

Steven A Carr

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5843024/publications.pdf>

Version: 2024-02-01

165
papers

38,642
citations

4942

84
h-index

4978

167
g-index

192
all docs

192
docs citations

192
times ranked

49501
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2022, 40, 209-217. | 9.4 | 127 |
| 2 | Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. <i>Blood</i> , 2022, 139, 2534-2546. | 0.6 | 14 |
| 3 | PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. <i>Nature Communications</i> , 2022, 13, 604. | 5.8 | 22 |
| 4 | Cancer proteogenomics: current impact and future prospects. <i>Nature Reviews Cancer</i> , 2022, 22, 298-313. | 12.8 | 79 |
| 5 | Identification of R1OK2 as a master regulator of human blood cell development. <i>Nature Immunology</i> , 2022, 23, 109-121. | 7.0 | 13 |
| 6 | <i>BCOR</i> and <i>BCORL1</i> Mutations Drive Epigenetic Reprogramming and Oncogenic Signaling by Unlinking PRC1.1 from Target Genes. <i>Blood Cancer Discovery</i> , 2022, 3, 116-135. | 2.6 | 18 |
| 7 | A bidirectional switch in the Shank3 phosphorylation state biases synapses toward up- or downscaling. <i>ELife</i> , 2022, 11, . | 2.8 | 15 |
| 8 | Landscape of helper and regulatory antitumour CD4+ T cells in melanoma. <i>Nature</i> , 2022, 605, 532-538. | 13.7 | 70 |
| 9 | Degradation of GSPT1 causes TP53-independent cell death in leukemia while sparing normal hematopoietic stem cells. <i>Journal of Clinical Investigation</i> , 2022, 132, . | 3.9 | 17 |
| 10 | Proteomics and Population Biology in the Cardiovascular Health Study (CHS): design of a study with mentored access and active data sharing. <i>European Journal of Epidemiology</i> , 2022, 37, 755-765. | 2.5 | 6 |
| 11 | Reversal of viral and epigenetic HLA class I repression in Merkel cell carcinoma. <i>Journal of Clinical Investigation</i> , 2022, 132, . | 3.9 | 10 |
| 12 | The SARS-CoV-2 RNA-protein interactome in infected human cells. <i>Nature Microbiology</i> , 2021, 6, 339-353. | 5.9 | 245 |
| 13 | MS-Based HLA-II Peptidomics Combined With Multiomics Will Aid the Development of Future Immunotherapies. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100116. | 2.5 | 13 |
| 14 | Optimized Liquid and Gas Phase Fractionation Increases HLA-Peptidome Coverage for Primary Cell and Tissue Samples. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100133. | 2.5 | 32 |
| 15 | The Conserved Translation Factor LepA Is Required for Optimal Synthesis of a Porin Family in <i>Mycobacterium smegmatis</i> . <i>Journal of Bacteriology</i> , 2021, 203, . | 1.0 | 5 |
| 16 | Dual functions of SPOP and ERG dictate androgen therapy responses in prostate cancer. <i>Nature Communications</i> , 2021, 12, 734. | 5.8 | 26 |
| 17 | Cohesin mutations alter DNA damage repair and chromatin structure and create therapeutic vulnerabilities in MDS/AML. <i>JCI Insight</i> , 2021, 6, . | 2.3 | 39 |
| 18 | Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16. | 7.7 | 189 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Avadomide Induces Degradation of ZMYM2 Fusion Oncoproteins in Hematologic Malignancies. <i>Blood Cancer Discovery</i> , 2021, 2, 250-265. | 2.6 | 19 |
| 20 | Targeting acute myeloid leukemia dependency on VCP-mediated DNA repair through a selective second-generation small-molecule inhibitor. <i>Science Translational Medicine</i> , 2021, 13, . | 5.8 | 29 |
| 21 | Proteomic profiling reveals biomarkers and pathways in type 2 diabetes risk. <i>JCI Insight</i> , 2021, 6, . | 2.3 | 26 |
| 22 | Blockade of IL-22 signaling reverses erythroid dysfunction in stress-induced anemias. <i>Nature Immunology</i> , 2021, 22, 520-529. | 7.0 | 11 |
| 23 | Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20. | 7.7 | 327 |
| 24 | Suppression of pancreatic ductal adenocarcinoma growth and metastasis by fibrillar collagens produced selectively by tumor cells. <i>Nature Communications</i> , 2021, 12, 2328. | 5.8 | 45 |
| 25 | Cell-specific transcriptional control of mitochondrial metabolism by TIF1 β drives erythropoiesis. <i>Science</i> , 2021, 372, 716-721. | 6.0 | 25 |
| 26 | Identification of a Novel Regulator of <i>Clostridioides difficile</i> Cortex Formation. <i>MSphere</i> , 2021, 6, e0021121. | 1.3 | 6 |
| 27 | Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314. | 13.7 | 181 |
| 28 | PANOPLY: a cloud-based platform for automated and reproducible proteogenomic data analysis. <i>Nature Methods</i> , 2021, 18, 580-582. | 9.0 | 11 |
| 29 | STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. <i>Cancer Cell</i> , 2021, 39, 827-844.e10. | 7.7 | 49 |
| 30 | Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics. <i>Nature Communications</i> , 2021, 12, 3346. | 5.8 | 90 |
| 31 | Targeted mass-spectrometry-based assays enable multiplex quantification of receptor tyrosine kinase, MAP kinase, and AKT signaling. <i>Cell Reports Methods</i> , 2021, 1, 100015. | 1.4 | 10 |
| 32 | <i>ZBTB33</i> Is Mutated in Clonal Hematopoiesis and Myelodysplastic Syndromes and Impacts RNA Splicing. <i>Blood Cancer Discovery</i> , 2021, 2, 500-517. | 2.6 | 17 |
| 33 | Profiling SARS-CoV-2 HLA-I peptidome reveals T β cell epitopes from out-of-frame ORFs. <i>Cell</i> , 2021, 184, 3962-3980.e17. | 13.5 | 98 |
| 34 | Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. <i>Nature Communications</i> , 2021, 12, 4375. | 5.8 | 39 |
| 35 | Phenotype, specificity and avidity of antitumour CD8 $^{+}$ T cells in melanoma. <i>Nature</i> , 2021, 596, 119-125. | 13.7 | 239 |
| 36 | Spatiotemporally-resolved mapping of RNA binding proteins via functional proximity labeling reveals a mitochondrial mRNA anchor promoting stress recovery. <i>Nature Communications</i> , 2021, 12, 4980. | 5.8 | 47 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 37 | An engineered transcriptional reporter of protein localization identifies regulators of mitochondrial and ER membrane protein trafficking in high-throughput CRISPRi screens. <i>ELife</i> , 2021, 10, . | 2.8 | 17 |
| 38 | A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40. | 13.5 | 170 |
| 39 | Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26. | 13.5 | 236 |
| 40 | A highly multiplexed quantitative phosphosite assay for biology and preclinical studies. <i>Molecular Systems Biology</i> , 2021, 17, e10156. | 3.2 | 12 |
| 41 | Genomic Profiling of Lung Adenocarcinoma in Never-Smokers. <i>Journal of Clinical Oncology</i> , 2021, 39, 3747-3758. | 0.8 | 38 |
| 42 | Automating UbiFast for High-throughput and Multiplexed Ubiquitin Enrichment. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100154. | 2.5 | 12 |
| 43 | Novel Antibodies for the Simple and Efficient Enrichment of Native O-GlcNAc Modified Peptides. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100167. | 2.5 | 23 |
| 44 | Multiomic characterization of oncogenic signaling mediated by wild-type and mutant RIT1. <i>Science Signaling</i> , 2021, 14, eabc4520. | 1.6 | 6 |
| 45 | Spontaneous Glycan Reattachment Following N-Glycanase Treatment of Influenza and HIV Vaccine Antigens. <i>Journal of Proteome Research</i> , 2020, 19, 733-743. | 1.8 | 5 |
| 46 | A large peptidome dataset improves HLA class I epitope prediction across most of the human population. <i>Nature Biotechnology</i> , 2020, 38, 199-209. | 9.4 | 324 |
| 47 | BRG1 Loss Predisposes Lung Cancers to Replicative Stress and ATR Dependency. <i>Cancer Research</i> , 2020, 80, 3841-3854. | 0.4 | 32 |
| 48 | Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31. | 13.5 | 273 |
| 49 | Avant-garde: an automated data-driven DIA data curation tool. <i>Nature Methods</i> , 2020, 17, 1237-1244. | 9.0 | 22 |
| 50 | Proximity labeling in mammalian cells with TurboID and split-TurboID. <i>Nature Protocols</i> , 2020, 15, 3971-3999. | 5.5 | 171 |
| 51 | Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276. | 2.9 | 83 |
| 52 | RNA-protein interaction mapping via MS2- or Cas13-based APEX targeting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22068-22079. | 3.3 | 105 |
| 53 | Split-TurboID enables contact-dependent proximity labeling in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12143-12154. | 3.3 | 179 |
| 54 | CITED4 Protects Against Adverse Remodeling in Response to Physiological and Pathological Stress. <i>Circulation Research</i> , 2020, 127, 631-646. | 2.0 | 29 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 55 | Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020, 181, 1464-1474. | 13.5 | 147 |
| 56 | From Skepticism to Embrace: The Role of Targeted Mass Spectrometry in Validating Proteomics. <i>Clinical Chemistry</i> , 2020, 66, 973-974. | 1.5 | 5 |
| 57 | Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35. | 13.5 | 410 |
| 58 | Proteomic Profiling of the ECM of Xenograft Breast Cancer Metastases in Different Organs Reveals Distinct Metastatic Niches. <i>Cancer Research</i> , 2020, 80, 1475-1485. | 0.4 | 79 |
| 59 | Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26. | 13.5 | 296 |
| 60 | Rapid and deep-scale ubiquitylation profiling for biology and translational research. <i>Nature Communications</i> , 2020, 11, 359. | 5.8 | 75 |
| 61 | Cell-Surface Proteomic Profiling in the Fly Brain Uncovers Wiring Regulators. <i>Cell</i> , 2020, 180, 373-386.e15. | 13.5 | 118 |
| 62 | Microscaled proteogenomic methods for precision oncology. <i>Nature Communications</i> , 2020, 11, 532. | 5.8 | 78 |
| 63 | Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation. <i>Nature Genetics</i> , 2020, 52, 138-145. | 9.4 | 73 |
| 64 | Virtual Issue: Technological Innovations. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 572-573. | 2.5 | 0 |
| 65 | Steroid resistance in Diamond Blackfan anemia associates with p57Kip2 dysregulation in erythroid progenitors. <i>Journal of Clinical Investigation</i> , 2020, 130, 2097-2110. | 3.9 | 29 |
| 66 | Evaluation of Advanced Precursor Determination for Tandem Mass Tag (TMT)-Based Quantitative Proteomics across Instrument Platforms. <i>Journal of Proteome Research</i> , 2019, 18, 542-547. | 1.8 | 18 |
| 67 | Combined Analysis of Metabolomes, Proteomes, and Transcriptomes of Hepatitis C Virus-Infected Cells and Liver to Identify Pathways Associated With Disease Development. <i>Gastroenterology</i> , 2019, 157, 537-551.e9. | 0.6 | 71 |
| 68 | A rapid triage test for active pulmonary tuberculosis in adult patients with persistent cough. <i>Science Translational Medicine</i> , 2019, 11, . | 5.8 | 44 |
| 69 | Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31. | 13.5 | 430 |
| 70 | SMAC mimetics promote NIK-dependent inhibition of CD4 ⁺ T _H 17 cell differentiation. <i>Science Signaling</i> , 2019, 12, . | 1.6 | 14 |
| 71 | Proteomic analyses of ECM during pancreatic ductal adenocarcinoma progression reveal different contributions by tumor and stromal cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19609-19618. | 3.3 | 244 |
| 72 | Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. <i>Cancer Cell</i> , 2019, 36, 369-384.e13. | 7.7 | 224 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 73 | Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19. | 13.5 | 498 |
| 74 | Patterns of substrate affinity, competition, and degradation kinetics underlie biological activity of thalidomide analogs. <i>Blood</i> , 2019, 134, 160-170. | 0.6 | 41 |
| 75 | Trio Haploinsufficiency Causes Neurodevelopmental Disease-Associated Deficits. <i>Cell Reports</i> , 2019, 26, 2805-2817.e9. | 2.9 | 39 |
| 76 | Streamlined Protocol for Deep Proteomic Profiling of FAC-sorted Cells and Its Application to Freshly Isolated Murine Immune Cells*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 995a-1009. | 2.5 | 69 |
| 77 | TMT Labeling for the Masses: A Robust and Cost-efficient, In-solution Labeling Approach. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1468-1478. | 2.5 | 245 |
| 78 | Domain-specific Quantification of Prion Protein in Cerebrospinal Fluid by Targeted Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2388-2400. | 2.5 | 22 |
| 79 | A Curated Resource for Phosphosite-specific Signature Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 576-593. | 2.5 | 197 |
| 80 | Mass Spectrometry-Based Proteomics Reveals Potential Roles of NEK9 and MAP2K4 in Resistance to PI3K Inhibition in Triple-Negative Breast Cancers. <i>Cancer Research</i> , 2018, 78, 2732-2746. | 0.4 | 52 |
| 81 | A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. <i>Cell Systems</i> , 2018, 6, 424-443.e7. | 2.9 | 68 |
| 82 | <i>Clorf106</i> is a colitis risk gene that regulates stability of epithelial adherens junctions. <i>Science</i> , 2018, 359, 1161-1166. | 6.0 | 95 |
| 83 | Specter: linear deconvolution for targeted analysis of data-independent acquisition mass spectrometry proteomics. <i>Nature Methods</i> , 2018, 15, 371-378. | 9.0 | 58 |
| 84 | Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018, 173, 90-103.e19. | 13.5 | 296 |
| 85 | Antigen discovery and specification of immunodominance hierarchies for MHCII-restricted epitopes. <i>Nature Medicine</i> , 2018, 24, 1762-1772. | 15.2 | 64 |
| 86 | Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2018, 34, 396-410.e8. | 7.7 | 146 |
| 87 | Targeting wild-type KRAS-amplified gastroesophageal cancer through combined MEK and SHP2 inhibition. <i>Nature Medicine</i> , 2018, 24, 968-977. | 15.2 | 196 |
| 88 | Anti-apoptotic Protein BIRC5 Maintains Survival of HIV-1-Infected CD4+ T Cells. <i>Immunity</i> , 2018, 48, 1183-1194.e5. | 6.6 | 109 |
| 89 | <i>Crbn</i> I391V is sufficient to confer in vivo sensitivity to thalidomide and its derivatives in mice. <i>Blood</i> , 2018, 132, 1535-1544. | 0.6 | 71 |
| 90 | Noncanonical translation via deadenylated 3' UTRs maintains primordial germ cells. <i>Nature Chemical Biology</i> , 2018, 14, 844-852. | 3.9 | 5 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|------|-----------|
| 91 | Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatography–mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1632-1661. | 5.5 | 377 |
| 92 | Discovery of proteins associated with a predefined genomic locus via dCas9–APEX-mediated proximity labeling. <i>Nature Methods</i> , 2018, 15, 437-439. | 9.0 | 133 |
| 93 | The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. <i>Nature</i> , 2018, 561, 132-136. | 13.7 | 303 |
| 94 | GeNets: a unified web platform for network-based genomic analyses. <i>Nature Methods</i> , 2018, 15, 543-546. | 9.0 | 62 |
| 95 | Mass Spectrometry Profiling of HLA-Associated Peptidomes in Mono-allelic Cells Enables More Accurate Epitope Prediction. <i>Immunity</i> , 2017, 46, 315-326. | 6.6 | 596 |
| 96 | New Guidelines for Publication of Manuscripts Describing Development and Application of Targeted Mass Spectrometry Measurements of Peptides and Proteins. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 327-328. | 2.5 | 33 |
| 97 | Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. <i>Nature Communications</i> , 2017, 8, 14864. | 5.8 | 112 |
| 98 | Antibodies to biotin enable large-scale detection of biotinylation sites on proteins. <i>Nature Methods</i> , 2017, 14, 1167-1170. | 9.0 | 114 |
| 99 | Opposing effects of cancer-type-specific SPOP mutants on BET protein degradation and sensitivity to BET inhibitors. <i>Nature Medicine</i> , 2017, 23, 1046-1054. | 15.2 | 145 |
| 100 | An Integrative Framework Reveals Signaling-to-Transcription Events in Toll-like Receptor Signaling. <i>Cell Reports</i> , 2017, 19, 2853-2866. | 2.9 | 26 |
| 101 | Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 121-134. | 2.5 | 111 |
| 102 | Proteomic mapping of cytosol-facing outer mitochondrial and ER membranes in living human cells by proximity biotinylation. <i>ELife</i> , 2017, 6, . | 2.8 | 276 |
| 103 | Proteogenomics connects somatic mutations to signalling in breast cancer. <i>Nature</i> , 2016, 534, 55-62. | 13.7 | 1,384 |
| 104 | Reduced-representation Phosphosignatures Measured by Quantitative Targeted MS Capture Cellular States and Enable Large-scale Comparison of Drug-induced Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1622-1641. | 2.5 | 92 |
| 105 | Proteomic Analysis of Unbounded Cellular Compartments: Synaptic Clefts. <i>Cell</i> , 2016, 166, 1295-1307.e21. | 13.5 | 324 |
| 106 | Aptamer-Based Proteomic Profiling Reveals Novel Candidate Biomarkers and Pathways in Cardiovascular Disease. <i>Circulation</i> , 2016, 134, 270-285. | 1.6 | 172 |
| 107 | Reconstituted B cell receptor signaling reveals carbohydrate-dependent mode of activation. <i>Scientific Reports</i> , 2016, 6, 36298. | 1.6 | 29 |
| 108 | Automated Microchromatography Enables Multiplexing of Immunoaffinity Enrichment of Peptides to Greater than 150 for Targeted MS-Based Assays. <i>Analytical Chemistry</i> , 2016, 88, 7548-7555. | 3.2 | 44 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 109 | Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765. | 13.5 | 804 |
| 110 | Identification of cancer-cytotoxic modulators of PDE3A by predictive chemogenomics. <i>Nature Chemical Biology</i> , 2016, 12, 102-108. | 3.9 | 72 |
| 111 | An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1060-1071. | 2.5 | 104 |
| 112 | Spatially resolved proteomic mapping in living cells with the engineered peroxidase APEX2. <i>Nature Protocols</i> , 2016, 11, 456-475. | 5.5 | 411 |
| 113 | Multiplexed Immunoaffinity Enrichment of Peptides with Anti-peptide Antibodies and Quantification by Stable Isotope Dilution Multiple Reaction Monitoring Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2016, 1410, 135-167. | 0.4 | 12 |
| 114 | Targeted MS Assay Predicting Tamoxifen Resistance in Estrogen-Receptor-Positive Breast Cancer Tissues and Sera. <i>Journal of Proteome Research</i> , 2016, 15, 1230-1242. | 1.8 | 21 |
| 115 | Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry-Based Assays. <i>Clinical Chemistry</i> , 2016, 62, 48-69. | 1.5 | 187 |
| 116 | Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016, 15, 691-706. | 1.8 | 44 |
| 117 | The extracellular matrix: Tools and insights for the "omics" era. <i>Matrix Biology</i> , 2016, 49, 10-24. | 1.5 | 793 |
| 118 | Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays. <i>Methods in Molecular Biology</i> , 2016, 1410, 223-236. | 0.4 | 33 |
| 119 | A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. <i>Molecular Cell</i> , 2015, 60, 816-827. | 4.5 | 200 |
| 120 | Dynamic profiling of the protein life cycle in response to pathogens. <i>Science</i> , 2015, 347, 1259038. | 6.0 | 408 |
| 121 | Lenalidomide induces ubiquitination and degradation of CK1 β in del(5q) MDS. <i>Nature</i> , 2015, 523, 183-188. | 13.7 | 648 |
| 122 | Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2357-2374. | 2.5 | 153 |
| 123 | Deep, Quantitative Coverage of the Lysine Acetylome Using Novel Anti-acetyl-lysine Antibodies and an Optimized Proteomic Workflow. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2429-2440. | 2.5 | 147 |
| 124 | Multiplexed, Quantitative Workflow for Sensitive Biomarker Discovery in Plasma Yields Novel Candidates for Early Myocardial Injury. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2375-2393. | 2.5 | 175 |
| 125 | Building the Connectivity Map of epigenetics: Chromatin profiling by quantitative targeted mass spectrometry. <i>Methods</i> , 2015, 72, 57-64. | 1.9 | 55 |
| 126 | A framework for installable external tools in Skyline. <i>Bioinformatics</i> , 2014, 30, 2521-2523. | 1.8 | 36 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 127 | Demonstrating the feasibility of large-scale development of standardized assays to quantify human proteins. <i>Nature Methods</i> , 2014, 11, 149-155. | 9.0 | 178 |
| 128 | Lenalidomide Causes Selective Degradation of IKZF1 and IKZF3 in Multiple Myeloma Cells. <i>Science</i> , 2014, 343, 301-305. | 6.0 | 1,371 |
| 129 | Proteogenomic characterization of human colon and rectal cancer. <i>Nature</i> , 2014, 513, 382-387. | 13.7 | 1,219 |
| 130 | Ischemia in Tumors Induces Early and Sustained Phosphorylation Changes in Stress Kinase Pathways but Does Not Affect Global Protein Levels. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1690-1704. | 2.5 | 323 |
| 131 | Panorama: A Targeted Proteomics Knowledge Base. <i>Journal of Proteome Research</i> , 2014, 13, 4205-4210. | 1.8 | 205 |
| 132 | Extracellular matrix signatures of human primary metastatic colon cancers and their metastases to liver. <i>BMC Cancer</i> , 2014, 14, 518. | 1.1 | 204 |
| 133 | Proteomic Mapping of the Human Mitochondrial Intermembrane Space in Live Cells via Ratiometric APEX Tagging. <i>Molecular Cell</i> , 2014, 55, 332-341. | 4.5 | 414 |
| 134 | Simplified and Efficient Quantification of Low-abundance Proteins at Very High Multiplex via Targeted Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1137-1149. | 2.5 | 63 |
| 135 | Extracellular matrix signatures of human mammary carcinoma identify novel metastasis promoters. <i>ELife</i> , 2014, 3, e01308. | 2.8 | 291 |
| 136 | Refined Preparation and Use of Anti-diglycine Remnant (K- μ -GG) Antibody Enables Routine Quantification of 10,000s of Ubiquitination Sites in Single Proteomics Experiments. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 825-831. | 2.5 | 279 |
| 137 | Large-scale identification of ubiquitination sites by mass spectrometry. <i>Nature Protocols</i> , 2013, 8, 1950-1960. | 5.5 | 256 |
| 138 | Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1386-1391. | 9.4 | 238 |
| 139 | Proteomic Mapping of Mitochondria in Living Cells via Spatially Restricted Enzymatic Tagging. <i>Science</i> , 2013, 339, 1328-1331. | 6.0 | 1,023 |
| 140 | Quantitative analysis of peptides and proteins in biomedicine by targeted mass spectrometry. <i>Nature Methods</i> , 2013, 10, 28-34. | 9.0 | 412 |
| 141 | Integrated proteomic analysis of post-translational modifications by serial enrichment. <i>Nature Methods</i> , 2013, 10, 634-637. | 9.0 | 534 |
| 142 | Design, Implementation and Multisite Evaluation of a System Suitability Protocol for the Quantitative Assessment of Instrument Performance in Liquid Chromatography-Multiple Reaction Monitoring-MS (LC-MRM-MS). <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2623-2639. | 2.5 | 100 |
| 143 | The Matrisome: In Silico Definition and In Vivo Characterization by Proteomics of Normal and Tumor Extracellular Matrices. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014647. | 2.5 | 920 |
| 144 | iTRAQ Labeling is Superior to mTRAQ for Quantitative Global Proteomics and Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014423. | 2.5 | 159 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|------|-----------|
| 145 | Methods for Quantification of in vivo Changes in Protein Ubiquitination following Proteasome and Deubiquitinase Inhibition. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 148-159. | 2.5 | 140 |
| 146 | Statistical characterization of multiple-reaction monitoring mass spectrometry (MRM-MS) assays for quantitative proteomics. <i>BMC Bioinformatics</i> , 2012, 13, S9. | 1.2 | 91 |
| 147 | Interlaboratory Evaluation of Automated, Multiplexed Peptide Immunoaffinity Enrichment Coupled to Multiple Reaction Monitoring Mass Spectrometry for Quantifying Proteins in Plasma. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013854. | 2.5 | 176 |
| 148 | A pipeline that integrates the discovery and verification of plasma protein biomarkers reveals candidate markers for cardiovascular disease. <i>Nature Biotechnology</i> , 2011, 29, 635-643. | 9.4 | 229 |
| 149 | Evaluation of Large Scale Quantitative Proteomic Assay Development Using Peptide Affinity-based Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005645. | 2.5 | 130 |
| 150 | Lipid profiling identifies a triacylglycerol signature of insulin resistance and improves diabetes prediction in humans. <i>Journal of Clinical Investigation</i> , 2011, 121, 1402-1411. | 3.9 | 537 |
| 151 | Automated Detection of Inaccurate and Imprecise Transitions in Peptide Quantification by Multiple Reaction Monitoring Mass Spectrometry. <i>Clinical Chemistry</i> , 2010, 56, 291-305. | 1.5 | 182 |
| 152 | Overview of Peptide and Protein Analysis by Mass Spectrometry. <i>Current Protocols in Protein Science</i> , 2010, 62, Unit16.1. | 2.8 | 44 |
| 153 | Effect of Collision Energy Optimization on the Measurement of Peptides by Selected Reaction Monitoring (SRM) Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 10116-10124. | 3.2 | 220 |
| 154 | Repeatability and Reproducibility in Proteomic Identifications by Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 761-776. | 1.8 | 505 |
| 155 | Developing Multiplexed Assays for Troponin I and Interleukin-33 in Plasma by Peptide Immunoaffinity Enrichment and Targeted Mass Spectrometry. <i>Clinical Chemistry</i> , 2009, 55, 1108-1117. | 1.5 | 243 |
| 156 | Quantification of Cardiovascular Biomarkers in Patient Plasma by Targeted Mass Spectrometry and Stable Isotope Dilution. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2339-2349. | 2.5 | 263 |
| 157 | Prediction of high-responding peptides for targeted protein assays by mass spectrometry. <i>Nature Biotechnology</i> , 2009, 27, 190-198. | 9.4 | 273 |
| 158 | Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. <i>Nature Biotechnology</i> , 2009, 27, 633-641. | 9.4 | 958 |
| 159 | A Mitochondrial Protein Compendium Elucidates Complex I Disease Biology. <i>Cell</i> , 2008, 134, 112-123. | 13.5 | 1,766 |
| 160 | Accurate Inclusion Mass Screening. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1952-1962. | 2.5 | 147 |
| 161 | Quantitative, Multiplexed Assays for Low Abundance Proteins in Plasma by Targeted Mass Spectrometry and Stable Isotope Dilution. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 2212-2229. | 2.5 | 619 |
| 162 | The Connectivity Map: Using Gene-Expression Signatures to Connect Small Molecules, Genes, and Disease. <i>Science</i> , 2006, 313, 1929-1935. | 6.0 | 4,472 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 163 | Protein biomarker discovery and validation: the long and uncertain path to clinical utility. <i>Nature Biotechnology</i> , 2006, 24, 971-983. | 9.4 | 1,577 |
| 164 | New mass spectral approaches to complex carbohydrate structure. <i>Mass Spectrometry Reviews</i> , 1983, 2, 153-221. | 2.8 | 84 |
| 165 | New Techniques for Oligosaccharide Sequencing. <i>Journal of Carbohydrate Chemistry</i> , 1983, 2, 1-18. | 0.4 | 24 |