

Sophia Doll

List of Publications by Year in descending order

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Version: 2024-02-01

242
papers

51,033
citations

3919

88
h-index

1895

208
g-index

253
all docs

253
docs citations

253
times ranked

63471
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Mass spectrometry-based proteomics. <i>Nature</i> , 2003, 422, 198-207. | 13.7 | 6,282 |
| 2 | The Perseus computational platform for comprehensive analysis of (prote)omics data. <i>Nature Methods</i> , 2016, 13, 731-740. | 9.0 | 6,181 |
| 3 | Accurate Proteome-wide Label-free Quantification by Delayed Normalization and Maximal Peptide Ratio Extraction, Termed MaxLFQ. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2513-2526. | 2.5 | 4,178 |
| 4 | Mass-spectrometric exploration of proteome structure and function. <i>Nature</i> , 2016, 537, 347-355. | 13.7 | 1,573 |
| 5 | Minimal, encapsulated proteomic-sample processing applied to copy-number estimation in eukaryotic cells. <i>Nature Methods</i> , 2014, 11, 319-324. | 9.0 | 1,447 |
| 6 | The growing landscape of lysine acetylation links metabolism and cell signalling. <i>Nature Reviews Molecular Cell Biology</i> , 2014, 15, 536-550. | 16.1 | 1,153 |
| 7 | A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. <i>Cell</i> , 2015, 163, 712-723. | 13.5 | 1,132 |
| 8 | L-Arginine Modulates T Cell Metabolism and Enhances Survival and Anti-tumor Activity. <i>Cell</i> , 2016, 167, 829-842.e13. | 13.5 | 1,077 |
| 9 | Circular non-coding RNA ANRIL modulates ribosomal RNA maturation and atherosclerosis in humans. <i>Nature Communications</i> , 2016, 7, 12429. | 5.8 | 859 |
| 10 | Phosphoproteomics reveals that Parkinson's disease kinase LRRK2 regulates a subset of Rab GTPases. <i>ELife</i> , 2016, 5, . | 2.8 | 766 |
| 11 | A proteomics strategy to elucidate functional protein-protein interactions applied to EGF signaling. <i>Nature Biotechnology</i> , 2003, 21, 315-318. | 9.4 | 702 |
| 12 | Direct identification of clinically relevant neopeptides presented on native human melanoma tissue by mass spectrometry. <i>Nature Communications</i> , 2016, 7, 13404. | 5.8 | 613 |
| 13 | Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2534-2545. | 2.5 | 602 |
| 14 | Revisiting biomarker discovery by plasma proteomics. <i>Molecular Systems Biology</i> , 2017, 13, 942. | 3.2 | 597 |
| 15 | Plasma Proteome Profiling to Assess Human Health and Disease. <i>Cell Systems</i> , 2016, 2, 185-195. | 2.9 | 549 |
| 16 | A Mammalian Organelle Map by Protein Correlation Profiling. <i>Cell</i> , 2006, 125, 187-199. | 13.5 | 538 |
| 17 | A "Proteomic Ruler" for Protein Copy Number and Concentration Estimation without Spike-in Standards. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3497-3506. | 2.5 | 530 |
| 18 | Widespread Proteome Remodeling and Aggregation in Aging <i>C.Âlegans</i> . <i>Cell</i> , 2015, 161, 919-932. | 13.5 | 478 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Mass Spectrometry of Human Leukocyte Antigen Class I Peptidomes Reveals Strong Effects of Protein Abundance and Turnover on Antigen Presentation. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 658-673. | 2.5 | 445 |
| 20 | Uncovering global SUMOylation signaling networks in a site-specific manner. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 927-936. | 3.6 | 408 |
| 21 | High-throughput phosphoproteomics reveals in vivo insulin signaling dynamics. <i>Nature Biotechnology</i> , 2015, 33, 990-995. | 9.4 | 408 |
| 22 | An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics. <i>Nature Communications</i> , 2019, 10, 963. | 5.8 | 408 |
| 23 | Protein Phosphorylation: A Major Switch Mechanism for Metabolic Regulation. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 676-687. | 3.1 | 402 |
| 24 | Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020, 367, 1140-1146. | 6.0 | 400 |
| 25 | The mitochondrial contact site complex, a determinant of mitochondrial architecture. <i>EMBO Journal</i> , 2011, 30, 4356-4370. | 3.5 | 395 |
| 26 | Precision proteomics: The case for high resolution and high mass accuracy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18132-18138. | 3.3 | 388 |
| 27 | diaPASEF: parallel accumulation ⁺ serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236. | 9.0 | 387 |
| 28 | Systematic proteomic analysis of LRRK2-mediated Rab GTPase phosphorylation establishes a connection to ciliogenesis. <i>ELife</i> , 2017, 6, . | 2.8 | 344 |
| 29 | Cytoplasmic protein aggregates interfere with nucleocytoplasmic transport of protein and RNA. <i>Science</i> , 2016, 351, 173-176. | 6.0 | 336 |
| 30 | Proteomics reveals NNMT as a master metabolic regulator of cancer-associated fibroblasts. <i>Nature</i> , 2019, 569, 723-728. | 13.7 | 330 |
| 31 | The Coming Age of Complete, Accurate, and Ubiquitous Proteomes. <i>Molecular Cell</i> , 2013, 49, 583-590. | 4.5 | 329 |
| 32 | TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. <i>Nature</i> , 2012, 488, 508-511. | 13.7 | 323 |
| 33 | A genome-wide resource for the analysis of protein localisation in <i>Drosophila</i> . <i>ELife</i> , 2016, 5, e12068. | 2.8 | 315 |
| 34 | BoxCar acquisition method enables single-shot proteomics at a depth of 10,000 proteins in 100 minutes. <i>Nature Methods</i> , 2018, 15, 440-448. | 9.0 | 303 |
| 35 | Phosphorylation Is a Central Mechanism for Circadian Control of Metabolism and Physiology. <i>Cell Metabolism</i> , 2017, 25, 118-127. | 7.2 | 297 |
| 36 | Social network architecture of human immune cells unveiled by quantitative proteomics. <i>Nature Immunology</i> , 2017, 18, 583-593. | 7.0 | 296 |

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|----|---|------|-----------|
| 37 | The Q Exactive HF, a Benchtop Mass Spectrometer with a Pre-filter, High-performance Quadrupole and an Ultra-high-field Orbitrap Analyzer. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3698-3708. | 2.5 | 285 |
| 38 | Parallel Accumulation-Serial Fragmentation (PASEF): Multiplying Sequencing Speed and Sensitivity by Synchronized Scans in a Trapped Ion Mobility Device. <i>Journal of Proteome Research</i> , 2015, 14, 5378-5387. | 1.8 | 281 |
| 39 | Inflammatory signaling in human tuberculosis granulomas is spatially organized. <i>Nature Medicine</i> , 2016, 22, 531-538. | 15.2 | 273 |
| 40 | A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2284-2296. | 2.5 | 270 |
| 41 | Proteomic maps of breast cancer subtypes. <i>Nature Communications</i> , 2016, 7, 10259. | 5.8 | 256 |
| 42 | In Vivo Identification of Human Small Ubiquitin-like Modifier Polymerization Sites by High Accuracy Mass Spectrometry and an in Vitro to in Vivo Strategy. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 132-144. | 2.5 | 251 |
| 43 | High-throughput and high-sensitivity phosphoproteomics with the EasyPhos platform. <i>Nature Protocols</i> , 2018, 13, 1897-1916. | 5.5 | 238 |
| 44 | Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015, 33, 415-423. | 9.4 | 237 |
| 45 | Deep Proteomics of Mouse Skeletal Muscle Enables Quantitation of Protein Isoforms, Metabolic Pathways, and Transcription Factors*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 841-853. | 2.5 | 234 |
| 46 | Accurate Protein Complex Retrieval by Affinity Enrichment Mass Spectrometry (AE-MS) Rather than Affinity Purification Mass Spectrometry (AP-MS). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 120-135. | 2.5 | 231 |
| 47 | Functional classification of memory CD8+ T cells by CX3CR1 expression. <i>Nature Communications</i> , 2015, 6, 8306. | 5.8 | 231 |
| 48 | Single Muscle Fiber Proteomics Reveals Fiber-Type-Specific Features of Human Muscle Aging. <i>Cell Reports</i> , 2017, 19, 2396-2409. | 2.9 | 213 |
| 49 | Region and cell-type resolved quantitative proteomic map of the human heart. <i>Nature Communications</i> , 2017, 8, 1469. | 5.8 | 213 |
| 50 | Time- and compartment-resolved proteome profiling of the extracellular niche in lung injury and repair. <i>Molecular Systems Biology</i> , 2015, 11, 819. | 3.2 | 211 |
| 51 | Activation of the ATR kinase by the RPA-binding protein ETAA1. <i>Nature Cell Biology</i> , 2016, 18, 1196-1207. | 4.6 | 208 |
| 52 | Mass Spectrometry-Based Detection and Assignment of Protein Posttranslational Modifications. <i>ACS Chemical Biology</i> , 2015, 10, 63-71. | 1.6 | 193 |
| 53 | Circadian control of oscillations in mitochondrial rate-limiting enzymes and nutrient utilization by PERIOD proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1673-82. | 3.3 | 190 |
| 54 | Proteomics reveals the effects of sustained weight loss on the human plasma proteome. <i>Molecular Systems Biology</i> , 2016, 12, 901. | 3.2 | 188 |

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|----|--|------|-----------|
| 55 | Copy Number Analysis of the Murine Platelet Proteome Spanning the Complete Abundance Range. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3435-3445. | 2.5 | 187 |
| 56 | Novel and shared neoantigen derived from histone 3 variant H3.3K27M mutation for glioma T cell therapy. <i>Journal of Experimental Medicine</i> , 2018, 215, 141-157. | 4.2 | 186 |
| 57 | Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. <i>Science</i> , 2015, 348, 1253671. | 6.0 | 183 |
| 58 | Soluble Oligomers of PolyQ-Expanded Huntingtin Target a Multiplicity of Key Cellular Factors. <i>Molecular Cell</i> , 2016, 63, 951-964. | 4.5 | 181 |
| 59 | Plasma proteome profiling discovers novel proteins associated with non-alcoholic fatty liver disease. <i>Molecular Systems Biology</i> , 2019, 15, e8793. | 3.2 | 176 |
| 60 | OpenCell: Endogenous tagging for the cartography of human cellular organization. <i>Science</i> , 2022, 375, eabi6983. | 6.0 | 174 |
| 61 | Plasma Proteome Profiling to detect and avoid sample-related biases in biomarker studies. <i>EMBO Molecular Medicine</i> , 2019, 11, e10427. | 3.3 | 171 |
| 62 | Loss-less Nano-fractionator for High Sensitivity, High Coverage Proteomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 694-705. | 2.5 | 169 |
| 63 | The forebrain synaptic transcriptome is organized by clocks but its proteome is driven by sleep. <i>Science</i> , 2019, 366, . | 6.0 | 169 |
| 64 | Histone Variant H2A.Z.2 Mediates Proliferation and Drug Sensitivity of Malignant Melanoma. <i>Molecular Cell</i> , 2015, 59, 75-88. | 4.5 | 166 |
| 65 | Single muscle fiber proteomics reveals unexpected mitochondrial specialization. <i>EMBO Reports</i> , 2015, 16, 387-395. | 2.0 | 163 |
| 66 | Deep Visual Proteomics defines single-cell identity and heterogeneity. <i>Nature Biotechnology</i> , 2022, 40, 1231-1240. | 9.4 | 160 |
| 67 | Proteome profiling in cerebrospinal fluid reveals novel biomarkers of Alzheimer's disease. <i>Molecular Systems Biology</i> , 2020, 16, e9356. | 3.2 | 157 |
| 68 | The Impact II, a Very High-Resolution Quadrupole Time-of-Flight Instrument (QTOF) for Deep Shotgun Proteomics *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2014-2029. | 2.5 | 150 |
| 69 | Cell-Type- and Brain-Region-Resolved Mouse Brain Lipidome. <i>Cell Reports</i> , 2020, 32, 108132. | 2.9 | 147 |
| 70 | Limited Environmental Serine and Glycine Confer Brain Metastasis Sensitivity to PHGDH Inhibition. <i>Cancer Discovery</i> , 2020, 10, 1352-1373. | 7.7 | 145 |
| 71 | Cell-Type-Resolved Quantitative Proteomics of Murine Liver. <i>Cell Metabolism</i> , 2014, 20, 1076-1087. | 7.2 | 143 |
| 72 | The CMG Helicase Bypasses DNA-Protein Cross-Links to Facilitate Their Repair. <i>Cell</i> , 2019, 176, 167-181.e21. | 13.5 | 138 |

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|----|--|------|-----------|
| 73 | Trapped ion mobility spectrometry and PASEF enable in-depth lipidomics from minimal sample amounts. <i>Nature Communications</i> , 2020, 11, 331. | 5.8 | 138 |
| 74 | Evidence of Extrapaneacretic Glucagon Secretion in Man. <i>Diabetes</i> , 2016, 65, 585-597. | 0.3 | 136 |
| 75 | Replication-Coupled DNA-Protein Crosslink Repair by SPRTN and the Proteasome in <i>Xenopus</i> Egg Extracts. <i>Molecular Cell</i> , 2019, 73, 574-588.e7. | 4.5 | 135 |
| 76 | Organellar Proteomics and Phospho-Proteomics Reveal Subcellular Reorganization in Diet-Induced Hepatic Steatosis. <i>Developmental Cell</i> , 2018, 47, 205-221.e7. | 3.1 | 132 |
| 77 | C9ORF72 interaction with cofilin modulates actin dynamics in motor neurons. <i>Nature Neuroscience</i> , 2016, 19, 1610-1618. | 7.1 | 131 |
| 78 | Structural Model of a CRISPR RNA-Silencing Complex Reveals the RNA-Target Cleavage Activity in Cmr4. <i>Molecular Cell</i> , 2014, 56, 43-54. | 4.5 | 129 |
| 79 | The proteome landscape of the kingdoms of life. <i>Nature</i> , 2020, 582, 592-596. | 13.7 | 128 |
| 80 | Multi-level Proteomics Identifies CT45 as a Chemosensitivity Mediator and Immunotherapy Target in Ovarian Cancer. <i>Cell</i> , 2018, 175, 159-170.e16. | 13.5 | 127 |
| 81 | Development of phospho-specific Rab protein antibodies to monitor <i>in vivo</i> activity of the LRRK2 Parkinson's disease kinase. <i>Biochemical Journal</i> , 2018, 475, 1-22. | 1.7 | 123 |
| 82 | The Proteome of Primary Prostate Cancer. <i>European Urology</i> , 2016, 69, 942-952. | 0.9 | 122 |
| 83 | Dynamics in protein translation sustaining T cell preparedness. <i>Nature Immunology</i> , 2020, 21, 927-937. | 7.0 | 120 |
| 84 | Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. <i>Cell Systems</i> , 2019, 8, 427-445.e10. | 2.9 | 111 |
| 85 | Proteomics-Based Comparative Mapping of the Secretomes of Human Brown and White Adipocytes Reveals EPDR1 as a Novel Adipokine. <i>Cell Metabolism</i> , 2019, 30, 963-975.e7. | 7.2 | 109 |
| 86 | A streamlined mass spectrometry-based proteomics workflow for large-scale FFPE tissue analysis. <i>Journal of Pathology</i> , 2020, 251, 100-112. | 2.1 | 109 |
| 87 | Spatiotemporal Proteomic Profiling of Huntington's Disease Inclusions Reveals Widespread Loss of Protein Function. <i>Cell Reports</i> , 2017, 21, 2291-2303. | 2.9 | 107 |
| 88 | Artificial intelligence for proteomics and biomarker discovery. <i>Cell Systems</i> , 2021, 12, 759-770. | 2.9 | 106 |
| 89 | In vivo brain GPCR signaling elucidated by phosphoproteomics. <i>Science</i> , 2018, 360, . | 6.0 | 105 |
| 90 | Phosphorylation of Histone H3 Thr-45 Is Linked to Apoptosis. <i>Journal of Biological Chemistry</i> , 2009, 284, 16575-16583. | 1.6 | 98 |

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|-----|--|------|-----------|
| 91 | System-wide identification of wild-type SUMO-2 conjugation sites. <i>Nature Communications</i> , 2015, 6, 7289. | 5.8 | 97 |
| 92 | Deep Proteome Profiling Reveals Common Prevalence of MZB1-Positive Plasma B Cells in Human Lung and Skin Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 1298-1310. | 2.5 | 97 |
| 93 | A role of OCRL in clathrin-coated pit dynamics and uncoating revealed by studies of Lowe syndrome cells. <i>ELife</i> , 2014, 3, e02975. | 2.8 | 97 |
| 94 | A knowledge graph to interpret clinical proteomics data. <i>Nature Biotechnology</i> , 2022, 40, 692-702. | 9.4 | 97 |
| 95 | T Cells Engineered to Express a T-Cell Receptor Specific for Glypican-3 to Recognize and Kill Hepatoma Cells In Vitro and In Mice. <i>Gastroenterology</i> , 2015, 149, 1042-1052. | 0.6 | 96 |
| 96 | Antisense-mediated exon skipping: a therapeutic strategy for titin-based dilated cardiomyopathy. <i>EMBO Molecular Medicine</i> , 2015, 7, 562-576. | 3.3 | 94 |
| 97 | C/EBPβ creates elite cells for iPSC reprogramming by upregulating Klf4 and increasing the levels of Lsd1 and Brd4. <i>Nature Cell Biology</i> , 2016, 18, 371-381. | 4.6 | 94 |
| 98 | High-resolution serum proteome trajectories in COVID-19 reveal patient-specific seroconversion. <i>EMBO Molecular Medicine</i> , 2021, 13, e14167. | 3.3 | 92 |
| 99 | Noninvasive proteomic biomarkers for alcohol-related liver disease. <i>Nature Medicine</i> , 2022, 28, 1277-1287. | 15.2 | 91 |
| 100 | Quantitative shotgun proteomics: considerations for a high-quality workflow in immunology. <i>Nature Immunology</i> , 2014, 15, 112-117. | 7.0 | 90 |
| 101 | CRL2 ^{Lrr1} promotes unloading of the vertebrate replisome from chromatin during replication termination. <i>Genes and Development</i> , 2017, 31, 275-290. | 2.7 | 90 |
| 102 | Splicing factor YBX1 mediates persistence of JAK2-mutated neoplasms. <i>Nature</i> , 2020, 588, 157-163. | 13.7 | 90 |
| 103 | EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. <i>Nature Methods</i> , 2018, 15, 527-530. | 9.0 | 88 |
| 104 | The Case for Proteomics and Phospho-Proteomics in Personalized Cancer Medicine. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800113. | 0.8 | 88 |
| 105 | Urinary proteome profiling for stratifying patients with familial Parkinson's disease. <i>EMBO Molecular Medicine</i> , 2021, 13, e13257. | 3.3 | 88 |
| 106 | Proteomics and C9orf72 neuropathology identify ribosomes as poly-GR/PR interactors driving toxicity. <i>Life Science Alliance</i> , 2018, 1, e201800070. | 1.3 | 88 |
| 107 | Trapped Ion Mobility Spectrometry and Parallel Accumulation-Serial Fragmentation in Proteomics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100138. | 2.5 | 84 |
| 108 | Deep learning the collisional cross sections of the peptide universe from a million experimental values. <i>Nature Communications</i> , 2021, 12, 1185. | 5.8 | 81 |

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|-----|--|-----|-----------|
| 109 | Plasma Proteome Profiling Reveals Dynamics of Inflammatory and Lipid Homeostasis Markers after Roux-En-Y Gastric Bypass Surgery. <i>Cell Systems</i> , 2018, 7, 601-612.e3. | 2.9 | 80 |
| 110 | Molecular basis of PRC1 targeting to Polycomb response elements by PhoRC. <i>Genes and Development</i> , 2016, 30, 1116-1127. | 2.7 | 78 |
| 111 | Multi-omics profiling of living human pancreatic islet donors reveals heterogeneous beta cell trajectories towards type 2 diabetes. <i>Nature Metabolism</i> , 2021, 3, 1017-1031. | 5.1 | 76 |
| 112 | Specificity and Commonality of the Phosphoinositide-Binding Proteome Analyzed by Quantitative Mass Spectrometry. <i>Cell Reports</i> , 2014, 6, 578-591. | 2.9 | 75 |
| 113 | Absolute Proteome Analysis of Colorectal Mucosa, Adenoma, and Cancer Reveals Drastic Changes in Fatty Acid Metabolism and Plasma Membrane Transporters. <i>Journal of Proteome Research</i> , 2015, 14, 4005-4018. | 1.8 | 74 |
| 114 | Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. <i>Nature Communications</i> , 2016, 7, 13250. | 5.8 | 74 |
| 115 | Phosphoproteomic approach for agonist-specific signaling in mouse brains: mTOR pathway is involved in μ opioid aversion. <i>Neuropsychopharmacology</i> , 2019, 44, 939-949. | 2.8 | 74 |
| 116 | Defective glycosylation and multisystem abnormalities characterize the primary immunodeficiency XMEN disease. <i>Journal of Clinical Investigation</i> , 2019, 130, 507-522. | 3.9 | 74 |
| 117 | Spatially and cell-type resolved quantitative proteomic atlas of healthy human skin. <i>Nature Communications</i> , 2020, 11, 5587. | 5.8 | 72 |
| 118 | A Stat6/Pten Axis Links Regulatory T Cells with Adipose Tissue Function. <i>Cell Metabolism</i> , 2017, 26, 475-492.e7. | 7.2 | 71 |
| 119 | Data-independent acquisition method for ubiquitinome analysis reveals regulation of circadian biology. <i>Nature Communications</i> , 2021, 12, 254. | 5.8 | 71 |
| 120 | Molecular and structural architecture of polyQ aggregates in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3446-E3453. | 3.3 | 68 |
| 121 | The Proteome of Prostate Cancer Bone Metastasis Reveals Heterogeneity with Prognostic Implications. <i>Clinical Cancer Research</i> , 2018, 24, 5433-5444. | 3.2 | 68 |
| 122 | Proteomics for blood biomarker exploration of severe mental illness: pitfalls of the past and potential for the future. <i>Translational Psychiatry</i> , 2018, 8, 160. | 2.4 | 68 |
| 123 | A Cell-Autonomous Signature of Dysregulated Protein Phosphorylation Underlies Muscle Insulin Resistance in Type 2 Diabetes. <i>Cell Metabolism</i> , 2020, 32, 844-859.e5. | 7.2 | 68 |
| 124 | Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. <i>Journal of Proteome Research</i> , 2015, 14, 4885-4895. | 1.8 | 66 |
| 125 | TRAIPI is a PCNA-binding ubiquitin ligase that protects genome stability after replication stress. <i>Journal of Cell Biology</i> , 2016, 212, 63-75. | 2.3 | 65 |
| 126 | A Primer on Concepts and Applications of Proteomics in Neuroscience. <i>Neuron</i> , 2017, 96, 558-571. | 3.8 | 65 |

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|-----|---|-----|-----------|
| 127 | Protein profile of fiber types in human skeletal muscle: a single-fiber proteomics study. <i>Skeletal Muscle</i> , 2021, 11, 24. | 1.9 | 65 |
| 128 | Mit/ <scp>TFE</scp> factors control <scp>ER</scp> â€phagy via transcriptional regulation of <scp>FAM</scp> 134B. <i>EMBO Journal</i> , 2020, 39, e105696. | 3.5 | 60 |
| 129 | Parallel accumulation for 100% duty cycle trapped ion mobility-mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2017, 413, 168-175. | 0.7 | 59 |
| 130 | Comparative analysis to guide quality improvements in proteomics. <i>Nature Methods</i> , 2009, 6, 717-719. | 9.0 | 58 |
| 131 | <scp>PP</scp> 2A delays <scp>APC</scp> /Câ€dependent degradation of separaseâ€associated but not free securin. <i>EMBO Journal</i> , 2014, 33, 1134-1147. | 3.5 | 57 |
| 132 | FoxK1 and FoxK2 in insulin regulation of cellular and mitochondrial metabolism. <i>Nature Communications</i> , 2019, 10, 1582. | 5.8 | 57 |
| 133 | Efficient mitotic checkpoint signaling depends on integrated activities of Bub1 and the <scp>RZZ</scp> complex. <i>EMBO Journal</i> , 2019, 38, . | 3.5 | 56 |
| 134 | Oxyntomodulin Identified as a Marker of Type 2 Diabetes and Gastric Bypass Surgery by Mass-spectrometry Based Profiling of Human Plasma. <i>EBioMedicine</i> , 2016, 7, 112-120. | 2.7 | 53 |
| 135 | UBL3 modification influences protein sorting to small extracellular vesicles. <i>Nature Communications</i> , 2018, 9, 3936. | 5.8 | 53 |
| 136 | Cortical circuit alterations precede motor impairments in Huntingtonâ€™s disease mice. <i>Scientific Reports</i> , 2019, 9, 6634. | 1.6 | 53 |
| 137 | Quantitative and Dynamic Catalogs of Proteins Released during Apoptotic and Necroptotic Cell Death. <i>Cell Reports</i> , 2020, 30, 1260-1270.e5. | 2.9 | 53 |
| 138 | Integrative analysis of cell state changes in lung fibrosis with peripheral protein biomarkers. <i>EMBO Molecular Medicine</i> , 2021, 13, e12871. | 3.3 | 53 |
| 139 | Overexpression of Q-rich prion-like proteins suppresses polyQ cytotoxicity and alters the polyQ interactome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18219-18224. | 3.3 | 52 |
| 140 | A Proteomics Approach to the Protein Normalization Problem: Selection of Unvarying Proteins for MS-Based Proteomics and Western Blotting. <i>Journal of Proteome Research</i> , 2016, 15, 2321-2326. | 1.8 | 51 |
| 141 | Quantitative Proteomics Identifies Serum Response Factor Binding Protein 1 as a Host Factor for Hepatitis C Virus Entry. <i>Cell Reports</i> , 2015, 12, 864-878. | 2.9 | 50 |
| 142 | Mechanisms Preserving Insulin Action during High Dietary Fat Intake. <i>Cell Metabolism</i> , 2019, 29, 50-63.e4. | 7.2 | 50 |
| 143 | Interconversion between Anticipatory and Active GID E3â€Ubiquitin Ligase Conformations via Metabolically Driven Substrate Receptor Assembly. <i>Molecular Cell</i> , 2020, 77, 150-163.e9. | 4.5 | 50 |
| 144 | The structural context of posttranslational modifications at a proteome-wide scale. <i>PLoS Biology</i> , 2022, 20, e3001636. | 2.6 | 50 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 145 | Multivalent binding of PWWP2A to H2A.Z regulates mitosis and neural crest differentiation. EMBO Journal, 2017, 36, 2263-2279. | 3.5 | 48 |
| 146 | Regulation of Liver Metabolism by the Endosomal GTPase Rab5. Cell Reports, 2015, 11, 884-892. | 2.9 | 47 |
| 147 | Large scale discovery of coronavirus-host factor protein interaction motifs reveals SARS-CoV-2 specific mechanisms and vulnerabilities. Nature Communications, 2021, 12, 6761. | 5.8 | 47 |
| 148 | Parasite-induced ER stress response in hepatocytes facilitates Plasmodium liver stage infection. EMBO Reports, 2015, 16, 955-964. | 2.0 | 46 |
| 149 | PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. Nature Communications, 2018, 9, 4300. | 5.8 | 46 |
| 150 | Minimal amounts of kindlin-3 suffice for basal platelet and leukocyte functions in mice. Blood, 2015, 126, 2592-2600. | 0.6 | 45 |
| 151 | Accurate MS-based Rab10 Phosphorylation Stoichiometry Determination as Readout for LRRK2 Activity in Parkinson's Disease. Molecular and Cellular Proteomics, 2020, 19, 1546-1560. | 2.5 | 45 |
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