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List of Publications by Year in descending order

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41
papers

5,436
citations

186209

28
h-index

276775

41
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all docs

42
docs citations

42
times ranked

7295
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Loss of TGF β 2 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
3	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
4	Targeted Mass Spectrometry Enables Quantification of Novel Pharmacodynamic Biomarkers of ATM Kinase Inhibition. <i>Cancers</i> , 2021, 13, 3843.	1.7	7
5	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
6	Targeted Mass Spectrometry Enables Multiplexed Quantification of Immunomodulatory Proteins in Clinical Biospecimens. <i>Frontiers in Immunology</i> , 2021, 12, 765898.	2.2	13
7	Multiomic 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
8	A dataset describing a suite of novel antibody reagents for the RAS signaling network. <i>Scientific Data</i> , 2019, 6, 160.	2.4	4
9	Clinical potential of mass spectrometry-based proteogenomics. <i>Nature Reviews Clinical Oncology</i> , 2019, 16, 256-268.	12.5	149
10	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
11	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
12	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
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	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
15	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
16	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
17	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
18	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	13.5	804

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19	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometryâ€”Based Assays. <i>Clinical Chemistry</i> , 2016, 62, 48-69.	1.5	187
20	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
21	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
22	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
23	CPTAC Assay Portal: a repository of targeted proteomic assays. <i>Nature Methods</i> , 2014, 11, 703-704.	9.0	150
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	Panorama: A Targeted Proteomics Knowledge Base. <i>Journal of Proteome Research</i> , 2014, 13, 4205-4210.	1.8	205
26	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
27	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
28	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
29	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
30	A targeted proteomicsâ€”based pipeline for verification of biomarkers in plasma. <i>Nature Biotechnology</i> , 2011, 29, 625-634.	9.4	336
31	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
32	Quantification of Proteins Using Peptide Immunoaffinity Enrichment Coupled with Mass Spectrometry. <i>Journal of Visualized Experiments</i> , 2011, , .	0.2	22
33	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
34	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
35	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
36	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

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37	The evolving role of mass spectrometry in cancer biomarker discovery. <i>Cancer Biology and Therapy</i> , 2009, 8, 1083-1094.	1.5	66
38	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
39	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
40	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
41	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