810	17.4	6
51	Elucidating essential kinases of endothelin signalling by logic modelling of phosphoproteomics data. <i>Molecular Systems Biology</i> , 2019 , 15, e8828	12.2	6
50	Protein Classifier for Thyroid Nodules Learned from Rapidly Acquired Proteotypes		5
49	Puf6 primes 60S pre-ribosome nuclear export at low temperature. <i>Nature Communications</i> , 2021 , 12, 4696	17.4	5
48	Spatial proteomic and phospho-proteomic organization in three prototypical cell migration modes. <i>Proteome Science</i> , 2014 , 12, 23	2.6	4
47	Genomic, Proteomic and Phenotypic Heterogeneity in HeLa Cells across Laboratories: Implications for Reproducibility of Research Results		4
46	PGC1 β and Exercise Adaptations in Zebrafish		4
45	Structural and functional dissection of reovirus capsid folding and assembly by the prefoldin-TRiC/CCT chaperone network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	4
44	The SystemMHC Atlas: a Computational Pipeline, a Website, and a Data Repository for Immunopeptidomic Analyses. <i>Methods in Molecular Biology</i> , 2020 , 2120, 173-181	1.4	4
43	Deciphering MET-dependent modulation of global cellular responses to DNA damage by quantitative phosphoproteomics. <i>Molecular Oncology</i> , 2020 , 14, 1185-1206	7.9	3
42	A Proteomic Connectivity Map. <i>Cell Systems</i> , 2018 , 6, 403-405	10.6	3
41	The mouse metallomic landscape of aging and metabolism.. <i>Nature Communications</i> , 2022 , 13, 607	17.4	3
40	Multilayered regulation of autophagy by the Atg1 kinase orchestrates spatial and temporal control of autophagosome formation. <i>Molecular Cell</i> , 2021 ,	17.6	3
39	Multi-Omic Profiling of the Liver Across Diets and Age in a Diverse Mouse Population		3
38	Rapid proteotyping reveals cancer biology and drug response determinants in the NCI-60 cells		3

37	Integration of transcriptome, proteome and phosphoproteome data elucidates the genetic control of molecular networks		3
36	Mapping specificity, cleavage entropy, allosteric changes and substrates of blood proteases in a high-throughput screen. <i>Nature Communications</i> , 2021 , 12, 1693	17.4	3
35	Reduced CXCL4/PF4 expression as a driver of increased human hematopoietic stem and progenitor cell proliferation in polycythemia vera. <i>Blood Cancer Journal</i> , 2021 , 11, 31	7	3
34	MINA-1 and WAGO-4 are part of regulatory network coordinating germ cell death and RNAi in <i>C. elegans</i> . <i>Cell Death and Differentiation</i> , 2019 , 26, 2157-2178	12.7	2
33	Identification of the target of monoclonal antibody A6H as dipeptidyl peptidase IV/CD26 by LC MSMS. <i>Hybridoma</i> , 2001 , 20, 231-6		2
32	Molecular architecture of the human tRNA ligase complex. <i>ELife</i> , 2021 , 10,	8.9	2
31	Multimic profiling of the liver across diets and age in a diverse mouse population. <i>Cell Systems</i> , 2021 ,	10.6	2
30	Accelerated Protein Biomarker Discovery from FFPE tissue samples using Single-shot, Short Gradient Microflow SWATH MS		2
29	Orthogonal proteomic platforms and their implications for the stable classification of high-grade serous ovarian cancer subtypes		2
28	A PKD-MFF signaling axis couples mitochondrial fission to mitotic progression. <i>Cell Reports</i> , 2021 , 35, 109129	10.6	2
27	Differential Expression Proteomic Analysis Using Isotope Coded Affinity Tags		1
26	Comparative omics analyses differentiate <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium bovis</i> and reveal distinct macrophage responses to infection with the human and bovine tubercle bacilli		1
25	Identification of protein abundance changes in biopsy-level hepatocellular carcinoma tissues using PCT-SWATH		1
24	A global screen for assembly state changes of the mitotic proteome by SEC-SWATH-MS		1
23	DPHL: A pan-human protein mass spectrometry library for robust biomarker discovery		1
22	Single Nucleotide Resolution RNA-Protein Cross-Linking Mass Spectrometry: A Simple Extension of the CLIR-MS Workflow. <i>Analytical Chemistry</i> , 2021 , 93, 14626-14634	7.8	1
21	Convergent network effects along the axis of gene expression during prostate cancer progression		1
20	Systematic protein complex profiling and differential analysis from co-fractionation mass spectrometry data		1

19	SWATH-MS co-expression profiles reveal paralogue interference in protein complex evolution		1
18	Systematic detection of functional proteoform groups from bottom-up proteomic datasets		1
17	High-throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification		1
16	System-Wide Profiling of Protein Complexes Via Size Exclusion Chromatography-Mass Spectrometry (SEC-MS). <i>Methods in Molecular Biology</i> , 2021 , 2259, 269-294	1.4	1
15	Expression Dysregulation as a Mediator of Fitness Costs in Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0050421	5.9	1
14	All Driven by Energy Demand? Integrative Comparison of Metabolism of <i>Enterococcus faecalis</i> Wildtype and a Glutamine Synthase Mutant.. <i>Microbiology Spectrum</i> , 2022 , e0240021	8.9	1
13	Nucleotide-amino acid π -stacking interactions initiate photo cross-linking in RNA-protein complexes.. <i>Nature Communications</i> , 2022 , 13, 2719	17.4	1
12	On the feasibility of deep learning applications using raw mass spectrometry data. <i>Bioinformatics</i> , 2021 , 37, i245-i253	7.2	0
11	The impact of genomic variation on protein phosphorylation states and regulatory networks.. <i>Molecular Systems Biology</i> , 2022 , 18, e10712	12.2	0
10	Mass Spectrometric Exploration of the Biochemical Basis of Living Systems. <i>Chimia</i> , 2019 , 73, 540-548	1.3	
9	P-003: Detection of bacterial and host proteins from a single colonic biopsy sample by a new mass spectrometry-based assay in pediatric ulcerative colitis. <i>Journal of Crohn's and Colitis</i> , 2014 , 8, S395	1.5	
8	Gene Expression: Basic Concepts 2008 , 1		
7	Basic Concepts of Gene Expression1-95		
6	QUANTITATIVE PROTEOMICS AND SYSTEMS BIOLOGY. <i>FASEB Journal</i> , 2007 , 21, A212	0.9	
5	Applications of Stable Isotope Tagging Based Quantitative Proteomics in Cancer Research121-143		
4	Mycobacterium tuberculosis in the Proteomics Era239-260		
3	Mapping and measuring molecular networks in cells. <i>FASEB Journal</i> , 2010 , 24, 66.1	0.9	
2	AN INTEGRATED EXPERIMENTAL WORKFLOW TO INCREASE THROUGHPUT AND DATA ROBUSTNESS FOR ANALYSIS OF MAMMALIAN PROTEIN INTERACTION NETWORKS. <i>FASEB Journal</i> , 2010 , 24, 1b165	0.9	

- 1 Horizontal Integration: OMICS Mass Spectrometry-Based Proteomics in Systems Biology Research
2022,