Brendan Maclean

List of Publications by Year in descending order

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36 papers	12,956 citations	136950 32 h-index	330143 37 g-index
38 all docs	38 docs citations	38 times ranked	20029 citing authors

#	Article	IF	Citations
1	The ProteomeXchange consortium in 2020: enabling â€˜big dataâ€™ approaches in proteomics. Nucleic Acids Research, 2020, 48, D1145-D1152.	14.5	491
2	The Skyline ecosystem: Informatics for quantitative mass spectrometry proteomics. Mass Spectrometry Reviews, 2020, 39, 229-244.	5.4	469
3	Avant-garde: an automated data-driven DIA data curation tool. Nature Methods, 2020, 17, 1237-1244.	19.0	22
4	LipidCreator workbench to probe the lipidomic landscape. Nature Communications, 2020, 11, 2057.	12.8	58
5	Panorama Public: A Public Repository for Quantitative Data Sets Processed in Skyline. Molecular and Cellular Proteomics, 2018, 17, 1239-1244.	3.8	177
6	Skyline Performs as Well as Vendor Software in the Quantitative Analysis of Serum 25-Hydroxy Vitamin D and Vitamin D Binding Globulin. Clinical Chemistry, 2018, 64, 408-410.	3.2	42
7	New Guidelines for Publication of Manuscripts Describing Development and Application of Targeted Mass Spectrometry Measurements of Peptides and Proteins. Molecular and Cellular Proteomics, 2017, 16, 327-328.	3.8	33
8	MSstatsQC: Longitudinal System Suitability Monitoring and Quality Control for Targeted Proteomic Experiments. Molecular and Cellular Proteomics, 2017, 16, 1335-1347.	3.8	21
9	ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of Differentially Abundant Proteins in Label-Free Quantitative LCâ€“MS/MS Experiments. Journal of Proteome Research, 2017, 16, 945-957.	3.7	42
10	An Automated Pipeline to Monitor System Performance in Liquid Chromatographyâ€“Tandem Mass Spectrometry Proteomic Experiments. Journal of Proteome Research, 2016, 15, 4763-4769.	3.7	56
11	A multicenter study benchmarks software tools for label-free proteome quantification. Nature Biotechnology, 2016, 34, 1130-1136.	17.5	321
12	Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays. Methods in Molecular Biology, 2016, 1410, 223-236.	0.9	33
13	Multiplexed peptide analysis using data-independent acquisition and Skyline. Nature Protocols, 2015, 10, 887-903.	12.0	174
14	Building high-quality assay libraries for targeted analysis of SWATH MS data. Nature Protocols, 2015, 10, 426-441.	12.0	319
15	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.	3.8	153
16	Multiplexed, Scheduled, High-Resolution Parallel Reaction Monitoring on a Full Scan QqTOF Instrument with Integrated Data-Dependent and Targeted Mass Spectrometric Workflows. Analytical Chemistry, 2015, 87, 10222-10229.	6.5	88
17	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. Molecular and Cellular Proteomics, 2015, 14, 2301-2307.	3.8	146
18	CPTAC Assay Portal: a repository of targeted proteomic assays. Nature Methods, 2014, 11, 703-704.	19.0	150

#	ARTICLE	IF	CITATIONS
19	Accounting for Population Variation in Targeted Proteomics. Journal of Proteome Research, 2014, 13, 321-323.	3.7	4
20	Implementation of Statistical Process Control for Proteomic Experiments Via LC MS/MS. Journal of the American Society for Mass Spectrometry, 2014, 25, 581-587.	2.8	36
21	MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments. Bioinformatics, 2014, 30, 2524-2526.	4.1	832
22	A framework for installable external tools in Skyline. Bioinformatics, 2014, 30, 2521-2523.	4.1	36
23	Panorama: A Targeted Proteomics Knowledge Base. Journal of Proteome Research, 2014, 13, 4205-4210.	3.7	205
24	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). Molecular and Cellular Proteomics, 2013, 12, 2623-2639.	3.8	100
25	A cross-platform toolkit for mass spectrometry and proteomics. Nature Biotechnology, 2012, 30, 918-920.	17.5	2,794
26	Label-Free Quantitation of Protein Modifications by Pseudo Selected Reaction Monitoring with Internal Reference Peptides. Journal of Proteome Research, 2012, 11, 3467-3479.	3.7	66
27	Using i<scp>RT</scp>, a normalized retention time for more targeted measurement of peptides. Proteomics, 2012, 12, 1111-1121.	2.2	517
28	The development of selected reaction monitoring methods for targeted proteomics via empirical refinement. Proteomics, 2012, 12, 1134-1141.	2.2	101
29	Rapid empirical discovery of optimal peptides for targeted proteomics. Nature Methods, 2011, 8, 1041-1043.	19.0	100
30	Comparison of Database Search Strategies for High Precursor Mass Accuracy MS/MS Data. Journal of Proteome Research, 2010, 9, 1138-1143.	3.7	109
31	Effect of Collision Energy Optimization on the Measurement of Peptides by Selected Reaction Monitoring (SRM) Mass Spectrometry. Analytical Chemistry, 2010, 82, 10116-10124.	6.5	220
32	Skyline: an open source document editor for creating and analyzing targeted proteomics experiments. Bioinformatics, 2010, 26, 966-968.	4.1	3,968
33	Expediting the Development of Targeted SRM Assays: Using Data from Shotgun Proteomics to Automate Method Development. Journal of Proteome Research, 2009, 8, 2733-2739.	3.7	137
34	Precursor-Ion Mass Re-Estimation Improves Peptide Identification on Hybrid Instruments. Journal of Proteome Research, 2008, 7, 4031-4039.	3.7	49
35	Computational Proteomics Analysis System (CPAS):â€‰ An Extensible, Open-Source Analytic System for Evaluating and Publishing Proteomic Data and High Throughput Biological Experiments. Journal of Proteome Research, 2006, 5, 112-121.	3.7	204
36	General framework for developing and evaluating database scoring algorithms using the TANDEM search engine. Bioinformatics, 2006, 22, 2830-2832.	4.1	209