## Nichollas E Scott

List of Publications by Year in descending order

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96 4,313 36 58
papers citations h-index g-index

119 119 5969
all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Getting more out of FLAG-Tag co-immunoprecipitation mass spectrometry experiments using FAIMS. Journal of Proteomics, 2022, 254, 104473.	2.4	2
2	Oxidative desulfurization pathway for complete catabolism of sulfoquinovose by bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	18
3	Characterization of the O-Glycoproteome of Porphyromonas gingivalis. Microbiology Spectrum, 2022, 10, e0150221.	3.0	11
4	Arginine glycosylation regulates UDP-GlcNAc biosynthesis in Salmonella enterica. Scientific Reports, 2022, 12, 5293.	3.3	7
5	The Phenylacetic Acid Catabolic Pathway Regulates Antibiotic and Oxidative Stress Responses in Acinetobacter. MBio, 2022, 13, e0186321.	4.1	18
6	Sculpting the Bacterial $\langle i \rangle O \langle  i \rangle$ -Glycoproteome: Functional Analyses of Orthologous Oligosaccharyltransferases with Diverse Targeting Specificities. MBio, 2022, 13, e0379721.	4.1	2
7	InvL, an Invasin-Like Adhesin, Is a Type II Secretion System Substrate Required for Acinetobacter baumannii Uropathogenesis. MBio, 2022, 13, .	4.1	11
8	Glycoproteomics. Nature Reviews Methods Primers, 2022, 2, .	21.2	61
9	Glycoproteomics: growing up fast. Current Opinion in Structural Biology, 2021, 68, 18-25.	5.7	33
10	Proteomic Identification of Coxiella burnetii Effector Proteins Targeted to the Host Cell Mitochondria During Infection. Molecular and Cellular Proteomics, 2021, 20, 100005.	3.8	12
11	What Are We Missing by Using Hydrophilic Enrichment? Improving Bacterial Glycoproteome Coverage Using Total Proteome and FAIMS Analyses. Journal of Proteome Research, 2021, 20, 599-612.	3.7	43
12	A glycoengineered antigen exploiting a conserved protein O-glycosylation pathway in the Burkholderia genus for detection of glanders infections. Virulence, 2021, 12, 493-506.	4.4	5
13	SUGAR-seq enables simultaneous detection of glycans, epitopes, and the transcriptome in single cells. Science Advances, 2021, 7, .	10.3	46
14	Editorial overview: Systems biology and the rise and rise of omics approaches. Current Opinion in Chemical Biology, 2021, 60, A1-A3.	6.1	1
15	Arginine glycosylation enhances methylglyoxal detoxification. Scientific Reports, 2021, 11, 3834.	3.3	10
16	Yeast- and antibody-based tools for studying tryptophan C-mannosylation. Nature Chemical Biology, 2021, 17, 428-437.	8.0	17
17	TLR2-mediated activation of innate responses in the upper airways confers antiviral protection of the lungs. JCI Insight, $2021, 6, .$	5.0	15
18	Nanobody cocktails potently neutralize SARS-CoV-2 D614G N501Y variant and protect mice. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	109

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19	NleB2 from enteropathogenic Escherichia coli is a novel arginine-glucose transferase effector. PLoS Pathogens, 2021, 17, e1009658.	4.7	9
20	An atlas of protein-protein interactions across mouse tissues. Cell, 2021, 184, 4073-4089.e17.	28.9	59
21	Synthesis of C-Mannosylated Glycopeptides Enabled by Ni-Catalyzed Photoreductive Cross-Coupling Reactions. Journal of the American Chemical Society, 2021, 143, 12699-12707.	13.7	39
22	Modern Acinetobacter baumannii clinical isolates replicate inside spacious vacuoles and egress from macrophages. PLoS Pathogens, 2021, 17, e1009802.	4.7	21
23	BonA from <i>Acinetobacter baumannii</i> Forms a Divisome-Localized Decamer That Supports Outer Envelope Function. MBio, 2021, 12, e0148021.	4.1	5
24	Characterization of the O-Glycoproteome of Tannerella forsythia. MSphere, 2021, 6, e0064921.	2.9	5
25	Burkholderia PglL enzymes are Serine preferring oligosaccharyltransferases which target conserved proteins across the Burkholderia genus. Communications Biology, 2021, 4, 1045.	4.4	4
26	Development and Immunogenicity of a Prototype Multivalent Group B <i>Streptococcus</i> Bioconjugate Vaccine. ACS Infectious Diseases, 2021, 7, 3111-3123.	3.8	7
27	Community evaluation of glycoproteomics informatics solutions reveals high-performance search strategies for serum glycopeptide analysis. Nature Methods, 2021, 18, 1304-1316.	19.0	74
28	The Application of Open Searching-based Approaches for the Identification of <em>Acinetobacter baumannii</em> O-linked Glycopeptides. Journal of Visualized Experiments, 2021, , .	0.3	2
29	Biogenesis of the Spacious <i>Coxiella</i> -Containing Vacuole Depends on Host Transcription Factors TFEB and TFE3. Infection and Immunity, 2020, 88, .	2.2	12
30	Humoral and circulating follicular helper T cell responses in recovered patients with COVID-19. Nature Medicine, 2020, 26, 1428-1434.	30.7	400
31	2020 FASEB Science Research Conference on Microbial Glycobiology, July 13â€14, 2020. FASEB Journal, 2020, 34, 14069-14072.	0.5	0
32	The Glycoprotease CpaA Secreted by Medically Relevant Acinetobacter Species Targets Multiple $<$ i> $>$ O $<$ /i> $>$ -Linked Host Glycoproteins. MBio, 2020, 11, .	4.1	31
33	The Salmonella Effector SseK3 Targets Small Rab GTPases. Frontiers in Cellular and Infection Microbiology, 2020, 10, 419.	3.9	16
34	CDK13 cooperates with CDK12 to control global RNA polymerase II processivity. Science Advances, 2020, 6, .	10.3	79
35	Open Database Searching Enables the Identification and Comparison of Bacterial Glycoproteomes without Defining Glycan Compositions Prior to Searching. Molecular and Cellular Proteomics, 2020, 19, 1561-1574.	3.8	28
36	Trefoil factors share a lectin activity that defines their role in mucus. Nature Communications, 2020, 11, 2265.	12.8	34

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37	Influence of Protein Glycosylation on Campylobacter fetus Physiology. Frontiers in Microbiology, 2020, 11, 1191.	3.5	7
38	An intra-bacterial activity for a T3SS effector. Scientific Reports, 2020, 10, 1073.	3.3	30
39	A Sulfoglycolytic Entner-Doudoroff Pathway in Rhizobium leguminosarum bv. trifolii SRDI565. Applied and Environmental Microbiology, 2020, 86, .	3.1	14
40	Characterization of the <i>Citrobacter rodentium</i> Cpx regulon and its role in host infection. Molecular Microbiology, 2019, 111, 700-716.	2.5	15
41	A general protein O-glycosylation machinery conserved in Burkholderia species improves bacterial fitness and elicits glycan immunogenicity in humans. Journal of Biological Chemistry, 2019, 294, 13248-13268.	3.4	27
42	Expanding our understanding of the role of microbial glycoproteomes through high-throughput mass spectrometry approaches. Glycoconjugate Journal, 2019, 36, 259-266.	2.7	2
43	Peptidyl-Prolyl Isomerase $\langle i \rangle$ ppiB $\langle  i \rangle$ Is Essential for Proteome Homeostasis and Virulence in Burkholderia pseudomallei. Infection and Immunity, 2019, 87, .	2.2	12
44	Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. IScience, 2019, 19, 1114-1132.	4.1	38
45	Urinary tract colonization is enhanced by a plasmid that regulates uropathogenic Acinetobacter baumannii chromosomal genes. Nature Communications, 2019, 10, 2763.	12.8	80
46	Salmonella Effectors SseK1 and SseK3 Target Death Domain Proteins in the TNF and TRAIL Signaling Pathways*. Molecular and Cellular Proteomics, 2019, 18, 1138-1156.	3.8	55
47	A platform for glycoengineering a polyvalent pneumococcal bioconjugate vaccine using E. coli as a host. Nature Communications, 2019, 10, 891.	12.8	60
48	A promising bioconjugate vaccine against hypervirulent <i>Klebsiella pneumoniae</i> h. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18655-18663.	7.1	116
49	Low pH Exposure During Immunoglobulin G Purification Methods Results in Aggregates That Avidly Bind FcÎ <sup>3</sup> Receptors: Implications for Measuring Fc Dependent Antibody Functions. Frontiers in Immunology, 2019, 10, 2415.	4.8	35
50	Loss of $\langle i \rangle O \langle  i \rangle$ -Linked Protein Glycosylation in Burkholderia cenocepacia Impairs Biofilm Formation and Siderophore Activity and Alters Transcriptional Regulators. MSphere, 2019, 4, .	2.9	12
51	Proteomics Reveals Multiple Phenotypes Associated with N-linked Glycosylation in Campylobacter jejuni. Molecular and Cellular Proteomics, 2019, 18, 715-734.	3.8	70
52	Protein O-fucosyltransferase 2–mediated O-glycosylation of the adhesin MIC2 is dispensable for Toxoplasma gondii tachyzoite infection. Journal of Biological Chemistry, 2019, 294, 1541-1553.	3.4	20
53	Profiling the Escherichia coli membrane protein interactome captured in Peptidisc libraries. ELife, 2019, 8, .	6.0	54
54	Surface Exposure and Packing of Lipoproteins into Outer Membrane Vesicles Are Coupled Processes in <i>Bacteroides</i> . MSphere, 2018, 3, .	2.9	57

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55	Transmission of Cricket paralysis virus via exosome-like vesicles during infection of Drosophila cells. Scientific Reports, 2018, 8, 17353.	3.3	8
56	Synthesis and use of 6,6,6-trifluoro-L-fucose to block core-fucosylation in hybridoma cell lines. Carbohydrate Research, 2018, 465, 4-9.	2.3	13
57	Interactome disassembly during apoptosis occurs independent of caspase cleavage. Molecular Systems Biology, 2017, 13, 906.	7.2	49
58	A forward genetic screen identifies a negative regulator of rapid Ca2+-dependent cell egress (MS1) in the intracellular parasite Toxoplasma gondii. Journal of Biological Chemistry, 2017, 292, 7662-7674.	3.4	27
59	Pathogenic Acinetobacter species have a functional type I secretion system and contact-dependent inhibition systems. Journal of Biological Chemistry, 2017, 292, 9075-9087.	3.4	73
60	The Type III Effector NIeD from Enteropathogenic Escherichia coli Differentiates between Host Substrates p38 and JNK. Infection and Immunity, 2017, 85, .	2.2	13
61	Protein O-fucosylation in Plasmodium falciparum ensures efficient infection of mosquito and vertebrate hosts. Nature Communications, 2017, 8, 561.	12.8	63
62	The bacterial arginine glycosyltransferase effector NleB preferentially modifies Fas-associated death domain protein (FADD). Journal of Biological Chemistry, 2017, 292, 17337-17350.	3.4	53
63	The role of mass spectrometry analysis in bacterial effector characterization. Biochemical Journal, 2017, 474, 2779-2784.	3.7	2
64	Post-translational Mechanisms of Host Subversion by Bacterial Effectors. Trends in Molecular Medicine, 2017, 23, 1088-1102.	6.7	17
65	A Map of Human Mitochondrial Protein Interactions Linked to Neurodegeneration Reveals New Mechanisms of Redox Homeostasis and NF-κB Signaling. Cell Systems, 2017, 5, 564-577.e12.	6.2	44
66	Characterizing Glycoproteins by Mass Spectrometry in Campylobacter jejuni. Methods in Molecular Biology, 2017, 1512, 211-232.	0.9	1
67	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). BMC Bioinformatics, 2017, 18, 457.	2.6	54
68	Protein O-linked glycosylation in the plant pathogen <i>Ralstonia solanacearum</i> . Glycobiology, 2016, 26, cwv098.	2.5	32
69	Genetic Dissection of the Type VI Secretion System in <i>Acinetobacter</i> and Identification of a Novel Peptidoglycan Hydrolase, TagX, Required for Its Biogenesis. MBio, 2016, 7, .	4.1	110
70	Cardiac Ryanodine Receptor (Ryr2)-mediated Calcium Signals Specifically Promote Glucose Oxidation via Pyruvate Dehydrogenase. Journal of Biological Chemistry, 2016, 291, 23490-23505.	3.4	23
71	<scp><i>A</i><fi><scp><i>A</i><fi>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<i>cop&gt;<ip><ip><ip><ip><ip><ip><ip><ip><ip><i< td=""><td>2.5</td><td>90</td></i<></ip></ip></ip></ip></ip></ip></ip></ip></ip></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></i></fi></scp></fi></scp>	2.5	90
72	Structure of human ST8Sialll sialyltransferase provides insight into cell-surface polysialylation. Nature Structural and Molecular Biology, 2015, 22, 627-635.	8.2	62

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73	Development of a computational framework for the analysis of protein correlation profiling and spatial proteomics experiments. Journal of Proteomics, 2015, 118, 112-129.	2.4	30
74	Novel Host Proteins and Signaling Pathways in Enteropathogenic E. coli Pathogenesis Identified by Global Phosphoproteome Analysis *. Molecular and Cellular Proteomics, 2015, 14, 1927-1945.	3.8	32
75	Clinical implications of glycoproteomics for <i> Acinetobacter baumannii </i> ). Expert Review of Proteomics, 2015, 12, 1-3.	3.0	11
76	High-Frequency Variation of Purine Biosynthesis Genes Is a Mechanism of Success in Campylobacter jejuni. MBio, 2015, 6, e00612-15.	4.1	13
77	Enrichment and Identification of Bacterial Glycopeptides by Mass Spectrometry. Methods in Molecular Biology, 2015, 1295, 355-368.	0.9	13
78	A general protein <scp><i>O</i></scp> â€glycosylation system within the <scp><i>B</i></scp> <ii>Urkholderia cepacia<ii>B<ii>Urkholderia cepacia   Molecular Microbiology, 2014, 92, 116-137.</ii></ii></ii>	2.5	56
79	Comparative Proteomics and Glycoproteomics Reveal Increased N-Linked Glycosylation and Relaxed Sequon Specificity in Campylobacter jejuni NCTC11168 O. Journal of Proteome Research, 2014, 13, 5136-5150.	3.7	48
80	Diversity Within the O-linked Protein Glycosylation Systems of Acinetobacter Species. Molecular and Cellular Proteomics, 2014, 13, 2354-2370.	3.8	64
81	Site-Specific Glycan-Peptide Analysis for Determination of <i>N</i> Journal of Proteome Research, 2013, 12, 5791-5800.	3.7	153
82	In Vitro Activity of Neisseria meningitidis PglL O-Oligosaccharyltransferase with Diverse Synthetic Lipid Donors and a UDP-activated Sugar. Journal of Biological Chemistry, 2013, 288, 10578-10587.	3.4	22
83	A common pathway for <i><scp>O</scp></i> â€linked proteinâ€glycosylation and synthesis of capsule in <i><scp>A</scp>cinetobacter baumannii</i> < Molecular Microbiology, 2013, 89, 816-830.	2.5	158
84	Secretome of Transmissible Pseudomonas aeruginosa AES-1R Grown in a Cystic Fibrosis Lung-Like Environment. Journal of Proteome Research, 2013, 12, 5357-5369.	3.7	18
85	Identification of a General O-linked Protein Glycosylation System in Acinetobacter baumannii and Its Role in Virulence and Biofilm Formation. PLoS Pathogens, 2012, 8, e1002758.	4.7	196
86	Diversity in the Protein N-Glycosylation Pathways Within the Campylobacter Genus. Molecular and Cellular Proteomics, 2012, 11, 1203-1219.	3.8	84
87	Modification of the Campylobacter jejuni N-Linked Glycan by EptC Protein-mediated Addition of Phosphoethanolamine. Journal of Biological Chemistry, 2012, 287, 29384-29396.	3.4	63
88	Simultaneous Glycan-Peptide Characterization Using Hydrophilic Interaction Chromatography and Parallel Fragmentation by CID, Higher Energy Collisional Dissociation, and Electron Transfer Dissociation MS Applied to the N-Linked Glycoproteome of Campylobacter jejuni. Molecular and Cellular Proteomics, 2011, 10, S1-S18.	3.8	265
89	Proteomics of the oxidative stress response induced by hydrogen peroxide and paraquat reveals a novel AhpCâ€ike protein in ⟨i⟩Pseudomonas aeruginosa⟨/i⟩. Proteomics, 2011, 11, 3056-3069.	2.2	27
90	Quantitative N-linked Glycoproteomics of Myocardial Ischemia and Reperfusion Injury Reveals Early Remodeling in the Extracellular Environment. Molecular and Cellular Proteomics, 2011, 10, M110.006833.	3.8	101

#	ARTICLE	IF	CITATION
91	Sequence TTKF↓QE Defines the Site of Proteolytic Cleavage in Mhp683 Protein, a Novel Glycosaminoglycan and Cilium Adhesin of Mycoplasma hyopneumoniae. Journal of Biological Chemistry, 2011, 286, 41217-41229.	3.4	47
92	Mass spectrometric characterization of the <i>Campylobacter jejuni</i> adherence factor CadF reveals post-translational processing that removes immunogenicity while retaining fibronectin binding. Proteomics, 2010, 10, 277-288.	2.2	30
93	Mass Spectrometric Characterization of the Surface-Associated 42 kDa Lipoprotein JlpA as a Glycosylated Antigen in Strains of <i>Campylobacter jejuni</i> . Journal of Proteome Research, 2009, 8, 4654-4664.	3.7	41
94	<i>Campylobacter</i> proteomics: guidelines, challenges and future perspectives. Expert Review of Proteomics, 2009, 6, 61-74.	3.0	16
95	Identification of membraneâ€associated proteins from <b><i>Campylobacter jejuni</i></b> strains using complementary proteomics technologies. Proteomics, 2008, 8, 122-139.	2.2	87
96	An Atlas of Protein-Protein Interactions Across Mammalian Tissues. SSRN Electronic Journal, 0, , .	0.4	8