D R Mani

List of Publications by Year
in descending order

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65 papers	14,230 citations	38660 50 h-index	102304 66 g-index
72 all docs	72 docs citations	72 times ranked	19369 citing authors

#	Article	IF	Citations
1	Cancer proteogenomics: current impact and future prospects. Nature Reviews Cancer, 2022, 22, 298-313.	12.8	79
2	Biomarkers to Distinguish Bacterial From Viral Pediatric Clinical Pneumonia in a Malaria-Endemic Setting. Clinical Infectious Diseases, 2021, 73, e3939-e3948.	2.9	6
3	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. Cancer Cell, 2021, 39, 361-379.e16.	7.7	189
4	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	7.7	327
5	PANOPLY: a cloud-based platform for automated and reproducible proteogenomic data analysis. Nature Methods, 2021, 18, 580-582.	9.0	11
6	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
7	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	13.5	236
8	A highly multiplexed quantitative phosphosite assay for biology and preclinical studies. Molecular Systems Biology, 2021, 17, e10156.	3.2	12
9	BRG1 Loss Predisposes Lung Cancers to Replicative Stress and ATR Dependency. Cancer Research, 2020, 80, 3841-3854.	0.4	32
10	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. Cell, 2020, 183, 1436-1456.e31.	13.5	273
11	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	13.5	177
12	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	13.5	410
13	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	13.5	296
14	Microscaled proteogenomic methods for precision oncology. Nature Communications, 2020, 11, 532.	5.8	78
15	Proteomic analyses of ECM during pancreatic ductal adenocarcinoma progression reveal different contributions by tumor and stromal cells. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19609-19618.	3.3	244
16	Streamlined Protocol for Deep Proteomic Profiling of FAC-sorted Cells and Its Application to Freshly Isolated Murine Immune Cells*. Molecular and Cellular Proteomics, 2019, 18, 995a-1009.	2.5	69
17	A Curated Resource for Phosphosite-specific Signature Analysis. Molecular and Cellular Proteomics, 2019, 18, 576-593.	2.5	197
18	Mass Spectrometryâ€“Based Proteomics Reveals Potential Roles of NEK9 and MAP2K4 in Resistance to PI3K Inhibition in Triple-Negative Breast Cancers. Cancer Research, 2018, 78, 2732-2746.	0.4	52

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19	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. Cell, 2018, 173, 90-103.e19.	13.5	296
20	Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. Cancer Cell, 2018, 34, 396-410.e8.	7.7	146
21	Crbn I391V is sufficient to confer in vivo sensitivity to thalidomide and its derivatives in mice. Blood, 2018, 132, 1535-1544.	0.6	71
22	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatographyâ€“mass spectrometry. Nature Protocols, 2018, 13, 1632-1661.	5.5	377
23	Quantitative proteomic profiling of the extracellular matrix of pancreatic islets during the angiogenic switch and insulinoma progression. Scientific Reports, 2017, 7, 40495.	1.6	88
24	New Guidelines for Publication of Manuscripts Describing Development and Application of Targeted Mass Spectrometry Measurements of Peptides and Proteins. Molecular and Cellular Proteomics, 2017, 16, 327-328.	2.5	33
25	Methods, Tools and Current Perspectives in Proteogenomics. Molecular and Cellular Proteomics, 2017, 16, 959-981.	2.5	130
26	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. Nature Communications, 2017, 8, 14864.	5.8	112
27	Proteogenomics connects somatic mutations to signalling in breast cancer. Nature, 2016, 534, 55-62.	13.7	1,384
28	Transitioning from Targeted to Comprehensive Mass Spectrometry Using Genetic Algorithms. Journal of the American Society for Mass Spectrometry, 2016, 27, 1745-1751.	1.2	2
29	Automated Microchromatography Enables Multiplexing of Immunoaffinity Enrichment of Peptides to Greater than 150 for Targeted MS-Based Assays. Analytical Chemistry, 2016, 88, 7548-7555.	3.2	44
30	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	13.5	804
31	Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays. Methods in Molecular Biology, 2016, 1410, 223-236.	0.4	33
32	Lenalidomide induces ubiquitination and degradation of CK1Î± in del(5q) MDS. Nature, 2015, 523, 183-188.	13.7	648
33	Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. Molecular and Cellular Proteomics, 2015, 14, 2357-2374.	2.5	153
34	Multiplexed, Quantitative Workflow for Sensitive Biomarker Discovery in Plasma Yields Novel Candidates for Early Myocardial Injury. Molecular and Cellular Proteomics, 2015, 14, 2375-2393.	2.5	175
35	CPTAC Assay Portal: a repository of targeted proteomic assays. Nature Methods, 2014, 11, 703-704.	9.0	150
36	Ischemia in Tumors Induces Early and Sustained Phosphorylation Changes in Stress Kinase Pathways but Does Not Affect Global Protein Levels. Molecular and Cellular Proteomics, 2014, 13, 1690-1704.	2.5	323

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37	Simplified and Efficient Quantification of Low-abundance Proteins at Very High Multiplex via Targeted Mass Spectrometry. Molecular and Cellular Proteomics, 2014, 13, 1137-1149.	2.5	63
38	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. Molecular and Cellular Proteomics, 2013, 12, 825-831.	2.5	279
39	Parallel deterministic annealing clustering and its application to LC-MS data analysis. , 2013, , .		5
40	Integrated proteomic analysis of post-translational modifications by serial enrichment. Nature Methods, 2013, 10, 634-637.	9.0	534
41	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). Molecular and Cellular Proteomics, 2013, 12, 2623-2639.	2.5	100
42	Identification of apolipoprotein D as a cardioprotective gene using a mouse model of lethal atherosclerotic coronary artery disease. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17023-17028.	3.3	52
43	Functional analysis of receptor tyrosine kinase mutations in lung cancer identifies oncogenic extracellular domain mutations of <i>ERBB2</i>. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14476-14481.	3.3	246
44	iTRAQ Labeling is Superior to mTRAQ for Quantitative Global Proteomics and Phosphoproteomics. Molecular and Cellular Proteomics, 2012, 11, M111.014423.	2.5	159
45	Methods for Quantification of in vivo Changes in Protein Ubiquitination following Proteasome and Deubiquitinase Inhibition. Molecular and Cellular Proteomics, 2012, 11, 148-159.	2.5	140
46	Statistical characterization of multiple-reaction monitoring mass spectrometry (MRM-MS) assays for quantitative proteomics. BMC Bioinformatics, 2012, 13, S9.	1.2	91
47	Interlaboratory Evaluation of Automated, Multiplexed Peptide Immunoaffinity Enrichment Coupled to Multiple Reaction Monitoring Mass Spectrometry for Quantifying Proteins in Plasma. Molecular and Cellular Proteomics, 2012, 11, M111.013854.	2.5	176
48	A pipeline that integrates the discovery and verification of plasma protein biomarkers reveals candidate markers for cardiovascular disease. Nature Biotechnology, 2011, 29, 635-643.	9.4	229
49	Clustering with position-specific constraints on variance: Applying redescending M-estimators to label-free LC-MS data analysis. BMC Bioinformatics, 2011, 12, 358.	1.2	4
50	Automated Detection of Inaccurate and Imprecise Transitions in Peptide Quantification by Multiple Reaction Monitoring Mass Spectrometry. Clinical Chemistry, 2010, 56, 291-305.	1.5	182
51	Developing Multiplexed Assays for Troponin I and Interleukin-33 in Plasma by Peptide Immunoaffinity Enrichment and Targeted Mass Spectrometry. Clinical Chemistry, 2009, 55, 1108-1117.	1.5	243
52	Quantification of Cardiovascular Biomarkers in Patient Plasma by Targeted Mass Spectrometry and Stable Isotope Dilution. Molecular and Cellular Proteomics, 2009, 8, 2339-2349.	2.5	263
53	Bead-based profiling of tyrosine kinase phosphorylation identifies SRC as a potential target for glioblastoma therapy. Nature Biotechnology, 2009, 27, 77-83.	9.4	210
54	Prediction of high-responding peptides for targeted protein assays by mass spectrometry. Nature Biotechnology, 2009, 27, 190-198.	9.4	273

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55	Multi-site assessment of the precision and reproducibility of multiple reaction monitoringâ€“based measurements of proteins in plasma. Nature Biotechnology, 2009, 27, 633-641.	9.4	958
56	Identifying the proteins to which small-molecule probes and drugs bind in cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4617-4622.	3.3	282
57	Predicting Resource Usage for Capital Efficient Marketing. , 2009, , 1558-1569.		0
58	An Assessment of Software Solutions for the Analysis of Mass Spectrometry Based Quantitative Proteomics Data. Journal of Proteome Research, 2008, 7, 51-61.	1.8	423
59	PEPPeR, a Platform for Experimental Proteomic Pattern Recognition. Molecular and Cellular Proteomics, 2006, 5, 1927-1941.	2.5	133
60	Place of Pattern in Proteomic Biomarker Discoveryâ€. Journal of Proteome Research, 2005, 4, 1143-1154.	1.8	81
61	Gene expression-based classification of malignant gliomas correlates better with survival than histological classification. Cancer Research, 2003, 63, 1602-7.	0.4	617
62	Targeting Customers with Statistical and Data-Mining Techniques. Journal of Service Research, 2001, 3, 205-219.	7.8	52
63	Automated Cellular Modeling and Prediction on a Large Scale. Artificial Intelligence Review, 2000, 14, 485-502.	9.7	59
64	CHAMP: A Prototype for Automated Cellular Churn Prediction. Data Mining and Knowledge Discovery, 1999, 3, 219-225.	2.4	27
65	Reflexive Reasoning with Multiple Instantiation in a Connectionist Reasoning System with a Type Hierarchy. Connection Science, 1993, 5, 205-242.	1.8	34