Robert J Chalkley

List of Publications by Year
in descending order

67 papers	6,224 citations	117625 34 h-index	110387 64 g-index
73 all docs	73 docs citations	73 times ranked	12004 citing authors

#	Article	IF	Citations
1	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	17.5	2,505
2	O-Linked N-Acetylglucosamine Proteomics of Postsynaptic Density Preparations Using Lectin Weak Affinity Chromatography and Mass Spectrometry. Molecular and Cellular Proteomics, 2006, 5, 923-934.	3.8	312
3	Identification of protein O-GlcNAcylation sites using electron transfer dissociation mass spectrometry on native peptides. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8894-8899.	7.1	225
4	In-depth Analysis of Tandem Mass Spectrometry Data from Disparate Instrument Types. Molecular and Cellular Proteomics, 2008, 7, 2386-2398.	3.8	181
5	Comprehensive Analysis of a Multidimensional Liquid Chromatography Mass Spectrometry Dataset Acquired on a Quadrupole Selecting, Quadrupole Collision Cell, Time-of-flight Mass Spectrometer. Molecular and Cellular Proteomics, 2005, 4, 1194-1204.	3.8	171
6	Quantitative analysis of both protein expression and serine?/?threonine post-translational modifications through stable isotope labeling with dithiothreitol. Proteomics, 2005, 5, 388-398.	2.2	169
7	Lessons in *de novo* peptide sequencing by tandem mass spectrometry. Mass Spectrometry Reviews, 2015, 34, 43-63.	5.4	167
8	Matching Cross-linked Peptide Spectra: Only as Good as the Worse Identification. Molecular and Cellular Proteomics, 2014, 13, 420-434.	3.8	153
9	The PSI-MOD community standard for representation of protein modification data. Nature Biotechnology, 2008, 26, 864-866.	17.5	132
10	PPKs mediate direct signal transfer from phytochrome photoreceptors to transcription factor PIF3. Nature Communications, 2017, 8, 15236.	12.8	132
11	The DegraBase: A Database of Proteolysis in Healthy and Apoptotic Human Cells. Molecular and Cellular Proteomics, 2013, 12, 813-824.	3.8	124
12	MS-Viewer: A Web-based Spectral Viewer for Proteomics Results. Molecular and Cellular Proteomics, 2014, 13, 1392-1396.	3.8	122
13	Modification Site Localization Scoring Integrated into a Search Engine. Molecular and Cellular Proteomics, 2011, 10, M111.008078.	3.8	106
14	Proteomic analysis reveals O-GlcNAc modification on proteins with key regulatory functions in *Arabidopsis*. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1536-E1543.	7.1	101
15	Modification Site Localization Scoring: Strategies and Performance. Molecular and Cellular Proteomics, 2012, 11, 3-14.	3.8	100
16	Tissue-Specific Glycosylation at the Glycopeptide Level. Molecular and Cellular Proteomics, 2015, 14, 2103-2110.	3.8	97
17	NGF and ProNGF: Regulation of neuronal and neoplastic responses through receptor signaling. Advances in Biological Regulation, 2015, 58, 16-27.	2.3	91
18	Peripheral Elevation of a Klotho Fragment Enhances Brain Function and Resilience in Young, Aging, and Î±-Synuclein Transgenic Mice. Cell Reports, 2017, 20, 1360-1371.	6.4	84

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19	Identification of GlcNAcylation sites of peptides and α-crystallin using Q-TOF mass spectrometry. Journal of the American Society for Mass Spectrometry, 2001, 12, 1106-1113.	2.8	76
20	Community evaluation of glycoproteomics informatics solutions reveals high-performance search strategies for serum glycopeptide analysis. Nature Methods, 2021, 18, 1304-1316.	19.0	74
21	Finding Chimeras: a Bioinformatics Strategy for Identification of Cross-linked Peptides. Molecular and Cellular Proteomics, 2010, 9, 25-31.	3.8	67
22	Proteotranscriptomic Profiling of 231-BR Breast Cancer Cells: Identification of Potential Biomarkers and Therapeutic Targets for Brain Metastasis. Molecular and Cellular Proteomics, 2015, 14, 2316-2330.	3.8	59
23	Characterizing Sialic Acid Variants at the Glycopeptide Level. Analytical Chemistry, 2015, 87, 3064-3071.	6.5	57
24	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular and Cellular Proteomics, 2017, 16, 1275-1285.	3.8	55
25	Improving Software Performance for Peptide Electron Transfer Dissociation Data Analysis by Implementation of Charge State- and Sequence-Dependent Scoring. Molecular and Cellular Proteomics, 2010, 9, 1795-1803.	3.8	53
26	Hyper-O-GlcNAcylation activates nuclear factor κ-light-chain-enhancer of activated B cells (NF-κB) signaling through interplay with phosphorylation and acetylation. Journal of Biological Chemistry, 2017, 292, 9150-9163.	3.4	53
27	The Effect of Using an Inappropriate Protein Database for Proteomic Data Analysis. PLoS ONE, 2011, 6, e20873.	2.5	52
28	Revealing nascent proteomics in signaling pathways and cell differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2353-2358.	7.1	51
29	Bioinformatic Methods to Exploit Mass Spectrometric Data for Proteomic Applications. Methods in Enzymology, 2005, 402, 289-312.	1.0	46
30	Mass Spectrometric Analysis, Automated Identification and Complete Annotation of O-Linked Glycopeptides. European Journal of Mass Spectrometry, 2010, 16, 421-428.	1.0	41
31	Rearrangements within human spliceosomes captured after exon ligation. Rna, 2013, 19, 400-412.	3.5	41
32	N-Glycopeptide Profiling in Arabidopsis Inflorescence. Molecular and Cellular Proteomics, 2016, 15, 2048-2054.	3.8	41
33	Mass spectrometric analysis of histone posttranslational modifications. Methods, 2005, 36, 383-394.	3.8	39
34	Molecular Architecture of Photoreceptor Phosphodiesterase Elucidated by Chemical Cross-Linking and Integrative Modeling. Journal of Molecular Biology, 2014, 426, 3713-3728.	4.2	37
35	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
36	Human antibodies targeting cell surface antigens overexpressed by the hormone refractory metastatic prostate cancer cells: ICAM-1 is a tumor antigen that mediates prostate cancer cell invasion. Journal of Molecular Medicine, 2009, 87, 507-514.	3.9	24

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37	When Target–Decoy False Discovery Rate Estimations Are Inaccurate and How to Spot Instances. Journal of Proteome Research, 2013, 12, 1062-1064.	3.7	23
38	Use of a glycosylation site database to improve glycopeptide identification from complex mixtures. Analytical and Bioanalytical Chemistry, 2017, 409, 571-577.	3.7	23
39	Proteomics Standards Initiative Extended FASTA Format. Journal of Proteome Research, 2019, 18, 2686-2692.	3.7	22
40	Methods for Enrichment and Assignment of N-Acetylglucosamine Modification Sites. Molecular and Cellular Proteomics, 2021, 20, 100031.	3.8	21
41	Proteome Informatics Research Group (iPRG)_2012: A Study on Detecting Modified Peptides in a Complex Mixture. Molecular and Cellular Proteomics, 2014, 13, 360-371.	3.8	20
42	The Role of Exon Sequences in C Complex Spliceosome Structure. Journal of Molecular Biology, 2009, 394, 363-375.	4.2	19
43	Dissecting the Roles of Tyrosines 490 and 785 of TrkA Protein in the Induction of Downstream Protein Phosphorylation Using Chimeric Receptors. Journal of Biological Chemistry, 2013, 288, 16606-16618.	3.4	18
44	The Induction of Serine/Threonine Protein Phosphorylations by a PDGFR/TrkA Chimera in Stably Transfected PC12 Cells. Molecular and Cellular Proteomics, 2012, 11, 15-30.	3.8	17
45	Protein PTMs: post–translational modifications or pesky trouble makers?. Journal of Mass Spectrometry, 2010, 45, 1095-1097.	1.6	14
46	The effectiveness of filtering glycopeptide peak list files for Y ions. Molecular Omics, 2020, 16, 147-155.	2.8	14
47	Prp8 positioning of U5 snRNA is linked to 5′ splice site recognition. Rna, 2018, 24, 769-777.	3.5	13
48	Proteomic analysis of platelet-rich and platelet-poor plasma. Regenerative Therapy, 2020, 15, 226-235.	3.0	13
49	Instrumentation for LC-MS/MS in Proteomics. Methods in Molecular Biology, 2010, 658, 47-60.	0.9	12
50	Receptor tyrosine kinase signaling – a proteomic perspective. Advances in Enzyme Regulation, 2011, 51, 293-305.	2.6	11
51	Identification of O-linked β-d-N-acetylglucosamine-Modified Proteins from Arabidopsis. Methods in Molecular Biology, 2011, 876, 33-45.	0.9	11
52	Initial Guidelines for Manuscripts Employing Data-independent Acquisition Mass Spectrometry for Proteomic Analysis. Molecular and Cellular Proteomics, 2019, 18, 1-2.	3.8	11
53	15N Metabolic Labeling Quantification Workflow in Arabidopsis Using Protein Prospector. Frontiers in Plant Science, 2022, 13, 832562.	3.6	10
54	Breaking Up the C Complex Spliceosome Shows Stable Association of Proteins with the Lariat Intron Intermediate. PLoS ONE, 2011, 6, e19061.	2.5	8

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55	Glyco-centric lectin magnetic bead array (LeMBA) â˜’ proteomics dataset of human serum samples from healthy, Barrett×³s esophagus and esophageal adenocarcinoma individuals. Data in Brief, 2016, 7, 1058-1062.	1.0	6
56	Improving Peptide Identification Using Empirical Scoring Systems. Methods in Molecular Biology, 2013, 1007, 173-182.	0.9	5
57	Characterization of Prenylated C-terminal Peptides Using a Thiopropyl-based Capture Technique and LC-MS/MS. Molecular and Cellular Proteomics, 2020, 19, 1005-1016.	3.8	5
58	Application of Parallel Reaction Monitoring in 15N Labeled Samples for Quantification. Frontiers in Plant Science, 2022, 13, 832585.	3.6	4
59	TSAFinder: exhaustive tumor-specific antigen detection with RNAseq. Bioinformatics, 2022, 38, 2422-2427.	4.1	3
60	Modification Site Localization in Peptides. Advances in Experimental Medicine and Biology, 2016, 919, 243-247.	1.6	2
61	Use of a mutant OGA for detecting O-GlcNAc modified proteins. Biochemical Journal, 2015, 472, e25-e26.	3.7	1
62	Modulating environmental signals to reveal mechanisms and vulnerabilities of cancer persisters. Science Advances, 2022, 8, eabi7711.	10.3	1
63	Phosphoproteomics of Tyrosine Kinases in the Nervous System. Neuromethods, 2016, , 143-154.	0.3	0
64	A two-step probing method to compare lysine accessibility across macromolecular complex conformations. RNA Biology, 2019, 16, 1346-1354.	3.1	0
65	Using Mass Spectrometry to Characterize the Complex Posttranslational Modifications of Histones. FASEB Journal, 2006, 20, A100.	0.5	0
66	Mapping postâ€translational modifications of the histone variant macroH2A1 using tandem mass spectrometry. FASEB Journal, 2006, 20, A528.	0.5	0
67	Largeâ€scale Detection of Oâ€GlcNAc Modification Sites using Lectin Chromatography and Electron Transfer Dissociation Mass Spectrometry. FASEB Journal, 2009, 23, 878.3.	0.5	0