

D R Mani

List of Publications by Year in descending order

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Version: 2024-02-01

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	Proteogenomics connects somatic mutations to signalling in breast cancer. <i>Nature</i> , 2016, 534, 55-62.	13.7	1,384
2	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
3	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	13.5	804
4	Lenalidomide induces ubiquitination and degradation of CK1 δ in del(5q) MDS. <i>Nature</i> , 2015, 523, 183-188.	13.7	648
5	Gene expression-based classification of malignant gliomas correlates better with survival than histological classification. <i>Cancer Research</i> , 2003, 63, 1602-7.	0.4	617
6	Integrated proteomic analysis of post-translational modifications by serial enrichment. <i>Nature Methods</i> , 2013, 10, 634-637.	9.0	534
7	An Assessment of Software Solutions for the Analysis of Mass Spectrometry Based Quantitative Proteomics Data. <i>Journal of Proteome Research</i> , 2008, 7, 51-61.	1.8	423
8	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	13.5	410
9	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
10	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	7.7	327
11	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
12	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018, 173, 90-103.e19.	13.5	296
13	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	13.5	296
14	Identifying the proteins to which small-molecule probes and drugs bind in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4617-4622.	3.3	282
15	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
16	Prediction of high-responding peptides for targeted protein assays by mass spectrometry. <i>Nature Biotechnology</i> , 2009, 27, 190-198.	9.4	273
17	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273
18	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

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19	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
20	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
21	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
22	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	13.5	236
23	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
24	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
25	A Curated Resource for Phosphosite-specific Signature Analysis. Molecular and Cellular Proteomics, 2019, 18, 576-593.	2.5	197
26	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
27	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
28	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	13.5	177
29	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, M1111.013854.	2.5	176
30	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
31	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
32	iTRAQ Labeling is Superior to mTRAQ for Quantitative Global Proteomics and Phosphoproteomics. Molecular and Cellular Proteomics, 2012, 11, M1111.014423.	2.5	159
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	CPTAC Assay Portal: a repository of targeted proteomic assays. Nature Methods, 2014, 11, 703-704.	9.0	150
35	Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. Cancer Cell, 2018, 34, 396-410.e8.	7.7	146
36	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

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37	PEPPeR, a Platform for Experimental Proteomic Pattern Recognition. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1927-1941.	2.5	133
38	Methods, Tools and Current Perspectives in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 959-981.	2.5	130
39	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. <i>Nature Communications</i> , 2017, 8, 14864.	5.8	112
40	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
41	Statistical characterization of multiple-reaction monitoring mass spectrometry (MRM-MS) assays for quantitative proteomics. <i>BMC Bioinformatics</i> , 2012, 13, S9.	1.2	91
42	Quantitative proteomic profiling of the extracellular matrix of pancreatic islets during the angiogenic switch and insulinoma progression. <i>Scientific Reports</i> , 2017, 7, 40495.	1.6	88
43	Place of Pattern in Proteomic Biomarker Discovery. <i>Journal of Proteome Research</i> , 2005, 4, 1143-1154.	1.8	81
44	Cancer proteogenomics: current impact and future prospects. <i>Nature Reviews Cancer</i> , 2022, 22, 298-313.	12.8	79
45	Microscaled proteogenomic methods for precision oncology. <i>Nature Communications</i> , 2020, 11, 532.	5.8	78
46	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
47	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
48	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
49	Automated Cellular Modeling and Prediction on a Large Scale. <i>Artificial Intelligence Review</i> , 2000, 14, 485-502.	9.7	59
50	Targeting Customers with Statistical and Data-Mining Techniques. <i>Journal of Service Research</i> , 2001, 3, 205-219.	7.8	52
51	Identification of apolipoprotein D as a cardioprotective gene using a mouse model of lethal atherosclerotic coronary artery disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17023-17028.	3.3	52
52	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
53	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
54	Reflexive Reasoning with Multiple Instantiation in a Connectionist Reasoning System with a Type Hierarchy. <i>Connection Science</i> , 1993, 5, 205-242.	1.8	34

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55	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
56	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
57	BRG1 Loss Predisposes Lung Cancers to Replicative Stress and ATR Dependency. <i>Cancer Research</i> , 2020, 80, 3841-3854.	0.4	32
58	CHAMP: A Prototype for Automated Cellular Churn Prediction. <i>Data Mining and Knowledge Discovery</i> , 1999, 3, 219-225.	2.4	27
59	A highly multiplexed quantitative phosphosite assay for biology and preclinical studies. <i>Molecular Systems Biology</i> , 2021, 17, e10156.	3.2	12
60	PANOPLY: a cloud-based platform for automated and reproducible proteogenomic data analysis. <i>Nature Methods</i> , 2021, 18, 580-582.	9.0	11
61	Biomarkers to Distinguish Bacterial From Viral Pediatric Clinical Pneumonia in a Malaria-Endemic Setting. <i>Clinical Infectious Diseases</i> , 2021, 73, e3939-e3948.	2.9	6
62	Parallel deterministic annealing clustering and its application to LC-MS data analysis. , 2013, , .		5
63	Clustering with position-specific constraints on variance: Applying redescending M-estimators to label-free LC-MS data analysis. <i>BMC Bioinformatics</i> , 2011, 12, 358.	1.2	4
64	Transitioning from Targeted to Comprehensive Mass Spectrometry Using Genetic Algorithms. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1745-1751.	1.2	2
65	Predicting Resource Usage for Capital Efficient Marketing. , 2009, , 1558-1569.		0