Brendan Maclean

List of Publications by Year
in descending order

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	Skyline: an open source document editor for creating and analyzing targeted proteomics experiments. Bioinformatics, 2010, 26, 966-968.	4.1	3,968
2	A cross-platform toolkit for mass spectrometry and proteomics. Nature Biotechnology, 2012, 30, 918-920.	17.5	2,794
3	MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments. Bioinformatics, 2014, 30, 2524-2526.	4.1	832
4	Using i<scp>RT</scp>, a normalized retention time for more targeted measurement of peptides. Proteomics, 2012, 12, 1111-1121.	2.2	517
5	The ProteomeXchange consortium in 2020: enabling â€˜big dataâ€™ approaches in proteomics. Nucleic Acids Research, 2020, 48, D1145-D1152.	14.5	491
6	The Skyline ecosystem: Informatics for quantitative mass spectrometry proteomics. Mass Spectrometry Reviews, 2020, 39, 229-244.	5.4	469
7	A multicenter study benchmarks software tools for label-free proteome quantification. Nature Biotechnology, 2016, 34, 1130-1136.	17.5	321
8	Building high-quality assay libraries for targeted analysis of SWATH MS data. Nature Protocols, 2015, 10, 426-441.	12.0	319
9	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
10	General framework for developing and evaluating database scoring algorithms using the TANDEM search engine. Bioinformatics, 2006, 22, 2830-2832.	4.1	209
11	Panorama: A Targeted Proteomics Knowledge Base. Journal of Proteome Research, 2014, 13, 4205-4210.	3.7	205
12	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
13	Panorama Public: A Public Repository for Quantitative Data Sets Processed in Skyline. Molecular and Cellular Proteomics, 2018, 17, 1239-1244.	3.8	177
14	Multiplexed peptide analysis using data-independent acquisition and Skyline. Nature Protocols, 2015, 10, 887-903.	12.0	174
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	CPTAC Assay Portal: a repository of targeted proteomic assays. Nature Methods, 2014, 11, 703-704.	19.0	150
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	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

#	Article	IF	Citations
19	Comparison of Database Search Strategies for High Precursor Mass Accuracy MS/MS Data. Journal of Proteome Research, 2010, 9, 1138-1143.	3.7	109
20	The development of selected reaction monitoring methods for targeted proteomics via empirical refinement. Proteomics, 2012, 12, 1134-1141.	2.2	101
21	Rapid empirical discovery of optimal peptides for targeted proteomics. Nature Methods, 2011, 8, 1041-1043.	19.0	100
22	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
23	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
24	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
25	LipidCreator workbench to probe the lipidomic landscape. Nature Communications, 2020, 11, 2057.	12.8	58
26	An Automated Pipeline to Monitor System Performance in Liquid Chromatography–Tandem Mass Spectrometry Proteomic Experiments. Journal of Proteome Research, 2016, 15, 4763-4769.	3.7	56
27	Precursor-Ion Mass Re-Estimation Improves Peptide Identification on Hybrid Instruments. Journal of Proteome Research, 2008, 7, 4031-4039.	3.7	49
28	ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of Differentially Abundant Proteins in Label-Free Quantitative LC–MS/MS Experiments. Journal of Proteome Research, 2017, 16, 945-957.	3.7	42
29	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
30	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
31	A framework for installable external tools in Skyline. Bioinformatics, 2014, 30, 2521-2523.	4.1	36
32	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
33	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
34	Avant-garde: an automated data-driven DIA data curation tool. Nature Methods, 2020, 17, 1237-1244.	19.0	22
35	MSstatsQC: Longitudinal System Suitability Monitoring and Quality Control for Targeted Proteomic Experiments. Molecular and Cellular Proteomics, 2017, 16, 1335-1347.	3.8	21
36	Accounting for Population Variation in Targeted Proteomics. Journal of Proteome Research, 2014, 13, 321-323.	3.7	4