

Amanda G Paulovich

List of Publications by Year in descending order

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83
papers

52,548
citations

43973

48
h-index

53109

85
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87
all docs

87
docs citations

87
times ranked

87771
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15545-15550.	3.3	38,922
2	Proteogenomics connects somatic mutations to signalling in breast cancer. <i>Nature</i> , 2016, 534, 55-62.	13.7	1,384
3	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
4	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	13.5	804
5	When Checkpoints Fail. <i>Cell</i> , 1997, 88, 315-321.	13.5	589
6	A checkpoint regulates the rate of progression through S phase in <i>S. cerevisiae</i> in Response to DNA damage. <i>Cell</i> , 1995, 82, 841-847.	13.5	577
7	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
8	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	13.5	430
9	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	13.5	410
10	A targeted proteomics-based pipeline for verification of biomarkers in plasma. <i>Nature Biotechnology</i> , 2011, 29, 625-634.	9.4	336
11	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	7.7	327
12	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
13	Phosphoproteomic analysis of chimeric antigen receptor signaling reveals kinetic and quantitative differences that affect cell function. <i>Science Signaling</i> , 2018, 11, .	1.6	323
14	An Automated and Multiplexed Method for High Throughput Peptide Immunoaffinity Enrichment and Multiple Reaction Monitoring Mass Spectrometry-based Quantification of Protein Biomarkers. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 184-196.	2.5	308
15	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	13.5	296
16	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	13.5	273
17	Antibody-based enrichment of peptides on magnetic beads for mass-spectrometry-based quantification of serum biomarkers. <i>Analytical Biochemistry</i> , 2007, 362, 44-54.	1.1	259
18	Connecting Genomic Alterations to Cancer Biology with Proteomics: The NCI Clinical Proteomic Tumor Analysis Consortium. <i>Cancer Discovery</i> , 2013, 3, 1108-1112.	7.7	243

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19	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
20	Panorama: A Targeted Proteomics Knowledge Base. <i>Journal of Proteome Research</i> , 2014, 13, 4205-4210.	1.8	205
21	Computational Proteomics Analysis System (CPAS): An Extensible, Open-Source Analytic System for Evaluating and Publishing Proteomic Data and High Throughput Biological Experiments. <i>Journal of Proteome Research</i> , 2006, 5, 112-121.	1.8	204
22	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
23	A Human Proteome Detection and Quantitation Project. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 883-886.	2.5	186
24	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
25	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	13.5	177
26	Cancer biomarkers: a systems approach. <i>Nature Biotechnology</i> , 2006, 24, 905-908.	9.4	176
27	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
28	Integrated Pipeline for Mass Spectrometry-Based Discovery and Confirmation of Biomarkers Demonstrated in a Mouse Model of Breast Cancer. <i>Journal of Proteome Research</i> , 2007, 6, 3962-3975.	1.8	171
29	Performance Metrics for Liquid Chromatography-Tandem Mass Spectrometry Systems in Proteomics Analyses. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 225-241.	2.5	167
30	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
31	Head-to-Head Comparison of Serum Fractionation Techniques. <i>Journal of Proteome Research</i> , 2007, 6, 828-836.	1.8	152
32	CPTAC Assay Portal: a repository of targeted proteomic assays. <i>Nature Methods</i> , 2014, 11, 703-704.	9.0	150
33	Clinical potential of mass spectrometry-based proteogenomics. <i>Nature Reviews Clinical Oncology</i> , 2019, 16, 256-268.	12.5	149
34	Interlaboratory Study Characterizing a Yeast Performance Standard for Benchmarking LC-MS Platform Performance. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 242-254.	2.5	148
35	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
36	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 121-134.	2.5	111

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37	Signal Maps for Mass Spectrometry-based Comparative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 423-432.	2.5	110
38	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015, 12, 725-731.	9.0	109
39	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
40	A Platform for Accurate Mass and Time Analyses of Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2007, 6, 2685-2694.	1.8	76
41	Comparative analysis of TCR and CAR signaling informs CAR designs with superior antigen sensitivity and in vivo function. <i>Science Signaling</i> , 2021, 14, .	1.6	67
42	The evolving role of mass spectrometry in cancer biomarker discovery. <i>Cancer Biology and Therapy</i> , 2009, 8, 1083-1094.	1.5	66
43	Sequential Multiplexed Analyte Quantification Using Peptide Immunoaffinity Enrichment Coupled to Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015347.	2.5	66
44	Peptide Immunoaffinity Enrichment and Targeted Mass Spectrometry Enables Multiplex, Quantitative Pharmacodynamic Studies of Phospho-Signaling. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2261-2273.	2.5	56
45	Automated screening of monoclonal antibodies for SISCAPA assays using a magnetic bead processor and liquid chromatography-selected reaction monitoring-mass spectrometry. <i>Journal of Immunological Methods</i> , 2010, 353, 49-61.	0.6	55
46	Assessing Bias in Experiment Design for Large Scale Mass Spectrometry-based Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1741-1748.	2.5	52
47	Quantification of ATP7B Protein in Dried Blood Spots by Peptide Immuno-SRM as a Potential Screen for Wilson's Disease. <i>Journal of Proteome Research</i> , 2017, 16, 862-871.	1.8	49
48	Immobilized Metal Affinity Chromatography Coupled to Multiple Reaction Monitoring Enables Reproducible Quantification of Phospho-signaling. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 726-739.	2.5	46
49	Multiplexed quantification of estrogen receptor and HER2/Neu in tissue and cell lysates by peptide immunoaffinity enrichment mass spectrometry. <i>Proteomics</i> , 2012, 12, 1253-1260.	1.3	45
50	Normalization regarding non-random missing values in high-throughput mass spectrometry data. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 315-26.	0.7	45
51	Rapid Multiplexed Proteomic Screening for Primary Immunodeficiency Disorders From Dried Blood Spots. <i>Frontiers in Immunology</i> , 2018, 9, 2756.	2.2	43
52	Peptide Immunoaffinity Enrichment Coupled with Mass Spectrometry for Peptide and Protein Quantification. <i>Clinics in Laboratory Medicine</i> , 2011, 31, 385-396.	0.7	42
53	The Preference for Error-Free or Error-Prone Postreplication Repair in <i>Saccharomyces cerevisiae</i> Exposed to Low-Dose Methyl Methanesulfonate Is Cell Cycle Dependent. <i>Molecular and Cellular Biology</i> , 2013, 33, 1515-1527.	1.1	42
54	High-Affinity Recombinant Antibody Fragments (Fabs) Can Be Applied in Peptide Enrichment Immuno-MRM Assays. <i>Journal of Proteome Research</i> , 2014, 13, 2187-2196.	1.8	42

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55	Optimized Protocol for Quantitative Multiple Reaction Monitoring-Based Proteomic Analysis of Formalin-Fixed, Paraffin-Embedded Tissues. <i>Journal of Proteome Research</i> , 2016, 15, 2717-2728.	1.8	42
56	A highly annotated database of genes associated with platinum resistance in cancer. <i>Oncogene</i> , 2021, 40, 6395-6405.	2.6	41
57	Loss of TGF β signaling increases alternative end-joining DNA repair that sensitizes to genotoxic therapies across cancer types. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	33
58	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
59	Quality Control Metrics for LC-MS Feature Detection Tools Demonstrated on <i>Saccharomyces cerevisiae</i> Proteomic Profiles. <i>Journal of Proteome Research</i> , 2006, 5, 1527-1534.	1.8	31
60	Anti-Peptide Monoclonal Antibodies Generated for Immuno-Multiple Reaction Monitoring-Mass Spectrometry Assays Have a High Probability of Supporting Western blot and ELISA. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 382-398.	2.5	31
61	Quantification of Human Epidermal Growth Factor Receptor 2 by Immunopeptide Enrichment and Targeted Mass Spectrometry in Formalin-Fixed Paraffin-Embedded and Frozen Breast Cancer Tissues. <i>Clinical Chemistry</i> , 2021, 67, 1008-1018.	1.5	29
62	pRAD50: a novel and clinically applicable pharmacodynamic biomarker of both ATM and ATR inhibition identified using mass spectrometry and immunohistochemistry. <i>British Journal of Cancer</i> , 2018, 119, 1233-1243.	2.9	27
63	Multimic analysis identifies CPT1A as a potential therapeutic target in platinum-refractory, high-grade serous ovarian cancer. <i>Cell Reports Medicine</i> , 2021, 2, 100471.	3.3	26
64	A Multiplexed Mass Spectrometry-Based Assay for Robust Quantification of Phosphosignaling in Response to DNA Damage. <i>Radiation Research</i> , 2018, 189, 505.	0.7	25
65	Multiplexed Proteomic Analysis for Diagnosis and Screening of Five Primary Immunodeficiency Disorders From Dried Blood Spots. <i>Frontiers in Immunology</i> , 2020, 11, 464.	2.2	24
66	Quantification of Proteins Using Peptide Immunoaffinity Enrichment Coupled with Mass Spectrometry. <i>Journal of Visualized Experiments</i> , 2011, , .	0.2	22
67	The <i>Saccharomyces cerevisiae</i> RAD9, RAD17 and RAD24 genes are required for suppression of mutagenic post-replicative repair during chronic DNA damage. <i>DNA Repair</i> , 2010, 9, 824-834.	1.3	20
68	Lymphatic Endothelial Murine Chloride Channel Calcium-Activated 1 Is a Ligand for Leukocyte LFA-1 and Mac-1. <i>Journal of Immunology</i> , 2010, 185, 5769-5777.	0.4	20
69	Targeted mass spectrometry enables robust quantification of FANCD2 mono-ubiquitination in response to DNA damage. <i>DNA Repair</i> , 2018, 65, 47-53.	1.3	18
70	Commercially available antibodies can be applied in quantitative multiplexed peptide immunoaffinity enrichment targeted mass spectrometry assays. <i>Proteomics</i> , 2016, 16, 2141-2145.	1.3	17
71	Antibody-Coupled Magnetic Beads Can Be Reused in Immuno-MRM Assays To Reduce Cost and Extend Antibody Supply. <i>Journal of Proteome Research</i> , 2015, 14, 4425-4431.	1.8	16
72	Peptide Immunoaffinity Enrichment with Targeted Mass Spectrometry: Application to Quantification of ATM Kinase Phospho-Signaling. <i>Methods in Molecular Biology</i> , 2017, 1599, 197-213.	0.4	15

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73	Targeted Mass Spectrometry Enables Multiplexed Quantification of Immunomodulatory Proteins in Clinical Biospecimens. <i>Frontiers in Immunology</i> , 2021, 12, 765898.	2.2	13
74	Internal Standard Triggered-Parallel Reaction Monitoring Mass Spectrometry Enables Multiplexed Quantification of Candidate Biomarkers in Plasma. <i>Analytical Chemistry</i> , 2022, 94, 9540-9547.	3.2	11
75	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
76	Novel Connections Between DNA Replication, Telomere Homeostasis, and the DNA Damage Response Revealed by a Genome-Wide Screen for TEL1/ATM Interactions in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013, 193, 1117-1133.	1.2	8
77	Quantifying the human proteome. <i>Nature Biotechnology</i> , 2016, 34, 1033-1034.	9.4	8
78	Targeted Mass Spectrometry Enables Quantification of Novel Pharmacodynamic Biomarkers of ATM Kinase Inhibition. <i>Cancers</i> , 2021, 13, 3843.	1.7	7
79	Integrative Proteo-genomic Analysis to Construct CNA-protein Regulatory Map in Breast and Ovarian Tumors. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S66-S81.	2.5	6
80	A dataset describing a suite of novel antibody reagents for the RAS signaling network. <i>Scientific Data</i> , 2019, 6, 160.	2.4	4
81	Quantification of Estrogen Receptor, Progesterone Receptor, and Human Epidermal Growth Factor Receptor 2 Protein Expression in Bone Biopsies by Targeted Mass Spectrometry without Acid Decalcification. <i>Clinical Chemistry</i> , 2020, 66, 1459-1461.	1.5	3
82	DNA Replication Stress Phosphoproteome Profiles Reveal Novel Functional Phosphorylation Sites on Xrs2 in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 203, 353-368.	1.2	2
83	Proteogenomic Characterization of Highly Enriched Viable Leukemic Blasts in Acute Myeloid Leukemia: A SWOG Report. <i>Blood</i> , 2021, 138, 522-522.	0.6	0