

# Ben C Collins

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7577033/publications.pdf>

Version: 2024-02-01

48  
papers

6,393  
citations

159525

30  
h-index

206029

48  
g-index

58  
all docs

58  
docs citations

58  
times ranked

7837  
citing authors

#	ARTICLE	IF	CITATIONS
1	System-Wide Profiling of Protein Complexes Via Size Exclusion Chromatographyâ€“Mass Spectrometry (SECâ€“MS). <i>Methods in Molecular Biology</i> , 2021, 2259, 269-294.	0.4	11
2	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
3	The Protein Landscape of Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2021, , .	0.6	17
4	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. <i>Nature Communications</i> , 2021, 12, 3810.	5.8	40
5	Expression Dysregulation as a Mediator of Fitness Costs in Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0050421.	1.4	5
6	Diagnostics and correction of batch effects in largeâ€“scale proteomic studies: a tutorial. <i>Molecular Systems Biology</i> , 2021, 17, e10240.	3.2	57
7	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
8	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
9	diaPASEF: parallel accumulationâ€“serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236.	9.0	387
10	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
11	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
12	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
13	Complexâ€“centric proteome profiling by <i>SEC</i> â€“ <i>SWATH</i> â€“ <i>MS</i> . <i>Molecular Systems Biology</i> , 2019, 15, e8438.	3.2	109
14	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
15	Proteomics goes parallel. <i>Nature Biotechnology</i> , 2018, 36, 1051-1053.	9.4	11
16	Dataâ€“independent acquisitionâ€“based <i>SWATH</i> â€“ <i>MS</i> for quantitative proteomics: a tutorial. <i>Molecular Systems Biology</i> , 2018, 14, e8126.	3.2	701
17	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
18	Quantitative proteomics: challenges and opportunities in basic and applied research. <i>Nature Protocols</i> , 2017, 12, 1289-1294.	5.5	200

#	ARTICLE	IF	CITATIONS
19	Inference and quantification of peptidoforms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017, 35, 781-788.	9.4	122
20	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. <i>Cell Reports</i> , 2017, 18, 3219-3226.	2.9	28
21	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
22	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
23	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291.	5.8	423
24	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
25	Absolute Quantification of Toxicological Biomarkers via Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1641, 337-348.	0.4	1
26	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
27	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , 2016, 13, 777-783.	9.0	173
28	Applications and Developments in Targeted Proteomics: From SRM to DIA/SWATH. <i>Proteomics</i> , 2016, 16, 2065-2067.	1.3	50
29	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
30	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015, 10, 426-441.	5.5	319
31	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
32	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
33	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
34	Quantitative variability of 342 plasma proteins in a human twin population. <i>Molecular Systems Biology</i> , 2015, 11, 786.	3.2	300
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , 2014, 32, 219-223.	9.4	692
39	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	2.4	370
40	Mass spectrometric protein maps for biomarker discovery and clinical research. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 811-825.	1.5	117
41	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
42	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
43	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
44	Sequence Tagging Reveals Unexpected Modifications in Toxicoproteomics. <i>Chemical Research in Toxicology</i> , 2011, 24, 204-216.	1.7	25
45	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
46	Differential Proteomics Incorporating iTRAQ Labeling and Multi-dimensional Separations. <i>Methods in Molecular Biology</i> , 2011, 691, 369-383.	0.4	3
47	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
48	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