

# Ben C Collins

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

6,393  
citations

159358

30  
h-index

205818

48  
g-index

58  
all docs

58  
docs citations

58  
times ranked

7837  
citing authors

#	ARTICLE	IF	CITATIONS
1	Data-independent acquisition-based <sc>SWATH</sc> &lt;sc>MS</sc> for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , 2018, 14, e8126.	3.2	701
2	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , 2014, 32, 219-223.	9.4	692
3	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291.	5.8	423
4	diaPASEF: parallel accumulation&quot;serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236.	9.0	387
5	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	2.4	370
6	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. <i>Nature Medicine</i> , 2015, 21, 407-413.	15.2	358
7	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015, 10, 426-441.	5.5	319
8	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. <i>Nature Methods</i> , 2013, 10, 1246-1253.	9.0	302
9	Quantitative variability of 342 plasma proteins in a human twin population. <i>Molecular Systems Biology</i> , 2015, 11, 786.	3.2	300
10	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of <i>Mycobacterium tuberculosis</i> . <i>Cell Host and Microbe</i> , 2015, 18, 96-108.	5.1	229
11	Quantitative proteomics: challenges and opportunities in basic and applied research. <i>Nature Protocols</i> , 2017, 12, 1289-1294.	5.5	200
12	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. <i>Nature Methods</i> , 2017, 14, 921-927.	9.0	189
13	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , 2016, 13, 777-783.	9.0	173
14	Glycoproteomic Analysis of Prostate Cancer Tissues by SWATH Mass Spectrometry Discovers N-acylethanolamine Acid Amidase and Protein Tyrosine Kinase 7 as Signatures for Tumor Aggressiveness. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1753-1768.	2.5	165
15	mapDIA: Preprocessing and statistical analysis of quantitative proteomics data from data independent acquisition mass spectrometry. <i>Journal of Proteomics</i> , 2015, 129, 108-120.	1.2	149
16	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017, 35, 781-788.	9.4	122
17	Mass spectrometric protein maps for biomarker discovery and clinical research. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 811-825.	1.5	117
18	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015, 12, 725-731.	9.0	109

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19	Complex-centric proteome profiling by SEC-SWATH-MS. <i>Molecular Systems Biology</i> , 2019, 15, e8438.	3.2	109
20	From coarse to fine: the absolute <i>Escherichia coli</i> proteome under diverse growth conditions. <i>Molecular Systems Biology</i> , 2021, 17, e9536.	3.2	82
21	Identification of a Set of Conserved Eukaryotic Internal Retention Time Standards for Data-independent Acquisition Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2800-2813.	2.5	76
22	Elucidation of host-pathogen protein-protein interactions to uncover mechanisms of host cell rewiring. <i>Current Opinion in Microbiology</i> , 2017, 39, 7-15.	2.3	61
23	Diagnostics and correction of batch effects in large-scale proteomic studies: a tutorial. <i>Molecular Systems Biology</i> , 2021, 17, e10240.	3.2	57
24	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. <i>Cell Systems</i> , 2020, 10, 133-155.e6.	2.9	57
25	Serum Proteomic Profiling Reveals That Pretreatment Complement Protein Levels are Predictive of Esophageal Cancer Patient Response to Neoadjuvant Chemoradiation. <i>Annals of Surgery</i> , 2011, 254, 809-817.	2.1	51
26	Applications and Developments in Targeted Proteomics: From SRM to DIA/SWATH. <i>Proteomics</i> , 2016, 16, 2065-2067.	1.3	50
27	Systems proteomics approaches to study bacterial pathogens: application to <i>Mycobacterium tuberculosis</i> . <i>Current Opinion in Microbiology</i> , 2017, 39, 64-72.	2.3	41
28	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. <i>Nature Communications</i> , 2021, 12, 3810.	5.8	40
29	Delayed effects of transcriptional responses in <i>Mycobacterium tuberculosis</i> exposed to nitric oxide suggest other mechanisms involved in survival. <i>Scientific Reports</i> , 2017, 7, 8208.	1.6	39
30	Range of protein detection by selected/multiple reaction monitoring mass spectrometry in an unfractionated human cell culture lysate. <i>Proteomics</i> , 2012, 12, 1185-1193.	1.3	37
31	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , 2019, 10, 2524.	5.8	35
32	Complex-centric proteome profiling by SEC-SWATH-MS for the parallel detection of hundreds of protein complexes. <i>Nature Protocols</i> , 2020, 15, 2341-2386.	5.5	34
33	Development of a Pharmaceutical Hepatotoxicity Biomarker Panel Using a Discovery to Targeted Proteomics Approach. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 394-410.	2.5	32
34	Integrating highly quantitative proteomics and genome-scale metabolic modeling to study pH adaptation in the human pathogen <i>Enterococcus faecalis</i> . <i>Npj Systems Biology and Applications</i> , 2016, 2, 16017.	1.4	28
35	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. <i>Cell Reports</i> , 2017, 18, 3219-3226.	2.9	28
36	AP-SWATH Reveals Direct Involvement of VCP/p97 in Integrated Stress Response Signaling Through Facilitating CReP/PPP1R15B Degradation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1295-1307.	2.5	26

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37	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. <i>Cell Systems</i> , 2020, 11, 589-607.e8.	2.9	26
38	Sequence Tagging Reveals Unexpected Modifications in Toxicoproteomics. <i>Chemical Research in Toxicology</i> , 2011, 24, 204-216.	1.7	25
39	Use of proteomics for the discovery of early markers of drug toxicity. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , 2007, 3, 689-704.	1.5	23
40	In Vivo and in Vitro Proteome Analysis of Human Immunodeficiency Virus (HIV)-1-infected, Human CD4+ T Cells. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S108-S123.	2.5	18
41	The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2021, , .	0.6	17
42	Use of SELDI MS to discover and identify potential biomarkers of toxicity in InnoMed PredTox: A multi-site, multi-compound study. <i>Proteomics</i> , 2010, 10, 1592-1608.	1.3	16
43	Multilayered regulation of autophagy by the Atg1 kinase orchestrates spatial and temporal control of autophagosome formation. <i>Molecular Cell</i> , 2021, 81, 5066-5081.e10.	4.5	13
44	Proteomics goes parallel. <i>Nature Biotechnology</i> , 2018, 36, 1051-1053.	9.4	11
45	System-Wide Profiling of Protein Complexes Via Size Exclusion Chromatography-Mass Spectrometry (SEC-MS). <i>Methods in Molecular Biology</i> , 2021, 2259, 269-294.	0.4	11
46	Expression Dysregulation as a Mediator of Fitness Costs in Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0050421.	1.4	5
47	Differential Proteomics Incorporating iTRAQ Labeling and Multi-dimensional Separations. <i>Methods in Molecular Biology</i> , 2011, 691, 369-383.	0.4	3
48	Absolute Quantification of Toxicological Biomarkers via Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1641, 337-348.	0.4	1