

Steven A Carr

List of Publications by Year in descending order

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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	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
2	A Mitochondrial Protein Compendium Elucidates Complex I Disease Biology. <i>Cell</i> , 2008, 134, 112-123.	13.5	1,766
3	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
4	Proteogenomics connects somatic mutations to signalling in breast cancer. <i>Nature</i> , 2016, 534, 55-62.	13.7	1,384
5	Lenalidomide Causes Selective Degradation of IKZF1 and IKZF3 in Multiple Myeloma Cells. <i>Science</i> , 2014, 343, 301-305.	6.0	1,371
6	Proteogenomic characterization of human colon and rectal cancer. <i>Nature</i> , 2014, 513, 382-387.	13.7	1,219
7	Proteomic Mapping of Mitochondria in Living Cells via Spatially Restricted Enzymatic Tagging. <i>Science</i> , 2013, 339, 1328-1331.	6.0	1,023
8	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
9	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
10	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	13.5	804
11	The extracellular matrix: Tools and insights for the "omics" era. <i>Matrix Biology</i> , 2016, 49, 10-24.	1.5	793
12	Lenalidomide induces ubiquitination and degradation of CK1 δ in del(5q) MDS. <i>Nature</i> , 2015, 523, 183-188.	13.7	648
13	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
14	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
15	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
16	Integrated proteomic analysis of post-translational modifications by serial enrichment. <i>Nature Methods</i> , 2013, 10, 634-637.	9.0	534
17	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
18	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	13.5	498

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19	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	13.5	430
20	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
21	Quantitative analysis of peptides and proteins in biomedicine by targeted mass spectrometry. <i>Nature Methods</i> , 2013, 10, 28-34.	9.0	412
22	Spatially resolved proteomic mapping in living cells with the engineered peroxidase APEX2. <i>Nature Protocols</i> , 2016, 11, 456-475.	5.5	411
23	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	13.5	410
24	Dynamic profiling of the protein life cycle in response to pathogens. <i>Science</i> , 2015, 347, 1259038.	6.0	408
25	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
26	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	7.7	327
27	Proteomic Analysis of Unbounded Cellular Compartments: Synaptic Clefts. <i>Cell</i> , 2016, 166, 1295-1307.e21.	13.5	324
28	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
29	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
30	The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. <i>Nature</i> , 2018, 561, 132-136.	13.7	303
31	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018, 173, 90-103.e19.	13.5	296
32	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	13.5	296
33	Extracellular matrix signatures of human mammary carcinoma identify novel metastasis promoters. <i>ELife</i> , 2014, 3, e01308.	2.8	291
34	Refined Preparation and Use of Anti-diglycine Remnant (K-Îµ-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
35	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
36	Prediction of high-responding peptides for targeted protein assays by mass spectrometry. <i>Nature Biotechnology</i> , 2009, 27, 190-198.	9.4	273

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37	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273
38	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
39	Large-scale identification of ubiquitination sites by mass spectrometry. <i>Nature Protocols</i> , 2013, 8, 1950-1960.	5.5	256
40	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
41	The SARS-CoV-2 RNA-protein interactome in infected human cells. <i>Nature Microbiology</i> , 2021, 6, 339-353.	5.9	245
42	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
43	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
44	Phenotype, specificity and avidity of antitumour CD8+ T cells in melanoma. <i>Nature</i> , 2021, 596, 119-125.	13.7	239
45	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1386-1391.	9.4	238
46	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	13.5	236
47	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
48	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. <i>Cancer Cell</i> , 2019, 36, 369-384.e13.	7.7	224
49	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
50	Panorama: A Targeted Proteomics Knowledge Base. <i>Journal of Proteome Research</i> , 2014, 13, 4205-4210.	1.8	205
51	Extracellular matrix signatures of human primary metastatic colon cancers and their metastases to liver. <i>BMC Cancer</i> , 2014, 14, 518.	1.1	204
52	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
53	A Curated Resource for Phosphosite-specific Signature Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 576-593.	2.5	197
54	Targeting wild-type KRAS-amplified gastroesophageal cancer through combined MEK and SHP2 inhibition. <i>Nature Medicine</i> , 2018, 24, 968-977.	15.2	196

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55	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
56	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
57	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
58	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314.	13.7	181
59	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
60	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
61	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
62	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
63	Aptamer-Based Proteomic Profiling Reveals Novel Candidate Biomarkers and Pathways in Cardiovascular Disease. <i>Circulation</i> , 2016, 134, 270-285.	1.6	172
64	Proximity labeling in mammalian cells with TurboID and split-TurboID. <i>Nature Protocols</i> , 2020, 15, 3971-3999.	5.5	171
65	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	13.5	170
66	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
67	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
68	Accurate Inclusion Mass Screening. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1952-1962.	2.5	147
69	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
70	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020, 181, 1464-1474.	13.5	147
71	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
72	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

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73	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
74	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
75	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
76	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2022, 40, 209-217.	9.4	127
77	Cell-Surface Proteomic Profiling in the Fly Brain Uncovers Wiring Regulators. <i>Cell</i> , 2020, 180, 373-386.e15.	13.5	118
78	Antibodies to biotin enable large-scale detection of biotinylation sites on proteins. <i>Nature Methods</i> , 2017, 14, 1167-1170.	9.0	114
79	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. <i>Nature Communications</i> , 2017, 8, 14864.	5.8	112
80	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 121-134.	2.5	111
81	Anti-apoptotic Protein BIRC5 Maintains Survival of HIV-1-Infected CD4+ T Cells. <i>Immunity</i> , 2018, 48, 1183-1194.e5.	6.6	109
82	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
83	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
84	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
85	Profiling SARS-CoV-2 HLA-I peptidome reveals T cell epitopes from out-of-frame ORFs. <i>Cell</i> , 2021, 184, 3962-3980.e17.	13.5	98
86	<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
87	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
88	Statistical characterization of multiple-reaction monitoring mass spectrometry (MRM-MS) assays for quantitative proteomics. <i>BMC Bioinformatics</i> , 2012, 13, S9.	1.2	91
89	Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics. <i>Nature Communications</i> , 2021, 12, 3346.	5.8	90
90	New mass spectral approaches to complex carbohydrate structure. <i>Mass Spectrometry Reviews</i> , 1983, 2, 153-221.	2.8	84

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91	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276.	2.9	83
92	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
93	Cancer proteogenomics: current impact and future prospects. <i>Nature Reviews Cancer</i> , 2022, 22, 298-313.	12.8	79
94	Microscaled proteogenomic methods for precision oncology. <i>Nature Communications</i> , 2020, 11, 532.	5.8	78
95	Rapid and deep-scale ubiquitylation profiling for biology and translational research. <i>Nature Communications</i> , 2020, 11, 359.	5.8	75
96	Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation. <i>Nature Genetics</i> , 2020, 52, 138-145.	9.4	73
97	Identification of cancer-cytotoxic modulators of PDE3A by predictive chemogenomics. <i>Nature Chemical Biology</i> , 2016, 12, 102-108.	3.9	72
98	Crbn 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
99	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
100	Landscape of helper and regulatory antitumour CD4+ T cells in melanoma. <i>Nature</i> , 2022, 605, 532-538.	18.7	70
101	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
102	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
103	Antigen discovery and specification of immunodominance hierarchies for MHCII-restricted epitopes. <i>Nature Medicine</i> , 2018, 24, 1762-1772.	15.2	64
104	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
105	GeNets: a unified web platform for network-based genomic analyses. <i>Nature Methods</i> , 2018, 15, 543-546.	9.0	62
106	Specter: linear deconvolution for targeted analysis of data-independent acquisition mass spectrometry proteomics. <i>Nature Methods</i> , 2018, 15, 371-378.	9.0	58
107	Building the Connectivity Map of epigenetics: Chromatin profiling by quantitative targeted mass spectrometry. <i>Methods</i> , 2015, 72, 57-64.	1.9	55
108	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

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109	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
110	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
111	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
112	Overview of Peptide and Protein Analysis by Mass Spectrometry. <i>Current Protocols in Protein Science</i> , 2010, 62, Unit16.1.	2.8	44
113	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
114	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016, 15, 691-706.	1.8	44
115	A rapid triage test for active pulmonary tuberculosis in adult patients with persistent cough. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	44
116	Patterns of substrate affinity, competition, and degradation kinetics underlie biological activity of thalidomide analogs. <i>Blood</i> , 2019, 134, 160-170.	0.6	41
117	Trio Haploinsufficiency Causes Neurodevelopmental Disease-Associated Deficits. <i>Cell Reports</i> , 2019, 26, 2805-2817.e9.	2.9	39
118	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
119	Structure of PDE3A-SLFN12 complex reveals requirements for activation of SLFN12 RNase. <i>Nature Communications</i> , 2021, 12, 4375.	5.8	39
120	Genomic Profiling of Lung Adenocarcinoma in Never-Smokers. <i>Journal of Clinical Oncology</i> , 2021, 39, 3747-3758.	0.8	38
121	A framework for installable external tools in Skyline. <i>Bioinformatics</i> , 2014, 30, 2521-2523.	1.8	36
122	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
123	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
124	BRG1 Loss Predisposes Lung Cancers to Replicative Stress and ATR Dependency. <i>Cancer Research</i> , 2020, 80, 3841-3854.	0.4	32
125	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
126	Reconstituted B cell receptor signaling reveals carbohydrate-dependent mode of activation. <i>Scientific Reports</i> , 2016, 6, 36298.	1.6	29

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127	CITED4 Protects Against Adverse Remodeling in Response to Physiological and Pathological Stress. <i>Circulation Research</i> , 2020, 127, 631-646.	2.0	29
128	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
129	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
130	An Integrative Framework Reveals Signaling-to-Transcription Events in Toll-like Receptor Signaling. <i>Cell Reports</i> , 2017, 19, 2853-2866.	2.9	26
131	Dual functions of SPOP and ERG dictate androgen therapy responses in prostate cancer. <i>Nature Communications</i> , 2021, 12, 734.	5.8	26
132	Proteomic profiling reveals biomarkers and pathways in type 2 diabetes risk. <i>JCI Insight</i> , 2021, 6, .	2.3	26
133	Cell-specific transcriptional control of mitochondrial metabolism by TIF1 ^β drives erythropoiesis. <i>Science</i> , 2021, 372, 716-721.	6.0	25
134	New Techniques for Qligosaccharide Sequencing. <i>Journal of Carbohydrate Chemistry</i> , 1983, 2, 1-18.	0.4	24
135	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
136	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
137	Avant-garde: an automated data-driven DIA data curation tool. <i>Nature Methods</i> , 2020, 17, 1237-1244.	9.0	22
138	PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. <i>Nature Communications</i> , 2022, 13, 604.	5.8	22
139	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
140	Avadomide Induces Degradation of ZMYM2 Fusion Oncoproteins in Hematologic Malignancies. <i>Blood Cancer Discovery</i> , 2021, 2, 250-265.	2.6	19
141	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
142	<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
143	<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
144	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

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145	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
146	A bidirectional switch in the Shank3 phosphorylation state biases synapses toward up- or downscaling. <i>ELife</i> , 2022, 11, .	2.8	15
147	SMAC mimetics promote NIK-dependent inhibition of CD4 ⁺ T _H 17 cell differentiation. <i>Science Signaling</i> , 2019, 12, .	1.6	14
148	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. <i>Blood</i> , 2022, 139, 2534-2546.	0.6	14
149	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
150	Identification of R1OK2 as a master regulator of human blood cell development. <i>Nature Immunology</i> , 2022, 23, 109-121.	7.0	13
151	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
152	A highly multiplexed quantitative phosphosite assay for biology and preclinical studies. <i>Molecular Systems Biology</i> , 2021, 17, e10156.	3.2	12
153	Automating UbiFast for High-throughput and Multiplexed Ubiquitin Enrichment. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100154.	2.5	12
154	Blockade of IL-22 signaling reverses erythroid dysfunction in stress-induced anemias. <i>Nature Immunology</i> , 2021, 22, 520-529.	7.0	11
155	PANOPLY: a cloud-based platform for automated and reproducible proteogenomic data analysis. <i>Nature Methods</i> , 2021, 18, 580-582.	9.0	11
156	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
157	Reversal of viral and epigenetic HLA class I repression in Merkel cell carcinoma. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	10
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