

# Brian C Searle

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

3,032  
citations

361413

20  
h-index

395702

33  
g-index

45  
all docs

45  
docs citations

45  
times ranked

4519  
citing authors

#	ARTICLE	IF	CITATIONS
1	Recurrent Co-Option and Recombination of Cytokine and Three Finger Proteins in Multiple Reproductive Tissues Throughout Salamander Evolution. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 828947.	3.7	1
2	Data-Independent Acquisition Protease-Multiplexing Enables Increased Proteome Sequence Coverage Across Multiple Fragmentation Modes. <i>Journal of Proteome Research</i> , 2022, 21, 1124-1136.	3.7	8
3	CIDer: A Statistical Framework for Interpreting Differences in CID and HCD Fragmentation. <i>Journal of Proteome Research</i> , 2021, 20, 1951-1965.	3.7	9
4	Detection of Human Papillomavirus Integration in Brain Metastases from Oropharyngeal Tumors by Targeted Sequencing. <i>Viruses</i> , 2021, 13, 1536.	3.3	5
5	The Skyline ecosystem: Informatics for quantitative mass spectrometry proteomics. <i>Mass Spectrometry Reviews</i> , 2020, 39, 229-244.	5.4	469
6	An efficient solution for resolving iTRAQ and TMT channel cross-talk. <i>Journal of Mass Spectrometry</i> , 2020, 55, e4354.	1.6	11
7	Lysine and Arginine Protein Post-translational Modifications by Enhanced DIA Libraries: Quantification in Murine Liver Disease. <i>Journal of Proteome Research</i> , 2020, 19, 4163-4178.	3.7	18
8	Matrix-Matched Calibration Curves for Assessing Analytical Figures of Merit in Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 1147-1153.	3.7	41
9	Highly Parallel Quantification and Compartment Localization of Transcription Factors and Nuclear Proteins. <i>Cell Reports</i> , 2020, 30, 2463-2471.e5.	6.4	20
10	Generating high quality libraries for DIA MS with empirically corrected peptide predictions. <i>Nature Communications</i> , 2020, 11, 1548.	12.8	148
11	Acquiring and Analyzing Data Independent Acquisition Proteomics Experiments without Spectrum Libraries. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1088-1103.	3.8	164
12	Assessing Protein Sequence Database Suitability Using De Novo Sequencing. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 198-208.	3.8	21
13	A Review of the Scientific Rigor, Reproducibility, and Transparency Studies Conducted by the ABRF Research Groups. <i>Journal of Biomolecular Techniques</i> , 2020, 31, 11-26.	1.5	15
14	Thesaurus: quantifying phosphopeptide positional isomers. <i>Nature Methods</i> , 2019, 16, 703-706.	19.0	44
15	Team COUNCIL OF RICKS submission for EUPA YPIC 2017. <i>EuPA Open Proteomics</i> , 2019, 22-23, 22-24.	2.5	0
16	Incorporating In-Source Fragment Information Improves Metabolite Identification Accuracy in Untargeted LC-MS Data Sets. <i>Journal of Proteome Research</i> , 2019, 18, 791-796.	3.7	27
17	Data-Independent Acquisition Mass Spectrometry To Quantify Protein Levels in FFPE Tumor Biopsies for Molecular Diagnostics. <i>Journal of Proteome Research</i> , 2018, 18, 426-435.	3.7	18
18	Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. <i>Nature Communications</i> , 2018, 9, 5128.	12.8	337

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19	Calibration Using a Single-Point External Reference Material Harmonizes Quantitative Mass Spectrometry Proteomics Data between Platforms and Laboratories. <i>Analytical Chemistry</i> , 2018, 90, 13112-13117.	6.5	30
20	PECAN: library-free peptide detection for data-independent acquisition tandem mass spectrometry data. <i>Nature Methods</i> , 2017, 14, 903-908.	19.0	158
21	Detecting Sources of Transcriptional Heterogeneity in Large-Scale RNA-Seq Data Sets. <i>Genetics</i> , 2016, 204, 1391-1396.	2.9	11
22	ProteinProcessor: A probabilistic analysis using mass accuracy and the MS spectrum. <i>Proteomics</i> , 2016, 16, 2480-2490.	2.2	7
23	Plug-and-play analysis of the human phosphoproteome by targeted high-resolution mass spectrometry. <i>Nature Methods</i> , 2016, 13, 431-434.	19.0	106
24	Using Data Independent Acquisition (DIA) to Model High-responding Peptides for Targeted Proteomics Experiments. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2331-2340.	3.8	47
25	An Efficient Approach to Evaluate Reporter Ion Behavior from MALDI-MS/MS Data for Quantification Studies Using Isobaric Tags. <i>Journal of Proteome Research</i> , 2015, 14, 4169-4178.	3.7	5
26	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014, 14, 2389-2399.	2.2	23
27	Interlaboratory studies and initiatives developing standards for proteomics. <i>Proteomics</i> , 2013, 13, 904-909.	2.2	29
28	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M1111.014381-1-M1111.014381-10.	3.8	175
29	A Face in the Crowd: Recognizing Peptides Through Database Search. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R1111.009522.	3.8	147
30	Scaffold: A bioinformatic tool for validating MS/MS-based proteomic studies. <i>Proteomics</i> , 2010, 10, 1265-1269.	2.2	482
31	Improving Sensitivity by Probabilistically Combining Results from Multiple MS/MS Search Methodologies. <i>Journal of Proteome Research</i> , 2008, 7, 245-253.	3.7	154
32	Identification of Protein Modifications Using MS/MS de Novo Sequencing and the OpenSea Alignment Algorithm. <i>Journal of Proteome Research</i> , 2005, 4, 546-554.	3.7	119
33	High-Throughput Identification of Proteins and Unanticipated Sequence Modifications Using a Mass-Based Alignment Algorithm for MS/MS de Novo Sequencing Results. <i>Analytical Chemistry</i> , 2004, 76, 2220-2230.	6.5	134
34	Identification of respiratory vagal feedback in awake normal subjects using pseudorandom unloading. <i>Journal of Applied Physiology</i> , 2001, 90, 2330-2340.	2.5	25