

Robert J Chalkley

List of Publications by Year in descending order

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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	Modulating environmental signals to reveal mechanisms and vulnerabilities of cancer persisters. <i>Science Advances</i> , 2022, 8, eabi7711.	10.3	1
2	15N Metabolic Labeling Quantification Workflow in Arabidopsis Using Protein Prospector. <i>Frontiers in Plant Science</i> , 2022, 13, 832562.	3.6	10
3	TSAFinder: exhaustive tumor-specific antigen detection with RNAseq. <i>Bioinformatics</i> , 2022, 38, 2422-2427.	4.1	3
4	Application of Parallel Reaction Monitoring in 15N Labeled Samples for Quantification. <i>Frontiers in Plant Science</i> , 2022, 13, 832585.	3.6	4
5	Methods for Enrichment and Assignment of N-Acetylglucosamine Modification Sites. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100031.	3.8	21
6	Community evaluation of glycoproteomics informatics solutions reveals high-performance search strategies for serum glycopeptide analysis. <i>Nature Methods</i> , 2021, 18, 1304-1316.	19.0	74
7	Proteomic analysis of platelet-rich and platelet-poor plasma. <i>Regenerative Therapy</i> , 2020, 15, 226-235.	3.0	13
8	The effectiveness of filtering glycopeptide peak list files for Y ions. <i>Molecular Omics</i> , 2020, 16, 147-155.	2.8	14
9	Characterization of Prenylated C-terminal Peptides Using a Thiopropyl-based Capture Technique and LC-MS/MS. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1005-1016.	3.8	5
10	A two-step probing method to compare lysine accessibility across macromolecular complex conformations. <i>RNA Biology</i> , 2019, 16, 1346-1354.	3.1	0
11	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	3.7	22
12	Initial Guidelines for Manuscripts Employing Data-independent Acquisition Mass Spectrometry for Proteomic Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1-2.	3.8	11
13	Revealing nascent proteomics in signaling pathways and cell differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2353-2358.	7.1	51
14	Prp8 positioning of U5 snRNA is linked to 5' splice site recognition. <i>Rna</i> , 2018, 24, 769-777.	3.5	13
15	Proteomic analysis reveals O-GlcNAc modification on proteins with key regulatory functions in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1536-E1543.	7.1	101
16	New Guidelines for Publication of Manuscripts Describing Development and Application of Targeted Mass Spectrometry Measurements of Peptides and Proteins. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 327-328.	3.8	33
17	Hyper-O-GlcNAcylation activates nuclear factor κ B-light-chain-enhancer of activated B cells (NF- κ B) signaling through interplay with phosphorylation and acetylation. <i>Journal of Biological Chemistry</i> , 2017, 292, 9150-9163.	3.4	53
18	PPKs mediate direct signal transfer from phytochrome photoreceptors to transcription factor PIF3. <i>Nature Communications</i> , 2017, 8, 15236.	12.8	132

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19	Peripheral Elevation of a Klotho Fragment Enhances Brain Function and Resilience in Young, Aging, and I±-Synuclein Transgenic Mice. <i>Cell Reports</i> , 2017, 20, 1360-1371.	6.4	84
20	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1275-1285.	3.8	55
21	Use of a glycosylation site database to improve glycopeptide identification from complex mixtures. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 571-577.	3.7	23
22	Modification Site Localization in Peptides. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 243-247.	1.6	2
23	Phosphoproteomics of Tyrosine Kinases in the Nervous System. <i>NeuroMethods</i> , 2016, , 143-154.	0.3	0
24	N-Glycopeptide Profiling in Arabidopsis Inflorescence. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2048-2054.	3.8	41
25	Glyco-centric lectin magnetic bead array (LeMBA) ⁺ proteomics dataset of human serum samples from healthy, Barrett's esophagus and esophageal adenocarcinoma individuals. <i>Data in Brief</i> , 2016, 7, 1058-1062.	1.0	6
26	Proteotranscriptomic Profiling of 231-BR Breast Cancer Cells: Identification of Potential Biomarkers and Therapeutic Targets for Brain Metastasis. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2316-2330.	3.8	59
27	Use of a mutant OGA for detecting O-GlcNAc modified proteins. <i>Biochemical Journal</i> , 2015, 472, e25-e26.	3.7	1
28	Characterizing Sialic Acid Variants at the Glycopeptide Level. <i>Analytical Chemistry</i> , 2015, 87, 3064-3071.	6.5	57
29	Tissue-Specific Glycosylation at the Glycopeptide Level. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2103-2110.	3.8	97
30	NGF and ProNGF: Regulation of neuronal and neoplastic responses through receptor signaling. <i>Advances in Biological Regulation</i> , 2015, 58, 16-27.	2.3	91
31	Lessons in <i>de novo</i> peptide sequencing by tandem mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2015, 34, 43-63.	5.4	167
32	Matching Cross-linked Peptide Spectra: Only as Good as the Worst Identification. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 420-434.	3.8	153
33	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	17.5	2,505
34	Proteome Informatics Research Group (iPRG)_2012: A Study on Detecting Modified Peptides in a Complex Mixture. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 360-371.	3.8	20
35	Molecular Architecture of Photoreceptor Phosphodiesterase Elucidated by Chemical Cross-Linking and Integrative Modeling. <i>Journal of Molecular Biology</i> , 2014, 426, 3713-3728.	4.2	37
36	MS-Viewer: A Web-based Spectral Viewer for Proteomics Results. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1392-1396.	3.8	122

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37	Improving Peptide Identification Using Empirical Scoring Systems. <i>Methods in Molecular Biology</i> , 2013, 1007, 173-182.	0.9	5
38	When Targetâ€œDecoy False Discovery Rate Estimations Are Inaccurate and How to Spot Instances. <i>Journal of Proteome Research</i> , 2013, 12, 1062-1064.	3.7	23
39	The DegraBase: A Database of Proteolysis in Healthy and Apoptotic Human Cells. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 813-824.	3.8	124
40	Rearrangements within human spliceosomes captured after exon ligation. <i>Rna</i> , 2013, 19, 400-412.	3.5	41
41	Dissecting the Roles of Tyrosines 490 and 785 of TrkA Protein in the Induction of Downstream Protein Phosphorylation Using Chimeric Receptors. <i>Journal of Biological Chemistry</i> , 2013, 288, 16606-16618.	3.4	18
42	The Induction of Serine/Threonine Protein Phosphorylations by a PDGFR/TrkA Chimera in Stably Transfected PC12 Cells. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 15-30.	3.8	17
43	Modification Site Localization Scoring: Strategies and Performance. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 3-14.	3.8	100
44	Receptor tyrosine kinase signaling â€œ a proteomic perspective. <i>Advances in Enzyme Regulation</i> , 2011, 51, 293-305.	2.6	11
45	Breaking Up the C Complex Spliceosome Shows Stable Association of Proteins with the Lariat Intron Intermediate. <i>PLoS ONE</i> , 2011, 6, e19061.	2.5	8
46	Identification of O-linked Î²-d-N-acetylglucosamine-Modified Proteins from Arabidopsis. <i>Methods in Molecular Biology</i> , 2011, 876, 33-45.	0.9	11
47	Modification Site Localization Scoring Integrated into a Search Engine. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.008078.	3.8	106
48	The Effect of Using an Inappropriate Protein Database for Proteomic Data Analysis. <i>PLoS ONE</i> , 2011, 6, e20873.	2.5	52
49	Mass Spectrometric Analysis, Automated Identification and Complete Annotation of O-Linked Glycopeptides. <i>European Journal of Mass Spectrometry</i> , 2010, 16, 421-428.	1.0	41
50	Protein PTMs: postâ€œtranslational modifications or pesky trouble makers?. <i>Journal of Mass Spectrometry</i> , 2010, 45, 1095-1097.	1.6	14
51	Improving Software Performance for Peptide Electron Transfer Dissociation Data Analysis by Implementation of Charge State- and Sequence-Dependent Scoring. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1795-1803.	3.8	53
52	Finding Chimeras: a Bioinformatics Strategy for Identification of Cross-linked Peptides. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 25-31.	3.8	67
53	Instrumentation for LC-MS/MS in Proteomics. <i>Methods in Molecular Biology</i> , 2010, 658, 47-60.	0.9	12
54	Identification of protein O-GlcNAcylation sites using electron transfer dissociation mass spectrometry on native peptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8894-8899.	7.1	225

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55	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. <i>Journal of Molecular Medicine</i> , 2009, 87, 507-514.	3.9	24
56	The Role of Exon Sequences in C Complex Spliceosome Structure. <i>Journal of Molecular Biology</i> , 2009, 394, 363-375.	4.2	19
57	Large-scale Detection of O-GlcNAc Modification Sites using Lectin Chromatography and Electron Transfer Dissociation Mass Spectrometry. <i>FASEB Journal</i> , 2009, 23, 878.3.	0.5	0
58	The PSI-MOD community standard for representation of protein modification data. <i>Nature Biotechnology</i> , 2008, 26, 864-866.	17.5	132
59	In-depth Analysis of Tandem Mass Spectrometry Data from Disparate Instrument Types. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2386-2398.	3.8	181
60	O-Linked N-Acetylglucosamine Proteomics of Postsynaptic Density Preparations Using Lectin Weak Affinity Chromatography and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 923-934.	3.8	312
61	Using Mass Spectrometry to Characterize the Complex Posttranslational Modifications of Histones. <i>FASEB Journal</i> , 2006, 20, A100.	0.5	0
62	Mapping posttranslational modifications of the histone variant macroH2A1 using tandem mass spectrometry. <i>FASEB Journal</i> , 2006, 20, A528.	0.5	0
63	Quantitative analysis of both protein expression and serine/threonine post-translational modifications through stable isotope labeling with dithiothreitol. <i>Proteomics</i> , 2005, 5, 388-398.	2.2	169
64	Comprehensive Analysis of a Multidimensional Liquid Chromatography Mass Spectrometry Dataset Acquired on a Quadrupole Selecting, Quadrupole Collision Cell, Time-of-flight Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1194-1204.	3.8	171
65	Bioinformatic Methods to Exploit Mass Spectrometric Data for Proteomic Applications. <i>Methods in Enzymology</i> , 2005, 402, 289-312.	1.0	46
66	Mass spectrometric analysis of histone posttranslational modifications. <i>Methods</i> , 2005, 36, 383-394.	3.8	39
67	Identification of GlcNAcylation sites of peptides and Î±-crystallin using Q-TOF mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 1106-1113.	2.8	76