

Ruedi Aebersold

List of Publications by Year in descending order

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Version: 2024-02-01

293
papers

63,878
citations

1463

107
h-index

962

238
g-index

338
all docs

338
docs citations

338
times ranked

63522
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Mass spectrometry-based proteomics. <i>Nature</i> , 2003, 422, 198-207. | 27.8 | 6,282 |
| 2 | Empirical Statistical Model To Estimate the Accuracy of Peptide Identifications Made by MS/MS and Database Search. <i>Analytical Chemistry</i> , 2002, 74, 5383-5392. | 6.5 | 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. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.016717. | 3.8 | 2,285 |
| 4 | On the Dependency of Cellular Protein Levels on mRNA Abundance. <i>Cell</i> , 2016, 165, 535-550. | 28.9 | 2,216 |
| 5 | Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network. <i>Science</i> , 2001, 292, 929-934. | 12.6 | 1,921 |
| 6 | Checkpoint blockade cancer immunotherapy targets tumour-specific mutant antigens. <i>Nature</i> , 2014, 515, 577-581. | 27.8 | 1,705 |
| 7 | Mass-spectrometric exploration of proteome structure and function. <i>Nature</i> , 2016, 537, 347-355. | 27.8 | 1,573 |
| 8 | The CRAPome: a contaminant repository for affinity purification-based mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736. | 19.0 | 1,353 |
| 9 | Selected reaction monitoring for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , 2008, 4, 222. | 7.2 | 1,215 |
| 10 | Selected reaction monitoring-based proteomics: workflows, potential, pitfalls and future directions. <i>Nature Methods</i> , 2012, 9, 555-566. | 19.0 | 1,177 |
| 11 | Quantitative profiling of differentiation-induced microsomal proteins using isotope-coded affinity tags and mass spectrometry. <i>Nature Biotechnology</i> , 2001, 19, 946-951. | 17.5 | 913 |
| 12 | NAD ⁺ repletion improves mitochondrial and stem cell function and enhances life span in mice. <i>Science</i> , 2016, 352, 1436-1443. | 12.6 | 907 |
| 13 | Interpretation of Shotgun Proteomic Data. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1419-1440. | 3.8 | 904 |
| 14 | The PeptideAtlas project. <i>Nucleic Acids Research</i> , 2006, 34, D655-D658. | 14.5 | 733 |
| 15 | A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004, 22, 1459-1466. | 17.5 | 724 |
| 16 | A guided tour of the Trans-Proteomic Pipeline. <i>Proteomics</i> , 2010, 10, 1150-1159. | 2.2 | 710 |
| 17 | Data-independent acquisition-based SWATH-MS for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , 2018, 14, e8126. | 7.2 | 701 |
| 18 | The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893. | 17.5 | 694 |

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|----|--|------|-----------|
| 19 | OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , 2014, 32, 219-223. | 17.5 | 692 |
| 20 | The quantitative proteome of a human cell line. <i>Molecular Systems Biology</i> , 2011, 7, 549. | 7.2 | 691 |
| 21 | The quantitative and condition-dependent <i>Escherichia coli</i> proteome. <i>Nature Biotechnology</i> , 2016, 34, 104-110. | 17.5 | 655 |
| 22 | Options and considerations when selecting a quantitative proteomics strategy. <i>Nature Biotechnology</i> , 2010, 28, 710-721. | 17.5 | 581 |
| 23 | How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214. | 8.0 | 580 |
| 24 | Reproducible isolation of distinct, overlapping segments of the phosphoproteome. <i>Nature Methods</i> , 2007, 4, 231-237. | 19.0 | 555 |
| 25 | OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748. | 19.0 | 537 |
| 26 | Quantitative Analysis of Fission Yeast Transcriptomes and Proteomes in Proliferating and Quiescent Cells. <i>Cell</i> , 2012, 151, 671-683. | 28.9 | 513 |
| 27 | 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. | 3.8 | 490 |
| 28 | Development and validation of a spectral library searching method for peptide identification from MS/MS. <i>Proteomics</i> , 2007, 7, 655-667. | 2.2 | 487 |
| 29 | mProphet: automated data processing and statistical validation for large-scale SRM experiments. <i>Nature Methods</i> , 2011, 8, 430-435. | 19.0 | 481 |
| 30 | Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291. | 12.8 | 423 |
| 31 | 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, 1380-1387. | 7.1 | 422 |
| 32 | Probing Native Protein Structures by Chemical Cross-linking, Mass Spectrometry, and Bioinformatics. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1634-1649. | 3.8 | 407 |
| 33 | Proteome-wide cellular protein concentrations of the human pathogen <i>Leptospira interrogans</i> . <i>Nature</i> , 2009, 460, 762-765. | 27.8 | 402 |
| 34 | diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236. | 19.0 | 387 |
| 35 | Identification of cross-linked peptides from large sequence databases. <i>Nature Methods</i> , 2008, 5, 315-318. | 19.0 | 379 |
| 36 | A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031. | 5.3 | 370 |

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|----|--|------|-----------|
| 37 | Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. <i>Nature Medicine</i> , 2015, 21, 407-413. | 30.7 | 358 |
| 38 | Structural Probing of a Protein Phosphatase 2A Network by Chemical Cross-Linking and Mass Spectrometry. <i>Science</i> , 2012, 337, 1348-1352. | 12.6 | 357 |
| 39 | A Mass Spectrometric-Derived Cell Surface Protein Atlas. <i>PLoS ONE</i> , 2015, 10, e0121314. | 2.5 | 356 |
| 40 | The study of macromolecular complexes by quantitative proteomics. <i>Nature Genetics</i> , 2003, 33, 349-355. | 21.4 | 350 |
| 41 | The complete structure of the 55 <i>S</i> mammalian mitochondrial ribosome. <i>Science</i> , 2015, 348, 303-308. | 12.6 | 344 |
| 42 | 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. | 7.5 | 330 |
| 43 | A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , 2016, 34, 1130-1136. | 17.5 | 321 |
| 44 | Crucial HSP70 co-chaperone complex unlocks metazoan protein disaggregation. <i>Nature</i> , 2015, 524, 247-251. | 27.8 | 320 |
| 45 | Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015, 10, 426-441. | 12.0 | 319 |
| 46 | A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 2013, 494, 266-270. | 27.8 | 307 |
| 47 | Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. <i>Nature Methods</i> , 2013, 10, 1246-1253. | 19.0 | 302 |
| 48 | Quantitative variability of 342 plasma proteins in a human twin population. <i>Molecular Systems Biology</i> , 2015, 11, 786. | 7.2 | 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. <i>Journal of Proteome Research</i> , 2012, 11, 5145-5156. | 3.7 | 298 |
| 50 | Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016, 166, 766-778. | 28.9 | 295 |
| 51 | The Human Proteome Project: Current State and Future Direction. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009993. | 3.8 | 294 |
| 52 | Genome-wide Mapping of Transcriptional Start Sites Defines an Extensive Leaderless Transcriptome in <i>Mycobacterium tuberculosis</i> . <i>Cell Reports</i> , 2013, 5, 1121-1131. | 6.4 | 283 |
| 53 | Protein Identification False Discovery Rates for Very Large Proteomics Data Sets Generated by Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2405-2417. | 3.8 | 282 |
| 54 | Architecture and conformational switch mechanism of the ryanodine receptor. <i>Nature</i> , 2015, 517, 39-43. | 27.8 | 282 |

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|----|---|------|-----------|
| 55 | The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , 2012, 30, 221-223. | 17.5 | 281 |
| 56 | Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1214-1221. | 1.5 | 277 |
| 57 | Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. <i>Science Signaling</i> , 2010, 3, rs4. | 3.6 | 277 |
| 58 | Mapping differential interactomes by affinity purification coupled with data-independent mass spectrometry acquisition. <i>Nature Methods</i> , 2013, 10, 1239-1245. | 19.0 | 277 |
| 59 | Early Steps in Autophagy Depend on Direct Phosphorylation of Atg9 by the Atg1 Kinase. <i>Molecular Cell</i> , 2014, 53, 471-483. | 9.7 | 274 |
| 60 | False discovery rate estimation for cross-linked peptides identified by mass spectrometry. <i>Nature Methods</i> , 2012, 9, 901-903. | 19.0 | 273 |
| 61 | Quantification of mRNA and protein and integration with protein turnover in a bacterium. <i>Molecular Systems Biology</i> , 2011, 7, 511. | 7.2 | 267 |
| 62 | Mass Spectrometry Applied to Bottom-Up Proteomics: Entering the High-Throughput Era for Hypothesis Testing. <i>Annual Review of Analytical Chemistry</i> , 2016, 9, 449-472. | 5.4 | 266 |
| 63 | 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. | 3.8 | 264 |
| 64 | The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. <i>Structure</i> , 2012, 20, 814-825. | 3.3 | 261 |
| 65 | Systems proteomics of liver mitochondria function. <i>Science</i> , 2016, 352, aad0189. | 12.6 | 257 |
| 66 | Building consensus spectral libraries for peptide identification in proteomics. <i>Nature Methods</i> , 2008, 5, 873-875. | 19.0 | 255 |
| 67 | Multi-omic measurements of heterogeneity in HeLa cells across laboratories. <i>Nature Biotechnology</i> , 2019, 37, 314-322. | 17.5 | 254 |
| 68 | An integrated workflow for charting the human interaction proteome: insights into the PP2A system. <i>Molecular Systems Biology</i> , 2009, 5, 237. | 7.2 | 253 |
| 69 | ATM-Dependent and -Independent Dynamics of the Nuclear Phosphoproteome After DNA Damage. <i>Science Signaling</i> , 2010, 3, rs3. | 3.6 | 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. <i>Nature Protocols</i> , 2014, 9, 120-137. | 12.0 | 244 |
| 71 | A High-Density Map for Navigating the Human Polycomb Complexome. <i>Cell Reports</i> , 2016, 17, 583-595. | 6.4 | 234 |
| 72 | The complete structure of the large subunit of the mammalian mitochondrial ribosome. <i>Nature</i> , 2014, 515, 283-286. | 27.8 | 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. | 11.0 | 229 |
| 74 | TRIM24 Is an Oncogenic Transcriptional Activator in Prostate Cancer. Cancer Cell, 2016, 29, 846-858. | 16.8 | 228 |
| 75 | Multilayered Genetic and Omics Dissection of Mitochondrial Activity in a Mouse Reference Population. Cell, 2014, 158, 1415-1430. | 28.9 | 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. | 7.1 | 213 |
| 77 | Architecture of the large subunit of the mammalian mitochondrial ribosome. Nature, 2014, 505, 515-519. | 27.8 | 207 |
| 78 | Quantitative proteomics: challenges and opportunities in basic and applied research. Nature Protocols, 2017, 12, 1289-1294. | 12.0 | 200 |
| 79 | Molecular Architecture of the 40Sâ€¦eIF1â€¦eIF3 Translation Initiation Complex. Cell, 2014, 158, 1123-1135. | 28.9 | 193 |
| 80 | Quantitative measurements of <i>N</i> -linked glycoproteins in human plasma by SWATH-MS. Proteomics, 2013, 13, 1247-1256. | 2.2 | 190 |
| 81 | Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. Nature Methods, 2017, 14, 921-927. | 19.0 | 189 |
| 82 | Analysis of Major Histocompatibility Complex (MHC) Immunopeptidomes Using Mass Spectrometry*. Molecular and Cellular Proteomics, 2015, 14, 3105-3117. | 3.8 | 188 |
| 83 | Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry-Based Assays. Clinical Chemistry, 2016, 62, 48-69. | 3.2 | 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. | 3.7 | 185 |
| 85 | Generating and navigating proteome maps using mass spectrometry. Nature Reviews Molecular Cell Biology, 2010, 11, 789-801. | 37.0 | 181 |
| 86 | The Protein Interaction Landscape of the Human CMGC Kinase Group. Cell Reports, 2013, 3, 1306-1320. | 6.4 | 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. | 7.1 | 175 |
| 88 | TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. Nature Methods, 2016, 13, 777-783. | 19.0 | 173 |
| 89 | Structures of human PRC2 with its cofactors AEBP2 and JARID2. Science, 2018, 359, 940-944. | 12.6 | 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. | 11.0 | 165 |

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|-----|--|------|-----------|
| 91 | Glycoproteomic Analysis of Prostate Cancer Tissues by SWATH Mass Spectrometry Discovers N-acyl ethanolamine Acid Amidase and Protein Tyrosine Kinase 7 as Signatures for Tumor Aggressiveness. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1753-1768. | 3.8 | 165 |
| 92 | 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. | 7.1 | 159 |
| 93 | Reproducible and Consistent Quantification of the <i>Saccharomyces cerevisiae</i> Proteome by SWATH-mass spectrometry *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 739-749. | 3.8 | 158 |
| 94 | Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016, 15, 3961-3970. | 3.7 | 158 |
| 95 | Proteomic and interactomic insights into the molecular basis of cell functional diversity. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 327-340. | 37.0 | 156 |
| 96 | A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301. | 12.8 | 152 |
| 97 | A Class of Environmental and Endogenous Toxins Induces BRCA2 Haploinsufficiency and Genome Instability. <i>Cell</i> , 2017, 169, 1105-1118.e15. | 28.9 | 149 |
| 98 | RNF168 Promotes Noncanonical K27 ^{ub} Ubiquitination to Signal DNA Damage. <i>Cell Reports</i> , 2015, 10, 226-238. | 6.4 | 147 |
| 99 | An Automated Pipeline for High-Throughput Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 1628-1644. | 3.7 | 146 |
| 100 | Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2301-2307. | 3.8 | 146 |
| 101 | Impact of Alternative Splicing on the Human Proteome. <i>Cell Reports</i> , 2017, 20, 1229-1241. | 6.4 | 145 |
| 102 | Proteomics meets the scientific method. <i>Nature Methods</i> , 2013, 10, 24-27. | 19.0 | 139 |
| 103 | JARID2 and AEBP2 regulate PRC2 in the presence of H2AK119ub1 and other histone modifications. <i>Science</i> , 2021, 371, . | 12.6 | 137 |
| 104 | Standard Guidelines for the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2012, 11, 2005-2013. | 3.7 | 135 |
| 105 | The Structural Basis of Substrate Recognition by the Eukaryotic Chaperonin TRiC/CCT. <i>Cell</i> , 2014, 159, 1042-1055. | 28.9 | 131 |
| 106 | Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017, 35, 781-788. | 17.5 | 122 |
| 107 | Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. <i>Molecular Cell</i> , 2015, 58, 977-988. | 9.7 | 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. <i>Nature Immunology</i> , 2014, 15, 384-392. | 14.5 | 119 |

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|-----|---|------|-----------|
| 109 | The SysteMHC Atlas project. <i>Nucleic Acids Research</i> , 2018, 46, D1237-D1247. | 14.5 | 119 |
| 110 | Estimation of Absolute Protein Quantities of Unlabeled Samples by Selected Reaction Monitoring Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013987. | 3.8 | 117 |
| 111 | Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. <i>Nature Communications</i> , 2017, 8, 1212. | 12.8 | 112 |
| 112 | Statistical protein quantification and significance analysis in label-free LC-MS experiments with complex designs. <i>BMC Bioinformatics</i> , 2012, 13, S6. | 2.6 | 110 |
| 113 | Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015, 12, 725-731. | 19.0 | 109 |
| 114 | Complex-centric proteome profiling by <i>SEC</i> <i>SWATH</i> <i>MS</i> . <i>Molecular Systems Biology</i> , 2019, 15, e8438. | 7.2 | 109 |
| 115 | Epigenetic stress responses induce muscle stem-cell ageing by Hoxa9 developmental signals. <i>Nature</i> , 2016, 540, 428-432. | 27.8 | 108 |
| 116 | An open-source computational and data resource to analyze digital maps of immunopeptidomes. <i>ELife</i> , 2015, 4, . | 6.0 | 107 |
| 117 | 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. | 6.4 | 106 |
| 118 | A mass spectrometric journey into protein and proteome research. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 685-695. | 2.8 | 105 |
| 119 | The Calcineurin Signaling Network Evolves via Conserved Kinase-Phosphatase Modules that Transcend Substrate Identity. <i>Molecular Cell</i> , 2014, 55, 422-435. | 9.7 | 102 |
| 120 | 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, 23-27. | 3.7 | 100 |
| 121 | High-throughput proteomic analysis of <i>FFPE</i> tissue samples facilitates tumor stratification. <i>Molecular Oncology</i> , 2019, 13, 2305-2328. | 4.6 | 100 |
| 122 | First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961. | 6.5 | 100 |
| 123 | The Chaperonin TRiC/CCT Associates with Prefoldin through a Conserved Electrostatic Interface Essential for Cellular Proteostasis. <i>Cell</i> , 2019, 177, 751-765.e15. | 28.9 | 98 |
| 124 | Insertion of the Biogenesis Factor Rei1 Probes the Ribosomal Tunnel during 60S Maturation. <i>Cell</i> , 2016, 164, 91-102. | 28.9 | 97 |
| 125 | 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, 2056-2071. | 3.8 | 96 |
| 126 | Structural basis of AAUAAA polyadenylation signal recognition by the human CPSF complex. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 135-138. | 8.2 | 96 |

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|-----|---|------|-----------|
| 127 | ChromID identifies the protein interactome at chromatin marks. <i>Nature Biotechnology</i> , 2020, 38, 728-736. | 17.5 | 90 |
| 128 | A Conserved Mito-Cytosolic Translational Balance Links Two Longevity Pathways. <i>Cell Metabolism</i> , 2020, 31, 549-563.e7. | 16.2 | 87 |
| 129 | A Case for a Human Immuno-Peptidome Project Consortium. <i>Immunity</i> , 2017, 47, 203-208. | 14.3 | 84 |
| 130 | From coarse to fine: the absolute <i>Escherichia coli</i> proteome under diverse growth conditions. <i>Molecular Systems Biology</i> , 2021, 17, e9536. | 7.2 | 82 |
| 131 | Prediction of colorectal cancer diagnosis based on circulating plasma proteins. <i>EMBO Molecular Medicine</i> , 2015, 7, 1166-1178. | 6.9 | 80 |
| 132 | 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, 2800-2813. | 3.8 | 76 |
| 133 | Structure of a human cap-dependent 48S translation pre-initiation complex. <i>Nucleic Acids Research</i> , 2018, 46, 2678-2689. | 14.5 | 76 |
| 134 | Strategies to enable large-scale proteomics for reproducible research. <i>Nature Communications</i> , 2020, 11, 3793. | 12.8 | 75 |
| 135 | Kinase Interaction Network Expands Functional and Disease Roles of Human Kinases. <i>Molecular Cell</i> , 2020, 79, 504-520.e9. | 9.7 | 74 |
| 136 | Target of Rapamycin Complex 2 Regulates Actin Polarization and Endocytosis via Multiple Pathways. <i>Journal of Biological Chemistry</i> , 2015, 290, 14963-14978. | 3.4 | 72 |
| 137 | Advancing translational research and precision medicine with targeted proteomics. <i>Journal of Proteomics</i> , 2018, 189, 1-10. | 2.4 | 72 |
| 138 | Breast Cancer Classification Based on Proteotypes Obtained by SWATH Mass Spectrometry. <i>Cell Reports</i> , 2019, 28, 832-843.e7. | 6.4 | 72 |
| 139 | Structural insights into the assembly and polyA signal recognition mechanism of the human CPSF complex. <i>ELife</i> , 2017, 6, . | 6.0 | 71 |
| 140 | Epigenetics and Proteomics Join Transcriptomics in the Quest for Tuberculosis Biomarkers. <i>MBio</i> , 2015, 6, e01187-15. | 4.1 | 70 |
| 141 | The interactome of <i>KRAB</i> zinc finger proteins reveals the evolutionary history of their functional diversification. <i>EMBO Journal</i> , 2019, 38, e101220. | 7.8 | 67 |
| 142 | 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. | 4.7 | 65 |
| 143 | Systematic Analysis of Human Protein Phosphatase Interactions and Dynamics. <i>Cell Systems</i> , 2017, 4, 430-444.e5. | 6.2 | 65 |
| 144 | Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. <i>Science Signaling</i> , 2015, 8, rs4. | 3.6 | 64 |

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|-----|---|------|-----------|
| 145 | Proteome-wide selected reaction monitoring assays for the human pathogen <i>Streptococcus pyogenes</i> . <i>Nature Communications</i> , 2012, 3, 1301. | 12.8 | 63 |
| 146 | aLFQ: an R-package for estimating absolute protein quantities from label-free LC-MS/MS proteomics data. <i>Bioinformatics</i> , 2014, 30, 2511-2513. | 4.1 | 63 |
| 147 | Mass spectrometry-driven phosphoproteomics: patterning the systems biology mosaic. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2014, 3, 83-112. | 5.9 | 63 |
| 148 | Phosphoproteomic analyses reveal novel cross-modulation mechanisms between two signaling pathways in yeast. <i>Molecular Systems Biology</i> , 2014, 10, 767. | 7.2 | 58 |
| 149 | Diagnostics and correction of batch effects in large-scale proteomic studies: a tutorial. <i>Molecular Systems Biology</i> , 2021, 17, e10240. | 7.2 | 57 |
| 150 | A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. <i>Cell Systems</i> , 2020, 10, 133-155.e6. | 6.2 | 57 |
| 151 | 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. <i>Microbial Genomics</i> , 2018, 4, . | 2.0 | 57 |
| 152 | Identification of <i>Cdk</i> targets that control cytokinesis. <i>EMBO Journal</i> , 2015, 34, 81-96. | 7.8 | 56 |
| 153 | Updated Reference Genome Sequence and Annotation of <i>Mycobacterium bovis</i> AF2122/97. <i>Genome Announcements</i> , 2017, 5, . | 0.8 | 55 |
| 154 | Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680. | 4.1 | 52 |
| 155 | Huntingtin's spherical solenoid structure enables polyglutamine tract-dependent modulation of its structure and function. <i>ELife</i> , 2016, 5, e11184. | 6.0 | 52 |
| 156 | Phosphoproteomic analysis identifies proteins involved in transcription-coupled mRNA decay as targets of Snf1 signaling. <i>Science Signaling</i> , 2014, 7, ra64. | 3.6 | 51 |
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