

Nicolas L Young

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

3,771
citations

218677

26
h-index

155660

55
g-index

59
all docs

59
docs citations

59
times ranked

5819
citing authors

#	ARTICLE	IF	CITATIONS
1	Histone variant-specific post-translational modifications. <i>Seminars in Cell and Developmental Biology</i> , 2023, 135, 73-84.	5.0	9
2	High-throughput profiling of histone post-translational modifications and chromatin modifying proteins by reverse phase protein array. <i>Journal of Proteomics</i> , 2022, 262, 104596.	2.4	10
3	Discovery of small molecules targeting the tandem tudor domain of the epigenetic factor UHRF1 using fragment-based ligand discovery. <i>Scientific Reports</i> , 2021, 11, 1121.	3.3	14
4	Expeditious Extraction of Histones from Limited Cells or Tissue Samples and Quantitative Top-Down Proteomic Analysis. <i>Current Protocols</i> , 2021, 1, e26.	2.9	11
5	Combinations of histone post-translational modifications. <i>Biochemical Journal</i> , 2021, 478, 511-532.	3.7	46
6	Gene therapy using AÎ ² variants for amyloid reduction. <i>Molecular Therapy</i> , 2021, 29, 2294-2307.	8.2	7
7	The histone H3.3 chaperone HIRA restrains erythroid-biased differentiation of adult hematopoietic stem cells. <i>Stem Cell Reports</i> , 2021, 16, 2014-2028.	4.8	9
8	Mechanistic insights into KDM4A driven genomic instability. <i>Biochemical Society Transactions</i> , 2021, 49, 93-105.	3.4	13
9	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1783-1802.	2.8	67
10	Orsay Virus CP-Î Adopts a Novel Î ² -Bracelet Structural Fold and Incorporates into Virions as a Head Fiber. <i>Journal of Virology</i> , 2020, 94, .	3.4	2
11	Characterization of SETD3 methyltransferase-mediated protein methionine methylation. <i>Journal of Biological Chemistry</i> , 2020, 295, 10901-10910.	3.4	14
12	Methodological innovations drive conceptual innovations forward in chromatin biology. <i>Methods</i> , 2020, 184, 1-3.	3.8	0
13	One-Pot Quantitative Top- and Middle-Down Analysis of GluC-Digested Histone H4. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2514-2525.	2.8	13
14	AMP-activated protein kinase links acetyl-CoA homeostasis to BRD4 recruitment in acute myeloid leukemia. <i>Blood</i> , 2019, 134, 2183-2194.	1.4	25
15	High-Throughput Quantitative Top-Down Proteomics: Histone H4. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2548-2560.	2.8	26
16	Middle-Down Characterization of the Cell Cycle Dependence of Histone H4 Posttranslational Modifications and Proteoforms. <i>Proteomics</i> , 2018, 18, e1700442.	2.2	31
17	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
18	The histone H4 proteoform dynamics in response to SUV4-20 inhibition reveals single molecule mechanisms of inhibitor resistance. <i>Epigenetics and Chromatin</i> , 2018, 11, 29.	3.9	24

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19	Control of Hexamerization, Assembly, and Excluded Strand Specificity for the <i>Sulfolobus solfataricus</i> MCM Helicase. <i>Biochemistry</i> , 2018, 57, 5672-5682.	2.5	4
20	Early butyrate induced acetylation of histone H4 is proteoform specific and linked to methylation state. <i>Epigenetics</i> , 2018, 13, 519-535.	2.7	26
21	Recent Advances in Understanding Histone Modification Events. <i>Current Molecular Biology Reports</i> , 2017, 3, 11-17.	1.6	3
22	Ultrahigh-resolution Fourier transform ion cyclotron resonance mass spectrometry and tandem mass spectrometry for peptide <i>de novo</i> amino acid sequencing for a seven-protein mixture by paired single-residue transposed Lys-N and Lys-C digestion. <i>Rapid Communications in Mass Spectrometry</i> , 2017, 31, 207-217.	1.5	3
23	Mapping the contact surfaces in the Lamin A:AIMP3 complex by hydrogen/deuterium exchange FT-ICR mass spectrometry. <i>PLoS ONE</i> , 2017, 12, e0181869.	2.5	5
24	Structure of a pentameric virion-associated fiber with a potential role in Orsay virus entry to host cells. <i>PLoS Pathogens</i> , 2017, 13, e1006231.	4.7	11
25	DNA Interactions Probed by Hydrogen-Deuterium Exchange (HDX) Fourier Transform Ion Cyclotron Resonance Mass Spectrometry Confirm External Binding Sites on the Minichromosomal Maintenance (MCM) Helicase. <i>Journal of Biological Chemistry</i> , 2016, 291, 12467-12480.	3.4	18
26	Label-Free Relative Quantitation of Isobaric and Isomeric Human Histone H2A and H2B Variants by Fourier Transform Ion Cyclotron Resonance Top-Down MS/MS. <i>Journal of Proteome Research</i> , 2016, 15, 3196-3203.	3.7	27
27	Quantitative Mass Spectrometry Reveals that Intact Histone H1 Phosphorylations are Variant Specific and Exhibit Single Molecule Hierarchical Dependence. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 818-833.	3.8	29
28	Epitope mapping of 7S cashew antigen in complex with antibody by solution-phase H/D exchange monitored by FT-ICR mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2015, 50, 812-819.	1.6	18
29	Paired single residue-transposed Lys-N and Lys-C digestions for label-free identification of N-terminal and C-terminal MS/MS peptide product ions: ultrahigh resolution Fourier transform ion cyclotron resonance mass spectrometry and tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2015, 29, 659-666.	1.5	5
30	The N-terminal Domain of Escherichia coli Assimilatory NADPH-Sulfite Reductase Hemoprotein Is an Oligomerization Domain That Mediates Holoenzyme Assembly. <i>Journal of Biological Chemistry</i> , 2015, 290, 19319-19333.	3.4	14
31	Ultraviolet photodissociation enhances top-down mass spectrometry as demonstrated on green fluorescent protein variants. <i>Proteomics</i> , 2014, 14, 1128-1129.	2.2	6
32	Chemical inhibition of prometastatic lysyl-tRNA synthetase-laminin receptor interaction. <i>Nature Chemical Biology</i> , 2014, 10, 29-34.	8.0	55
33	Protected Amine Labels: A Versatile Molecular Scaffold for Multiplexed Nominal Mass and Sub-Da Isotopologue Quantitative Proteomic Reagents. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 636-650.	2.8	6
34	The first pilot project of the consortium for top-down proteomics: <i>status report</i> . <i>Proteomics</i> , 2014, 14, 1130-1140.	2.2	90
35	Rapid Screening for Potential Epitopes Reactive with a Polyclonal Antibody by Solution-Phase H/D Exchange Monitored by FT-ICR Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1016-1025.	2.8	25
36	H1 histones: current perspectives and challenges. <i>Nucleic Acids Research</i> , 2013, 41, 9593-9609.	14.5	188

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37	Nucleotide-induced conformational changes of tetradecameric GroEL mapped by H/D exchange monitored by FT-ICR mass spectrometry. <i>Scientific Reports</i> , 2013, 3, 1247.	3.3	26
38	SIRT7 links H3K18 deacetylation to maintenance of oncogenic transformation. <i>Nature</i> , 2012, 487, 114-118.	27.8	503
39	Asymmetrically Modified Nucleosomes. <i>Cell</i> , 2012, 151, 181-193.	28.9	367
40	Methylation of H4 lysines 5, 8 and 12 by yeast Set5 calibrates chromatin stress responses. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 361-363.	8.2	49
41	Proteomic Interrogation of Human Chromatin. <i>PLoS ONE</i> , 2011, 6, e24747.	2.5	35
42	Methylation of H2AR29 is a novel repressive PRMT6 target. <i>Epigenetics and Chromatin</i> , 2011, 4, 11.	3.9	74
43	Histone Deacetylase 9 Deficiency Protects against Effector T Cell-mediated Systemic Autoimmunity. <i>Journal of Biological Chemistry</i> , 2011, 286, 28833-28843.	3.4	90
44	Quantitative Proteomic Approaches to Studying Histone Modifications. <i>Current Chemical Genomics</i> , 2011, 5, 106-114.	2.0	18
45	The significance, development and progress of high-throughput combinatorial histone code analysis. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 3983-4000.	5.4	90
46	Collective mass spectrometry approaches reveal broad and combinatorial modification of high mobility group protein A1a. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 960-970.	2.8	19
47	Systems-wide proteomic characterization of combinatorial post-translational modification patterns. <i>Expert Review of Proteomics</i> , 2010, 7, 79-92.	3.0	55
48	A Novel Approach for Untargeted Post-translational Modification Identification Using Integer Linear Optimization and Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 764-779.	3.8	42
49	Quantitative proteomics reveals direct and indirect alterations in the histone code following methyltransferase knockdown. <i>Molecular BioSystems</i> , 2010, 6, 1719.	2.9	36
50	Chromatin-Specific Remodeling by HMGB1 and Linker Histone H1 Silences Proinflammatory Genes during Endotoxin Tolerance. <i>Molecular and Cellular Biology</i> , 2009, 29, 1959-1971.	2.3	137
51	A Mixed Integer Linear Optimization Framework for the Identification and Quantification of Targeted Post-translational Modifications of Highly Modified Proteins Using Multiplexed Electron Transfer Dissociation Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2527-2543.	3.8	77
52	Heterochromatin Protein 1 Is Extensively Decorated with Histone Code-like Post-translational Modifications. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2432-2442.	3.8	88
53	One-Pot Shotgun Quantitative Mass Spectrometry Characterization of Histones. <i>Journal of Proteome Research</i> , 2009, 8, 5367-5374.	3.7	120
54	Histone H3 Lysine 56 Acetylation Is Linked to the Core Transcriptional Network in Human Embryonic Stem Cells. <i>Molecular Cell</i> , 2009, 33, 417-427.	9.7	176

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55	High Throughput Characterization of Combinatorial Histone Codes. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2266-2284.	3.8	271
56	Steady-State Asymmetric Nanospray Dual Ion Source for Accurate Mass Determination within a Chromatographic Separation. <i>Analytical Chemistry</i> , 2007, 79, 5711-5718.	6.5	8
57	Method to Site-Specifically Identify and Quantitate Carbonyl End Products of Protein Oxidation Using Oxidation-Dependent Element Coded Affinity Tags (O-ECAT) and NanoLiquid Chromatography Fourier Transform Mass Spectrometry. <i>Journal of Proteome Research</i> , 2006, 5, 539-547.	3.7	51