

D R Mani

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

14,230
citations

38742

50
h-index

102487

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. <i>Nature Reviews Cancer</i> , 2022, 22, 298-313.	28.4	79
2	Biomarkers to Distinguish Bacterial From Viral Pediatric Clinical Pneumonia in a Malaria-Endemic Setting. <i>Clinical Infectious Diseases</i> , 2021, 73, e3939-e3948.	5.8	6
3	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.	16.8	189
4	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	16.8	327
5	PANOPLY: a cloud-based platform for automated and reproducible proteogenomic data analysis. <i>Nature Methods</i> , 2021, 18, 580-582.	19.0	11
6	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	28.9	170
7	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
8	A highly multiplexed quantitative phosphosite assay for biology and preclinical studies. <i>Molecular Systems Biology</i> , 2021, 17, e10156.	7.2	12
9	BRG1 Loss Predisposes Lung Cancers to Replicative Stress and ATR Dependency. <i>Cancer Research</i> , 2020, 80, 3841-3854.	0.9	32
10	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
11	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	28.9	177
12	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	28.9	410
13	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
14	Microscaled proteogenomic methods for precision oncology. <i>Nature Communications</i> , 2020, 11, 532.	12.8	78
15	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.	7.1	244
16	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.	3.8	69
17	A Curated Resource for Phosphosite-specific Signature Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 576-593.	3.8	197
18	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.	0.9	52

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19	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018, 173, 90-103.e19.	28.9	296
20	Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2018, 34, 396-410.e8.	16.8	146
21	Crbn I391V is sufficient to confer in vivo sensitivity to thalidomide and its derivatives in mice. <i>Blood</i> , 2018, 132, 1535-1544.	1.4	71
22	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.	12.0	377
23	Quantitative proteomic profiling of the extracellular matrix of pancreatic islets during the angiogenic switch and insulinoma progression. <i>Scientific Reports</i> , 2017, 7, 40495.	3.3	88
24	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.	3.8	33
25	Methods, Tools and Current Perspectives in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 959-981.	3.8	130
26	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. <i>Nature Communications</i> , 2017, 8, 14864.	12.8	112
27	Proteogenomics connects somatic mutations to signalling in breast cancer. <i>Nature</i> , 2016, 534, 55-62.	27.8	1,384
28	Transitioning from Targeted to Comprehensive Mass Spectrometry Using Genetic Algorithms. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1745-1751.	2.8	2
29	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.	6.5	44
30	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
31	Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays. <i>Methods in Molecular Biology</i> , 2016, 1410, 223-236.	0.9	33
32	Lenalidomide induces ubiquitination and degradation of CK1 δ in del(5q) MDS. <i>Nature</i> , 2015, 523, 183-188.	27.8	648
33	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.	3.8	153
34	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.	3.8	175
35	CPTAC Assay Portal: a repository of targeted proteomic assays. <i>Nature Methods</i> , 2014, 11, 703-704.	19.0	150
36	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.	3.8	323

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37	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.	3.8	63
38	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.	3.8	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. <i>Nature Methods</i> , 2013, 10, 634-637.	19.0	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). <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2623-2639.	3.8	100
42	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.	7.1	52
43	Functional analysis of receptor tyrosine kinase mutations in lung cancer identifies oncogenic extracellular domain mutations of <i>ERBB2</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14476-14481.	7.1	246
44	iTRAQ Labeling is Superior to mTRAQ for Quantitative Global Proteomics and Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014423.	3.8	159
45	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.	3.8	140
46	Statistical characterization of multiple-reaction monitoring mass spectrometry (MRM-MS) assays for quantitative proteomics. <i>BMC Bioinformatics</i> , 2012, 13, S9.	2.6	91
47	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.	3.8	176
48	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.	17.5	229
49	Clustering with position-specific constraints on variance: Applying re-descending M-estimators to label-free LC-MS data analysis. <i>BMC Bioinformatics</i> , 2011, 12, 358.	2.6	4
50	Automated Detection of Inaccurate and Imprecise Transitions in Peptide Quantification by Multiple Reaction Monitoring Mass Spectrometry. <i>Clinical Chemistry</i> , 2010, 56, 291-305.	3.2	182
51	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.	3.2	243
52	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.	3.8	263
53	Bead-based profiling of tyrosine kinase phosphorylation identifies SRC as a potential target for glioblastoma therapy. <i>Nature Biotechnology</i> , 2009, 27, 77-83.	17.5	210
54	Prediction of high-responding peptides for targeted protein assays by mass spectrometry. <i>Nature Biotechnology</i> , 2009, 27, 190-198.	17.5	273

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55	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.	17.5	958
56	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.	7.1	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. <i>Journal of Proteome Research</i> , 2008, 7, 51-61.	3.7	423
59	PEPPER, a Platform for Experimental Proteomic Pattern Recognition. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1927-1941.	3.8	133
60	Place of Pattern in Proteomic Biomarker Discovery. <i>Journal of Proteome Research</i> , 2005, 4, 1143-1154.	3.7	81
61	Gene expression-based classification of malignant gliomas correlates better with survival than histological classification. <i>Cancer Research</i> , 2003, 63, 1602-7.	0.9	617
62	Targeting Customers with Statistical and Data-Mining Techniques. <i>Journal of Service Research</i> , 2001, 3, 205-219.	12.2	52
63	Automated Cellular Modeling and Prediction on a Large Scale. <i>Artificial Intelligence Review</i> , 2000, 14, 485-502.	15.7	59
64	CHAMP: A Prototype for Automated Cellular Churn Prediction. <i>Data Mining and Knowledge Discovery</i> , 1999, 3, 219-225.	3.7	27
65	Reflexive Reasoning with Multiple Instantiation in a Connectionist Reasoning System with a Type Hierarchy. <i>Connection Science</i> , 1993, 5, 205-242.	3.0	34