

Ruedi Aebersold

List of Publications by Year in Descending Order

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

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	The mouse metallomic landscape of aging and metabolism.. <i>Nature Communications</i> , 2022 , 13, 607	17.4	3
305	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
304	Nucleotide-amino acid π -stacking interactions initiate photo cross-linking in RNA-protein complexes.. <i>Nature Communications</i> , 2022 , 13, 2719	17.4	1
303	The impact of genomic variation on protein phosphorylation states and regulatory networks.. <i>Molecular Systems Biology</i> , 2022 , 18, e10712	12.2	0
302	Horizontal Integration: OMICS π Mass Spectrometry-Based Proteomics in Systems Biology Research 2022 ,		
301	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
300	Multilayered regulation of autophagy by the Atg1 kinase orchestrates spatial and temporal control of autophagosome formation. <i>Molecular Cell</i> , 2021 ,	17.6	3
299	Molecular architecture of the human tRNA ligase complex. <i>ELife</i> , 2021 , 10,	8.9	2
298	Progress Identifying and Analyzing the Human Proteome: 2021 π Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2021 , 20, 5227-5240	5.6	7
297	Multiomc profiling of the liver across diets and age in a diverse mouse population. <i>Cell Systems</i> , 2021 ,	10.6	2
296	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
295	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
294	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
293	PCprophet: a framework for protein complex prediction and differential analysis using proteomic data. <i>Nature Methods</i> , 2021 , 18, 520-527	21.6	7
292	A PKD-MFF signaling axis couples mitochondrial fission to mitotic progression. <i>Cell Reports</i> , 2021 , 35, 109129	10.6	2
291	From coarse to fine: the absolute <i>Escherichia coli</i> proteome under diverse growth conditions. <i>Molecular Systems Biology</i> , 2021 , 17, e9536	12.2	9
290	The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2021 ,	2.2	6

289	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. <i>Nature Communications</i> , 2021 , 12, 3810	17.4	6
288	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
287	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
286	JARID2 and AEBP2 regulate PRC2 in the presence of H2AK119ub1 and other histone modifications. <i>Science</i> , 2021 , 371,	33.3	41
285	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
284	On the feasibility of deep learning applications using raw mass spectrometry data. <i>Bioinformatics</i> , 2021 , 37, i245-i253	7.2	0
283	Puf6 primes 60S pre-ribosome nuclear export at low temperature. <i>Nature Communications</i> , 2021 , 12, 4696	17.4	5
282	Expression Dysregulation as a Mediator of Fitness Costs in Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0050421	5.9	1
281	Diagnostics and correction of batch effects in large-scale proteomic studies: a tutorial. <i>Molecular Systems Biology</i> , 2021 , 17, e10240	12.2	8
280	Convergent network effects along the axis of gene expression during prostate cancer progression. <i>Genome Biology</i> , 2020 , 21, 302	18.3	6
279	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
278	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
277	ChromID identifies the protein interactome at chromatin marks. <i>Nature Biotechnology</i> , 2020 , 38, 728-736	44.5	31
276	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
275	A Conserved Mito-Cytosolic Translational Balance Links Two Longevity Pathways. <i>Cell Metabolism</i> , 2020 , 31, 549-563.e7	24.6	36
274	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
273	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
272	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

271	The GTPase Nog1 co-ordinates the assembly, maturation and quality control of distant ribosomal functional centers. <i>ELife</i> , 2020 , 9,	8.9	18
270	Review of Batch Effects Prevention, Diagnostics, and Correction Approaches. <i>Methods in Molecular Biology</i> , 2020 , 2051, 373-387	1.4	12
269	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
268	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
267	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020 , 11, 5301	17.4	59
266	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
265	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
264	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
263	diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020 , 17, 1229-1236	21.6	85
262	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
261	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
260	The structure and symmetry of the radial spoke protein complex in flagella. <i>Journal of Cell Science</i> , 2020 , 133,	5.3	8
259	Kinase Interaction Network Expands Functional and Disease Roles of Human Kinases. <i>Molecular Cell</i> , 2020 , 79, 504-520.e9	17.6	22
258	Strategies to enable large-scale proteomics for reproducible research. <i>Nature Communications</i> , 2020 , 11, 3793	17.4	26
257	Mitochondrial translation and dynamics synergistically extend lifespan in <i>C. elegans</i> through HLH-30. <i>Journal of Cell Biology</i> , 2020 , 219,	7.3	16
256	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
255	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
254	CryoEM structures of Arabidopsis DDR complexes involved in RNA-directed DNA methylation. <i>Nature Communications</i> , 2019 , 10, 3916	17.4	12

253	Mass Spectrometric Exploration of the Biochemical Basis of Living Systems. <i>Chimia</i> , 2019 , 73, 540-548	1.3	
252	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
251	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
250	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
249	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. <i>Cell</i> , 2019 , 177, 1308-1318.e10	9.1	10
248	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019 , 91, 6953-6961	7.8	57
247	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
246	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
245	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
244	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
243	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
242	Breast Cancer Classification Based on Proteotypes Obtained by SWATH Mass Spectrometry. <i>Cell Reports</i> , 2019 , 28, 832-843.e7	10.6	40
241	High-throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification. <i>Molecular Oncology</i> , 2019 , 13, 2305-2328	7.9	43
240	Generation of a zebrafish SWATH-MS spectral library to quantify 10,000 proteins. <i>Scientific Data</i> , 2019 , 6, 190011	8.2	23
239	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. <i>Nature Biotechnology</i> , 2019 , 37, 314-322	44.5	129
238	The interactome of KRAB zinc finger proteins reveals the evolutionary history of their functional diversification. <i>EMBO Journal</i> , 2019 , 38, e101220	13	33
237	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>iScience</i> , 2019 , 21, 664-680	6.1	21
236	Arabidopsis proteome and the mass spectral assay library. <i>Scientific Data</i> , 2019 , 6, 278	8.2	24

235	Proteomic identification of a marker signature for MAPKi resistance in melanoma. <i>EMBO Journal</i> , 2019 , 38, e95874	13	11
234	Elucidating essential kinases of endothelin signalling by logic modelling of phosphoproteomics data. <i>Molecular Systems Biology</i> , 2019 , 15, e8828	12.2	6
233	Complex-centric proteome profiling by SEC-SWATH-MS. <i>Molecular Systems Biology</i> , 2019 , 15, e8438	12.2	61
232	Identification of Protein Abundance Changes in Hepatocellular Carcinoma Tissues Using PCT-SWATH. <i>Proteomics - Clinical Applications</i> , 2019 , 13, e1700179	3.1	19
231	Advancing translational research and precision medicine with targeted proteomics. <i>Journal of Proteomics</i> , 2018 , 189, 1-10	3.9	44
230	Structure of a human cap-dependent 48S translation pre-initiation complex. <i>Nucleic Acids Research</i> , 2018 , 46, 2678-2689	20.1	47
229	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
228	Structures of human PRC2 with its cofactors AEBP2 and JARID2. <i>Science</i> , 2018 , 359, 940-944	33.3	109
227	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
226	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
225	A Proteomic Connectivity Map. <i>Cell Systems</i> , 2018 , 6, 403-405	10.6	3
224	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
223	The SystemMHC Atlas project. <i>Nucleic Acids Research</i> , 2018 , 46, D1237-D1247	20.1	87
222	Systematic characterization of pan-cancer mutation clusters. <i>Molecular Systems Biology</i> , 2018 , 14, e7974	12.2	25
221	Systems pharmacology using mass spectrometry identifies critical response nodes in prostate cancer. <i>Npj Systems Biology and Applications</i> , 2018 , 4, 26	5	7
220	Data-independent acquisition-based SWATH-MS for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , 2018 , 14, e8126	12.2	389
219	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
218	A tissue-based draft map of the murine MHC class I immunopeptidome. <i>Scientific Data</i> , 2018 , 5, 180157	8.2	23

217	Comparative Proteomics 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
216	Proteomics goes parallel. <i>Nature Biotechnology</i> , 2018 , 36, 1051-1053	44.5	9
215	Separation of blood microsamples by exploiting sedimentation at the microscale. <i>Scientific Reports</i> , 2018 , 8, 14101	4.9	13
214	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
213	Molecular basis for disassembly of an importin:ribosomal protein complex by the escortin Tsr2. <i>Nature Communications</i> , 2018 , 9, 3669	17.4	11
212	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. <i>Life Science Alliance</i> , 2018 , 1,	5.8	38
211	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
210	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
209	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
208	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
207	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
206	Automated SWATH Data Analysis Using Targeted Extraction of Ion Chromatograms. <i>Methods in Molecular Biology</i> , 2017 , 1550, 289-307	1.4	23
205	Updated Reference Genome Sequence and Annotation of AF2122/97. <i>Genome Announcements</i> , 2017 , 5,		31
204	Application of SWATH Proteomics to Mouse Biology. <i>Current Protocols in Mouse Biology</i> , 2017 , 7, 130-143.1		7
203	A Class of Environmental and Endogenous Toxins Induces BRCA2 Haploinsufficiency and Genome Instability. <i>Cell</i> , 2017 , 169, 1105-1118.e15	56.2	93
202	Quantitative proteomics: challenges and opportunities in basic and applied research. <i>Nature Protocols</i> , 2017 , 12, 1289-1294	18.8	133
201	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017 , 35, 781-788	44.5	85
200	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

199	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. <i>Cell Reports</i> , 2017 , 18, 3219-3226	10.6	23
198	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
197	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
196	Systematic Analysis of Human Protein Phosphatase Interactions and Dynamics. <i>Cell Systems</i> , 2017 , 4, 430-444.e5	10.6	44
195	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
194	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. <i>Nature Communications</i> , 2017 , 8, 1212	17.4	59
193	Systems proteomics approaches to study bacterial pathogens: application to Mycobacterium tuberculosis. <i>Current Opinion in Microbiology</i> , 2017 , 39, 64-72	7.9	21
192	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
191	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017 , 8, 291	17.4	252
190	Delayed effects of transcriptional responses in Mycobacterium tuberculosis exposed to nitric oxide suggest other mechanisms involved in survival. <i>Scientific Reports</i> , 2017 , 7, 8208	4.9	27
189	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
188	Impact of Alternative Splicing on the Human Proteome. <i>Cell Reports</i> , 2017 , 20, 1229-1241	10.6	74
187	A Case for a Human Immuno-Peptidome Project Consortium. <i>Immunity</i> , 2017 , 47, 203-208	32.3	46
186	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
185	Molecular basis of AKAP79 regulation by calmodulin. <i>Nature Communications</i> , 2017 , 8, 1681	17.4	17
184	Structural insights into the assembly and polyA signal recognition mechanism of the human CPSF complex. <i>ELife</i> , 2017 , 6,	8.9	52
183	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
182	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016 , 13, 741-8	21.6	337

181	Mass-spectrometric exploration of proteome structure and function. <i>Nature</i> , 2016 , 537, 347-55	50.4	1070
180	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016 , 166, 766-778	56.2	236
179	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
178	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
177	Systems proteomics of liver mitochondria function. <i>Science</i> , 2016 , 352, aad0189	33.3	193
176	The quantitative and condition-dependent <i>Escherichia coli</i> proteome. <i>Nature Biotechnology</i> , 2016 , 34, 104-10	44.5	422
175	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
174	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
173	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
172	Insertion of the Biogenesis Factor Rei1 Probes the Ribosomal Tunnel during 60S Maturation. <i>Cell</i> , 2016 , 164, 91-102	56.2	75
171	Huntingtin β spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. <i>ELife</i> , 2016 , 5, e11184	8.9	32
170	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
169	Attenuation of pattern recognition receptor signaling is mediated by a MAP kinase kinase kinase. <i>EMBO Reports</i> , 2016 , 17, 441-54	6.5	39
168	Epigenetic stress responses induce muscle stem-cell ageing by Hoxa9 developmental signals. <i>Nature</i> , 2016 , 540, 428-432	50.4	79
167	The interdependence of transcript and protein abundance: new data--new complexities. <i>Molecular Systems Biology</i> , 2016 , 12, 856	12.2	15
166	Molecular Architecture of Yeast Chromatin Assembly Factor 1. <i>Scientific Reports</i> , 2016 , 6, 26702	4.9	19
165	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
164	TRIM24 Is an Oncogenic Transcriptional Activator in Prostate Cancer. <i>Cancer Cell</i> , 2016 , 29, 846-858	24.3	160

163	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
162	NAD ⁺ repletion improves mitochondrial and stem cell function and enhances life span in mice. <i>Science</i> , 2016 , 352, 1436-43	33.3	645
161	On the Dependency of Cellular Protein Levels on mRNA Abundance. <i>Cell</i> , 2016 , 165, 535-50	56.2	1235
160	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
159	A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , 2016 , 34, 1130-1136	44.5	202
158	A High-Density Map for Navigating the Human Polycomb Complexome. <i>Cell Reports</i> , 2016 , 17, 583-595	10.6	147
157	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , 2016 , 13, 777-83	21.6	122
156	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
155	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016 , 15, 3961-3970	5.6	130
154	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015 , 10, 426-41	18.8	229
153	Reproducible and consistent quantification of the <i>Saccharomyces cerevisiae</i> proteome by SWATH-mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 739-49	7.6	136
152	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
151	Inferring causal metabolic signals that regulate the dynamic TORC1-dependent transcriptome. <i>Molecular Systems Biology</i> , 2015 , 11, 802	12.2	26
150	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of <i>Mycobacterium tuberculosis</i> . <i>Cell Host and Microbe</i> , 2015 , 18, 96-108	23.4	155
149	Cooperative target mRNA destabilization and translation inhibition by miR-58 microRNA family in <i>C. elegans</i> . <i>Genome Research</i> , 2015 , 25, 1680-91	9.7	15
148	Crucial HSP70 co-chaperone complex unlocks metazoan protein disaggregation. <i>Nature</i> , 2015 , 524, 247-51	50.4	224
147	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
146	Identification of Cdk targets that control cytokinesis. <i>EMBO Journal</i> , 2015 , 34, 81-96	13	43

145	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
144	Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. <i>Science Signaling</i> , 2015 , 8, rs4	8.8	56
143	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. <i>Bioinformatics</i> , 2015 , 31, 2415-7	7.2	11
142	Ribosome. The complete structure of the 55S mammalian mitochondrial ribosome. <i>Science</i> , 2015 , 348, 303-8	33.3	275
141	Quantitative variability of 342 plasma proteins in a human twin population. <i>Molecular Systems Biology</i> , 2015 , 11, 786	12.2	222
140	Confident site localization using a simulated phosphopeptide spectral library. <i>Journal of Proteome Research</i> , 2015 , 14, 2348-59	5.6	22
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