

# Ben C Collins

## List of Publications by Year in Descending Order

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**Version:** 2024-04-24

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

51  
papers

4,133  
citations

26  
h-index

58  
g-index

58  
ext. papers

5,468  
ext. citations

13.2  
avg, IF

5.3  
L-index

#	Paper	IF	Citations
51	Multilayered regulation of autophagy by the Atg1 kinase orchestrates spatial and temporal control of autophagosome formation. <i>Molecular Cell</i> , <b>2021</b> ,	17.6	3
50	From coarse to fine: the absolute Escherichia coli proteome under diverse growth conditions. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e9536	12.2	9
49	The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , <b>2021</b> ,	2.2	6
48	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. <i>Nature Communications</i> , <b>2021</b> , 12, 3810	17.4	6
47	System-Wide Profiling of Protein Complexes Via Size Exclusion Chromatography-Mass Spectrometry (SEC-MS). <i>Methods in Molecular Biology</i> , <b>2021</b> , 2259, 269-294	1.4	1
46	Expression Dysregulation as a Mediator of Fitness Costs in Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2021</b> , 65, e0050421	5.9	1
45	Diagnostics and correction of batch effects in large-scale proteomic studies: a tutorial. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e10240	12.2	8
44	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. <i>Cell Systems</i> , <b>2020</b> , 10, 133-155.e6	10.6	24
43	Complex-centric proteome profiling by SEC-SWATH-MS for the parallel detection of hundreds of protein complexes. <i>Nature Protocols</i> , <b>2020</b> , 15, 2341-2386	18.8	17
42	diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , <b>2020</b> , 17, 1229-1236	21.6	85
41	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. <i>Cell Systems</i> , <b>2020</b> , 11, 589-607.e8	10.6	9
40	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , <b>2019</b> , 10, 2524	17.4	20
39	Complex-centric proteome profiling by SEC-SWATH-MS. <i>Molecular Systems Biology</i> , <b>2019</b> , 15, e8438	12.2	61
38	AP-SWATH Reveals Direct Involvement of VCP/p97 in Integrated Stress Response Signaling Through Facilitating CREP/PPP1R15B Degradation. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 1295-1307	7.6	18
37	Data-independent acquisition-based SWATH-MS for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , <b>2018</b> , 14, e8126	12.2	389
36	Proteomics goes parallel. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 1051-1053	44.5	9
35	and Proteome Analysis of Human Immunodeficiency Virus (HIV)-1-infected, Human CD4 T Cells. <i>Molecular and Cellular Proteomics</i> , <b>2017</b> , 16, S108-S123	7.6	15

34	Quantitative proteomics: challenges and opportunities in basic and applied research. <i>Nature Protocols</i> , <b>2017</b> , 12, 1289-1294	18.8	133
33	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 781-788	44.5	85
32	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. <i>Cell Reports</i> , <b>2017</b> , 18, 3219-3226	10.6	23
31	Systems proteomics approaches to study bacterial pathogens: application to Mycobacterium tuberculosis. <i>Current Opinion in Microbiology</i> , <b>2017</b> , 39, 64-72	7.9	21
30	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. <i>Nature Methods</i> , <b>2017</b> , 14, 921-927	21.6	129
29	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , <b>2017</b> , 8, 291	17.4	252
28	Delayed effects of transcriptional responses in Mycobacterium tuberculosis exposed to nitric oxide suggest other mechanisms involved in survival. <i>Scientific Reports</i> , <b>2017</b> , 7, 8208	4.9	27
27	Absolute Quantification of Toxicological Biomarkers via Mass Spectrometry. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1641, 337-348	1.4	1
26	Elucidation of host-pathogen protein-protein interactions to uncover mechanisms of host cell rewiring. <i>Current Opinion in Microbiology</i> , <b>2017</b> , 39, 7-15	7.9	34
25	Integrating highly quantitative proteomics and genome-scale metabolic modeling to study pH adaptation in the human pathogen. <i>Npj Systems Biology and Applications</i> , <b>2016</b> , 2, 16017	5	20
24	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , <b>2016</b> , 13, 777-83	21.6	122
23	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , <b>2015</b> , 10, 426-41	18.8	229
22	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. <i>Nature Medicine</i> , <b>2015</b> , 21, 407-13	50.5	250
21	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. <i>Cell Host and Microbe</i> , <b>2015</b> , 18, 96-108	23.4	155
20	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , <b>2015</b> , 12, 725-31	21.6	86
19	Quantitative variability of 342 plasma proteins in a human twin population. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 786	12.2	222
18	Identification of a Set of Conserved Eukaryotic Internal Retention Time Standards for Data-independent Acquisition Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 2800-13	7.6	51
17	mapDIA: Preprocessing and statistical analysis of quantitative proteomics data from data independent acquisition mass spectrometry. <i>Journal of Proteomics</i> , <b>2015</b> , 129, 108-120	3.9	101

16	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 219-23	44.5	508
15	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , <b>2014</b> , 1, 1400318.2		266
14	Glycoproteomic analysis of prostate cancer tissues by SWATH mass spectrometry discovers N-acyl ethanolamine acid amidase and protein tyrosine kinase 7 as signatures for tumor aggressiveness. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 1753-68	7.6	143
13	Mass spectrometric protein maps for biomarker discovery and clinical research. <i>Expert Review of Molecular Diagnostics</i> , <b>2013</b> , 13, 811-25	3.8	105
12	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. <i>Nature Methods</i> , <b>2013</b> , 10, 1246-53	21.6	249
11	Range of protein detection by selected/multiple reaction monitoring mass spectrometry in an unfractionated human cell culture lysate. <i>Proteomics</i> , <b>2012</b> , 12, 1185-93	4.8	35
10	Development of a pharmaceutical hepatotoxicity biomarker panel using a discovery to targeted proteomics approach. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, 394-410	7.6	32
9	Serum proteomic profiling reveals that pretreatment complement protein levels are predictive of esophageal cancer patient response to neoadjuvant chemoradiation. <i>Annals of Surgery</i> , <b>2011</b> , 254, 809-16; discussion 816-7	7.8	42
8	Sequence tagging reveals unexpected modifications in toxicoproteomics. <i>Chemical Research in Toxicology</i> , <b>2011</b> , 24, 204-16	4	24
7	Differential proteomics incorporating iTRAQ labeling and multi-dimensional separations. <i>Methods in Molecular Biology</i> , <b>2011</b> , 691, 369-83	1.4	2
6	Use of SELDI MS to discover and identify potential biomarkers of toxicity in InnoMed PredTox: a multi-site, multi-compound study. <i>Proteomics</i> , <b>2010</b> , 10, 1592-608	4.8	12
5	Use of proteomics for the discovery of early markers of drug toxicity. <i>Expert Opinion on Drug Metabolism and Toxicology</i> , <b>2007</b> , 3, 689-704	5.5	21
4	A global screen for assembly state changes of the mitotic proteome by SEC-SWATH-MS		1
3	Systematic detection of functional proteoform groups from bottom-up proteomic datasets		1
2	Parallel accumulation & serial fragmentation combined with data-independent acquisition (diaPASEF): Bottom-up proteomics with near optimal ion usage		18
1	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry		3