

Carrie D Nicora

List of Publications by Year in descending order

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93
papers

5,200
citations

87843

38
h-index

102432

66
g-index

111
all docs

111
docs citations

111
times ranked

8627
citing authors

#	ARTICLE	IF	CITATIONS
1	Auto-deconvolution and molecular networking of gas chromatography–mass spectrometry data. <i>Nature Biotechnology</i> , 2021, 39, 169-173.	9.4	78
2	Re-routing of Sugar Catabolism Provides a Better Insight Into Fungal Flexibility in Using Plant Biomass-Derived Monomers as Substrates. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 644216.	2.0	4
3	Parallel Multi-Omics in High-Risk Subjects for the Identification of Integrated Biomarker Signatures of Type 1 Diabetes. <i>Biomolecules</i> , 2021, 11, 383.	1.8	17
4	Integration of Proteomics and Metabolomics Into the Design, Build, Test, Learn Cycle to Improve 3-Hydroxypropionic Acid Production in <i>Aspergillus pseudoterreus</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 603832.	2.0	12
5	From Plants to Ants: Fungal Modification of Leaf Lipids for Nutrition and Communication in the Leaf-Cutter Ant Fungal Garden Ecosystem. <i>MSystems</i> , 2021, 6, .	1.7	11
6	Decrypting bacterial polyphenol metabolism in an anoxic wetland soil. <i>Nature Communications</i> , 2021, 12, 2466.	5.8	45
7	Further engineering of <i>R. toruloides</i> for the production of terpenes from lignocellulosic biomass. <i>Biotechnology for Biofuels</i> , 2021, 14, 101.	6.2	31
8	A Comprehensive Urine Proteome Database Generated From Patients With Various Renal Conditions and Prostate Cancer. <i>Frontiers in Medicine</i> , 2021, 8, 548212.	1.2	18
9	A Fungal Secretome Adapted for Stress Enabled a Radical Wood Decay Mechanism. <i>MBio</i> , 2021, 12, e0204021.	1.8	13
10	Moisture modulates soil reservoirs of active DNA and RNA viruses. <i>Communications Biology</i> , 2021, 4, 992.	2.0	33
11	A Pilot Study of Urine Proteomics in COVID-19–Associated Acute Kidney Injury. <i>Kidney International Reports</i> , 2021, 6, 3064-3069.	0.4	5
12	<i>De novo</i> sequencing and native mass spectrometry revealed hetero-association of dirigent protein homologs and potential interacting proteins in <i>Forsythia</i> – <i>intermedia</i> . <i>Analyst</i> , The, 2021, 146, 7670-7681.	1.7	0
13	Colonies of the fungus <i>Aspergillus niger</i> are highly differentiated to adapt to local carbon source variation. <i>Environmental Microbiology</i> , 2020, 22, 1154-1166.	1.8	15
14	Lignin induced iron reduction by novel sp., <i>Tolomonas lignolytic</i> BRL6-1. <i>PLoS ONE</i> , 2020, 15, e0233823.	1.1	8
15	Endophyte-Promoted Phosphorus Solubilization in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 567918.	1.7	54
16	Receptor-Driven ERK Pulses Reconfigure MAPK Signaling and Enable Persistence of Drug-Adapted BRAF-Mutant Melanoma Cells. <i>Cell Systems</i> , 2020, 11, 478-494.e9.	2.9	71
17	The Specific Carbohydrate Diet and Diet Modification as Induction Therapy for Pediatric Crohn’s Disease: A Randomized Diet Controlled Trial. <i>Nutrients</i> , 2020, 12, 3749.	1.7	62
18	Production of ent-kaurene from lignocellulosic hydrolysate in <i>Rhodospiridium toruloides</i> . <i>Microbial Cell Factories</i> , 2020, 19, 24.	1.9	30

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19	Integrated network modeling approach defines key metabolic responses of soil microbiomes to perturbations. <i>Scientific Reports</i> , 2020, 10, 10882.	1.6	9
20	Metabolite, Protein, and Lipid Extraction (MPLEx): A Method that Simultaneously Inactivates Middle East Respiratory Syndrome Coronavirus and Allows Analysis of Multiple Host Cell Components Following Infection. <i>Methods in Molecular Biology</i> , 2020, 2099, 173-194.	0.4	15
21	Tandem Mass Tag Labeling Facilitates Reversed-Phase Liquid Chromatography-Mass Spectrometry Analysis of Hydrophilic Phosphopeptides. <i>Analytical Chemistry</i> , 2019, 91, 11606-11613.	3.2	22
22	Proteomic Insights into Phycobilisome Degradation, A Selective and Tightly Controlled Process in The Fast-Growing Cyanobacterium <i>Synechococcus elongatus</i> UTEX 2973. <i>Biomolecules</i> , 2019, 9, 374.	1.8	13
23	Detection of Organohalide-Respiring Enzyme Biomarkers at a Bioaugmented TCE-Contaminated Field Site. <i>Frontiers in Microbiology</i> , 2019, 10, 1433.	1.5	10
24	Exploiting the Semidestructive Nature of Gas Cluster Ion Beam Time-of-Flight Secondary Ion Mass Spectrometry Imaging for Simultaneous Localization and Confident Lipid Annotations. <i>Analytical Chemistry</i> , 2019, 91, 15073-15080.	3.2	21
25	Multomics resolution of molecular events during a day in the life of <i>Chlamydomonas</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2374-2383.	3.3	133
26	In situ transformation of ethoxylate and glycol surfactants by shale-colonizing microorganisms during hydraulic fracturing. <i>ISME Journal</i> , 2019, 13, 2690-2700.	4.4	18
27	Ion mobility spectrometry and the omics: Distinguishing isomers, molecular classes and contaminant ions in complex samples. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 116, 292-299.	5.8	71
28	Gut anatomical properties and microbial functional assembly promote lignocellulose deconstruction and colony subsistence of a wood-feeding beetle. <i>Nature Microbiology</i> , 2019, 4, 864-875.	5.9	68
29	Deep-Subsurface Pressure Stimulates Metabolic Plasticity in Shale-Colonizing <i>Halanaerobium</i> spp. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	20
30	Insights into the histology of planarian flatworm <i>Phagocata gracilis</i> based on location specific, intact lipid information provided by GCIB-ToF-SIMS imaging. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 733-743.	1.2	9
31	Broad Substrate-Specific Phosphorylation Events Are Associated With the Initial Stage of Plant Cell Wall Recognition in <i>Neurospora crassa</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2317.	1.5	25
32	Proteomic Sample Preparation Techniques: Toward Forensic Proteomic Applications. <i>ACS Symposium Series</i> , 2019, , 29-46.	0.5	0
33	Genomes and secretomes of Ascomycota fungi reveal diverse functions in plant biomass decomposition and pathogenesis. <i>BMC Genomics</i> , 2019, 20, 976.	1.2	96
34	Carrier-Assisted Single-Tube Processing Approach for Targeted Proteomics Analysis of Low Numbers of Mammalian Cells. <i>Analytical Chemistry</i> , 2019, 91, 1441-1451.	3.2	24
35	Abstract LB-B09: ERK pulses drive non-genetic resistance in drug-adapted BRAFV600E melanoma cells. , 2019, , .		0
36	Salmonella-Mediated Inflammation Eliminates Competitors for Fructose-Asparagine in the Gut. <i>Infection and Immunity</i> , 2018, 86, .	1.0	12

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37	MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1012-E1021.	3.3	142
38	Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. <i>Nature Microbiology</i> , 2018, 3, 1274-1284.	5.9	144
39	Rare Earth Elements Alter Redox Balance in <i>Methylobacterium alcaliphilum</i> 20ZR. <i>Frontiers in Microbiology</i> , 2018, 9, 2735.	1.5	28
40	The MPLEx Protocol for Multi-omic Analyses of Soil Samples. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	19
41	Urinary Virome Perturbations in Kidney Transplantation. <i>Frontiers in Medicine</i> , 2018, 5, 72.	1.2	12
42	Structure Elucidation of Unknown Metabolites in Metabolomics by Combined NMR and MS/MS Prediction. <i>Metabolites</i> , 2018, 8, 8.	1.3	54
43	Genome-centric view of carbon processing in thawing permafrost. <i>Nature</i> , 2018, 560, 49-54.	13.7	337
44	Coupled laboratory and field investigations resolve microbial interactions that underpin persistence in hydraulically fractured shales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6585-E6594.	3.3	69
45	Addressing the challenge of soil metaproteome complexity by improving metaproteome depth of coverage through two-dimensional liquid chromatography. <i>Soil Biology and Biochemistry</i> , 2018, 125, 290-299.	4.2	37
46	Facile carrier-assisted targeted mass spectrometric approach for proteomic analysis of low numbers of mammalian cells. <i>Communications Biology</i> , 2018, 1, 103.	2.0	21
47	Multi 'omics comparison reveals metabolome biochemistry, not microbiome composition or gene expression, corresponds to elevated biogeochemical function in the hyporheic zone. <i>Science of the Total Environment</i> , 2018, 642, 742-753.	3.9	60
48	MPLEx: a method for simultaneous pathogen inactivation and extraction of samples for multi-omics profiling. <i>Analyst</i> , The, 2017, 142, 442-448.	1.7	43
49	New roles in hemicellulosic sugar fermentation for the uncultivated <i>Bacteroidetes</i> family BS11. <i>ISME Journal</i> , 2017, 11, 691-703.	4.4	115
50	Targeted quantification of functional enzyme dynamics in environmental samples for microbially mediated biogeochemical processes. <i>Environmental Microbiology Reports</i> , 2017, 9, 512-521.	1.0	16
51	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in <i>Yarrowia lipolytica</i> . <i>MBio</i> , 2017, 8, .	1.8	38
52	LC-SRM-Based Targeted Quantification of Urinary Protein Biomarkers. <i>Methods in Molecular Biology</i> , 2017, 1788, 145-156.	0.4	4
53	Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .	1.3	62
54	Optimization for Peptide Sample Preparation for Urine Peptidomics. <i>Methods in Molecular Biology</i> , 2017, 1788, 63-72.	0.4	5

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55	Effects of delayed NSAID administration after experimental eccentric contraction injury – A cellular and proteomics study. PLoS ONE, 2017, 12, e0172486.	1.1	14
56	Phycobilisome truncation causes widespread proteome changes in <i>Synechocystis</i> sp. PCC 6803. PLoS ONE, 2017, 12, e0173251.	1.1	24
57	Multiplexed targeted mass spectrometry assays for prostate cancer-associated urinary proteins. Oncotarget, 2017, 8, 101887-101898.	0.8	14
58	MPLEx: a Robust and Universal Protocol for Single-Sample Integrative Proteomic, Metabolomic, and Lipidomic Analyses. MSSystems, 2016, 1, .	1.7	166
59	The fungal cultivar of leaf-cutter ants produces specific enzymes in response to different plant substrates. Molecular Ecology, 2016, 25, 5795-5805.	2.0	37
60	Proteome Remodeling in Response to Sulfur Limitation in <i>Candidatus</i> <i>Pelagibacter ubique</i> . MSSystems, 2016, 1, .	1.7	18
61	Moleculo Long-Read Sequencing Facilitates Assembly and Genomic Binning from Complex Soil Metagenomes. MSSystems, 2016, 1, .	1.7	89
62	Unambiguous metabolite identification in high-throughput metabolomics by hybrid 1D ¹ H NMR/ESI MS ¹ approach. Magnetic Resonance in Chemistry, 2016, 54, 998-1003.	1.1	22
63	Comparative Community Proteomics Demonstrates the Unexpected Importance of Actinobacterial Glycoside Hydrolase Family 12 Protein for Crystalline Cellulose Hydrolysis. MBio, 2016, 7, .	1.8	17
64	The abundant marine bacterium <i>Pelagibacter</i> simultaneously catabolizes dimethylsulfoniopropionate to the gases dimethyl sulfide and methanethiol. Nature Microbiology, 2016, 1, 16065.	5.9	110
65	Conservation of protein abundance patterns reveals the regulatory architecture of the EGFR-MAPK pathway. Science Signaling, 2016, 9, rs6.	1.6	119
66	Multi-omics analysis reveals regulators of the response to nitrogen limitation in <i>Yarrowia lipolytica</i> . BMC Genomics, 2016, 17, 138.	1.2	62
67	Integrated Omics Analysis of Pathogenic Host Responses during Pandemic H1N1 Influenza Virus Infection: The Crucial Role of Lipid Metabolism. Cell Host and Microbe, 2016, 19, 254-266.	5.1	75
68	Mining the human urine proteome for monitoring renal transplant injury. Kidney International, 2016, 89, 1244-1252.	2.6	80
69	An efficient method for native protein purification in the selected range from prostate cancer tissue digests. Chinese Clinical Oncology, 2016, 5, 78-78.	0.4	4
70	Multi-Omic Dynamics Associate Oxygenic Photosynthesis with Nitrogenase-Mediated H ₂ Production in <i>Cyanospora</i> sp. ATCC 51142. Scientific Reports, 2015, 5, 16004.	1.6	13
71	Subunit compositions of Arabidopsis RNA polymerases I and III reveal Pol I- and Pol III-specific forms of the AC40 subunit and alternative forms of the C53 subunit. Nucleic Acids Research, 2015, 43, 4163-4178.	6.5	21
72	Sensitive Targeted Quantification of ERK Phosphorylation Dynamics and Stoichiometry in Human Cells without Affinity Enrichment. Analytical Chemistry, 2015, 87, 1103-1110.	3.2	32

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73	Diacyltransferase Activity and Chain Length Specificity of <i>Mycobacterium tuberculosis</i> PapA5 in the Synthesis of Alkyl $\hat{1}$ -Diol Lipids. <i>Biochemistry</i> , 2015, 54, 5457-5468.	1.2	9
74	Enrichment and Broad Representation of Plant Biomass-Degrading Enzymes in the Specialized Hyphal Swellings of <i>Leucoagaricus gongylophorus</i> , the Fungal Symbiont of Leaf-Cutter Ants. <i>PLoS ONE</i> , 2015, 10, e0134752.	1.1	28
75	Bayesian Proteoform Modeling Improves Protein Quantification of Global Proteomic Measurements. <i>Molecular and Cellular Proteomics</i> , 2014, , .	2.5	3
76	Bayesian Proteoform Modeling Improves Protein Quantification of Global Proteomic Measurements. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3639-3646.	2.5	38
77	Functional Diversification of Maize RNA Polymerase IV and V Subtypes via Alternative Catalytic Subunits. <i>Cell Reports</i> , 2014, 9, 378-390.	2.9	71
78	Protein and microRNA biomarkers from lavage, urine, and serum in military personnel evaluated for dyspnea. <i>BMC Medical Genomics</i> , 2014, 7, 58.	0.7	12
79	Proteomics informed by transcriptomics identifies novel secreted proteins in <i>Dermacentor andersoni</i> saliva. <i>International Journal for Parasitology</i> , 2014, 44, 1029-1037.	1.3	75
80	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.	4.4	170
81	The Identification of Novel Potential Injury Mechanisms and Candidate Biomarkers in Renal Allograft Rejection by Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 621-631.	2.5	73
82	Perturbations in the Urinary Exosome in Transplant Rejection. <i>Frontiers in Medicine</i> , 2014, 1, 57.	1.2	43
83	Long-Gradient Separations Coupled with Selected Reaction Monitoring for Highly Sensitive, Large Scale Targeted Protein Quantification in a Single Analysis. <i>Analytical Chemistry</i> , 2013, 85, 9196-9203.	3.2	41
84	<i>Leucoagaricus gongylophorus</i> Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3770-3778.	1.4	98
85	Evidence supporting dissimilatory and assimilatory lignin degradation in <i>Enterobacter lignolyticus</i> SCF1. <i>Frontiers in Microbiology</i> , 2013, 4, 280.	1.5	92
86	In Vitro Transcription Activities of Pol IV, Pol V, and RDR2 Reveal Coupling of Pol IV and RDR2 for dsRNA Synthesis in Plant RNA Silencing. <i>Molecular Cell</i> , 2012, 48, 811-818.	4.5	180
87	Simple Sodium Dodecyl Sulfate-Assisted Sample Preparation Method for LC-MS-Based Proteomics Applications. <i>Analytical Chemistry</i> , 2012, 84, 2862-2867.	3.2	74
88	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. <i>ISME Journal</i> , 2012, 6, 1688-1701.	4.4	126
89	Transport functions dominate the SAR11 metaproteome at low-nutrient extremes in the Sargasso Sea. <i>ISME Journal</i> , 2009, 3, 93-105.	4.4	295
90	Subunit Compositions of the RNA-Silencing Enzymes Pol IV and Pol V Reveal Their Origins as Specialized Forms of RNA Polymerase II. <i>Molecular Cell</i> , 2009, 33, 192-203.	4.5	225

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91	Proteogenomic Monitoring of <i>Geobacter</i> Physiology during Stimulated Uranium Bioremediation. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6591-6599.	1.4	136
92	Proteomic Analysis of Stationary Phase in the Marine Bacterium <i>Candidatus Pelagibacter ubique</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 4091-4100.	1.4	78
93	Phosphoproteome Profiling of Human Skin Fibroblast Cells in Response to Low- and High-Dose Irradiation. <i>Journal of Proteome Research</i> , 2006, 5, 1252-1260.	1.8	108