

Amanda G Paulovich

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

81
papers

34,395
citations

45
h-index

87
g-index

87
ext. papers

45,437
ext. citations

14.3
avg, IF

6.34
L-index

#	Paper	IF	Citations
81	Targeted Mass Spectrometry Enables Multiplexed Quantification of Immunomodulatory Proteins in Clinical Biospecimens. <i>Frontiers in Immunology</i> , 2021 , 12, 765898	8.4	3
80	Proteogenomic Characterization of Highly Enriched Viable Leukemic Blasts in Acute Myeloid Leukemia: A SWOG Report. <i>Blood</i> , 2021 , 138, 522-522	2.2	
79	A highly annotated database of genes associated with platinum resistance in cancer. <i>Oncogene</i> , 2021 , 40, 6395-6405	9.2	4
78	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021 , 39, 509-528.e30	14.3	71
77	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	5.5	3
76	Targeted mass spectrometry-based assays enable multiplex quantification of receptor tyrosine kinase, MAP Kinase, and AKT signaling. <i>Cell Reports Methods</i> , 2021 , 1,		4
75	Loss of TGFβ signaling increases alternative end-joining DNA repair that sensitizes to genotoxic therapies across cancer types. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	8
74	Comparative analysis of TCR and CAR signaling informs CAR designs with superior antigen sensitivity and in vivo function. <i>Science Signaling</i> , 2021 , 14,	8.8	11
73	Multomic analysis identifies CPT1A as a potential therapeutic target in platinum-refractory, high-grade serous ovarian cancer.. <i>Cell Reports Medicine</i> , 2021 , 2, 100471	18	2
72	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020 , 182, 200-225.e35	56.2	139
71	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020 , 180, 729-748.e26	56.2	122
70	Multiplexed Proteomic Analysis for Diagnosis and Screening of Five Primary Immunodeficiency Disorders From Dried Blood Spots. <i>Frontiers in Immunology</i> , 2020 , 11, 464	8.4	15
69	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020 , 183, 1436-1456.e31	56.2	71
68	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020 , 183, 1962-1985.e31	56.2	45
67	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	5.5	2
66	A dataset describing a suite of novel antibody reagents for the RAS signaling network. <i>Scientific Data</i> , 2019 , 6, 160	8.2	3
65	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	7.6	2

64	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019 , 179, 964-983. DOI	53.1	173
63	Clinical potential of mass spectrometry-based proteogenomics. <i>Nature Reviews Clinical Oncology</i> , 2019 , 16, 256-268	19.4	89
62	A Multiplexed Mass Spectrometry-Based Assay for Robust Quantification of Phosphosignaling in Response to DNA Damage. <i>Radiation Research</i> , 2018 , 189, 505-518	3.1	15
61	Targeted mass spectrometry enables robust quantification of FANCD2 mono-ubiquitination in response to DNA damage. <i>DNA Repair</i> , 2018 , 65, 47-53	4.3	8
60	Phosphoproteomic analysis of chimeric antigen receptor signaling reveals kinetic and quantitative differences that affect cell function. <i>Science Signaling</i> , 2018 , 11,	8.8	192
59	Rapid Multiplexed Proteomic Screening for Primary Immunodeficiency Disorders From Dried Blood Spots. <i>Frontiers in Immunology</i> , 2018 , 9, 2756	8.4	15
58	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	8.7	16
57	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	1.4	8
56	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	5.6	31
55	Proteome Profiling Outperforms Transcriptome Profiling for Coexpression Based Gene Function Prediction. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 121-134	7.6	67
54	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016 , 166, 755-765	56.2	544
53	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry-Based Assays. <i>Clinical Chemistry</i> , 2016 , 62, 48-69	5.5	135
52	Immobilized Metal Affinity Chromatography Coupled to Multiple Reaction Monitoring Enables Reproducible Quantification of Phospho-signaling. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 726-39	7.6	40
51	Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays. <i>Methods in Molecular Biology</i> , 2016 , 1410, 223-36	1.4	25
50	Commercially available antibodies can be applied in quantitative multiplexed peptide immunoaffinity enrichment targeted mass spectrometry assays. <i>Proteomics</i> , 2016 , 16, 2141-5	4.8	15
49	DNA Replication Stress Phosphoproteome Profiles Reveal Novel Functional Phosphorylation Sites on Xrs2 in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016 , 203, 353-68	4	2
48	Proteogenomics connects somatic mutations to signalling in breast cancer. <i>Nature</i> , 2016 , 534, 55-62	50.4	938
47	Quantifying the human proteome. <i>Nature Biotechnology</i> , 2016 , 34, 1033-1034	44.5	7

46	Optimized Protocol for Quantitative Multiple Reaction Monitoring-Based Proteomic Analysis of Formalin-Fixed, Paraffin-Embedded Tissues. <i>Journal of Proteome Research</i> , 2016 , 15, 2717-28	5.6	35
45	Peptide Immunoaffinity Enrichment and Targeted Mass Spectrometry Enables Multiplex, Quantitative Pharmacodynamic Studies of Phospho-Signaling. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2261-73	7.6	49
44	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, 2357-74	7.6	135
43	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015 , 12, 725-31	21.6	86
42	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, 4425-31	5.6	15
41	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, 382-98	7.6	29
40	Demonstrating the feasibility of large-scale development of standardized assays to quantify human proteins. <i>Nature Methods</i> , 2014 , 11, 149-55	21.6	145
39	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, 1690-704	7.6	239
38	Panorama: a targeted proteomics knowledge base. <i>Journal of Proteome Research</i> , 2014 , 13, 4205-10	5.6	149
37	High-affinity recombinant antibody fragments (Fabs) can be applied in peptide enrichment immuno-MRM assays. <i>Journal of Proteome Research</i> , 2014 , 13, 2187-96	5.6	30
36	CPTAC Assay Portal: a repository of targeted proteomic assays. <i>Nature Methods</i> , 2014 , 11, 703-4	21.6	113
35	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, 1117-33	4	8
34	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, 2623-39	7.6	87
33	Connecting genomic alterations to cancer biology with proteomics: the NCI Clinical Proteomic Tumor Analysis Consortium. <i>Cancer Discovery</i> , 2013 , 3, 1108-12	24.4	162
32	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, 1515-27	4.8	39
31	Multiplexed quantification of estrogen receptor and HER2/Neu in tissue and cell lysates by peptide immunoaffinity enrichment mass spectrometry. <i>Proteomics</i> , 2012 , 12, 1253-60	4.8	41
30	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	7.6	153
29	Sequential multiplexed analyte quantification using peptide immunoaffinity enrichment coupled to mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.015347	7.6	48

28	Quantification of proteins using peptide immunoaffinity enrichment coupled with mass spectrometry. <i>Journal of Visualized Experiments</i> , 2011 ,	1.6	16
27	A targeted proteomics-based pipeline for verification of biomarkers in plasma. <i>Nature Biotechnology</i> , 2011 , 29, 625-34	44.5	290
26	Peptide immunoaffinity enrichment coupled with mass spectrometry for peptide and protein quantification. <i>Clinics in Laboratory Medicine</i> , 2011 , 31, 385-96	2.1	38
25	Evaluation of large scale quantitative proteomic assay development using peptide affinity-based mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.005645	7.6	118
24	Interlaboratory study characterizing a yeast performance standard for benchmarking LC-MS platform performance. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 242-54	7.6	130
23	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, 184-96	7.6	276
22	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, 5769-77	5.3	18
21	Effect of collision energy optimization on the measurement of peptides by selected reaction monitoring (SRM) mass spectrometry. <i>Analytical Chemistry</i> , 2010 , 82, 10116-24	7.8	176
20	Repeatability and reproducibility in proteomic identifications by liquid chromatography-tandem mass spectrometry. <i>Journal of Proteome Research</i> , 2010 , 9, 761-76	5.6	377
19	Performance metrics for liquid chromatography-tandem mass spectrometry systems in proteomics analyses. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 225-41	7.6	147
18	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	2.5	48
17	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, 824-34	4.3	17
16	The evolving role of mass spectrometry in cancer biomarker discovery. <i>Cancer Biology and Therapy</i> , 2009 , 8, 1083-94	4.6	60
15	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. <i>Nature Biotechnology</i> , 2009 , 27, 633-41	44.5	859
14	A human proteome detection and quantitation project. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 883-67.6		167
13	A platform for accurate mass and time analyses of mass spectrometry data. <i>Journal of Proteome Research</i> , 2007 , 6, 2685-94	5.6	72
12	Antibody-based enrichment of peptides on magnetic beads for mass-spectrometry-based quantification of serum biomarkers. <i>Analytical Biochemistry</i> , 2007 , 362, 44-54	3.1	234
11	Head-to-head comparison of serum fractionation techniques. <i>Journal of Proteome Research</i> , 2007 , 6, 828-36	5.6	144

10	Assessing bias in experiment design for large scale mass spectrometry-based quantitative proteomics. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1741-8	7.6	44
9	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, 3962-75	5.6	156
8	Signal maps for mass spectrometry-based comparative proteomics. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 423-32	7.6	96
7	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, 112-21	5.6	183
6	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, 1527-34	5.6	27
5	Cancer biomarkers: a systems approach. <i>Nature Biotechnology</i> , 2006 , 24, 905-8	44.5	153
4	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	1.3	42
3	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, 15545-50	11.5	24578
2	When checkpoints fail. <i>Cell</i> , 1997 , 88, 315-21	56.2	535
1	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, 841-7	56.2	525