Nichollas E Scott

List of Publications by Year in descending order

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		101543	138484
96	4,313	36	58
papers	citations	h-index	g-index
119	119	119	5969
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Humoral and circulating follicular helper T cell responses in recovered patients with COVID-19. Nature Medicine, 2020, 26, 1428-1434.	30.7	400
2	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
3	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
4	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
5	Site-Specific Glycan-Peptide Analysis for Determination of <i>N</i> -Glycoproteome Heterogeneity. Journal of Proteome Research, 2013, 12, 5791-5800.	3.7	153
6	A promising bioconjugate vaccine against hypervirulent <i>Klebsiella pneumoniae</i> . Proceedings of the United States of America, 2019, 116, 18655-18663.	7.1	116
7	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
8	Nanobody cocktails potently neutralize SARS-CoV-2 D614G N501Y variant and protect mice. Proceedings of the United States of America, 2021, 118, .	7.1	109
9	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
10	<scp><i>A</i></scp> <i>ci>cinetobacter</i> strains carry two functional oligosaccharyltransferases, one devoted exclusively to type <scp>IV</scp> pilin, and the other one dedicated to <scp><i>O</i></scp> â€glycosylation of multiple proteins. Molecular Microbiology, 2015, 96, 1023-1041.	2.5	90
11	Identification of membraneâ€associated proteins from <i>Campylobacter jejuni</i> strains using complementary proteomics technologies. Proteomics, 2008, 8, 122-139.	2.2	87
12	Diversity in the Protein N-Glycosylation Pathways Within the Campylobacter Genus. Molecular and Cellular Proteomics, 2012, 11, 1203-1219.	3.8	84
13	Urinary tract colonization is enhanced by a plasmid that regulates uropathogenic Acinetobacter baumannii chromosomal genes. Nature Communications, 2019, 10, 2763.	12.8	80
14	CDK13 cooperates with CDK12 to control global RNA polymerase II processivity. Science Advances, 2020, 6, .	10.3	79
15	Community evaluation of glycoproteomics informatics solutions reveals high-performance search strategies for serum glycopeptide analysis. Nature Methods, 2021, 18, 1304-1316.	19.0	74
16	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
17	Proteomics Reveals Multiple Phenotypes Associated with N-linked Glycosylation in Campylobacter jejuni. Molecular and Cellular Proteomics, 2019, 18, 715-734.	3.8	70
18	Diversity Within the O-linked Protein Glycosylation Systems of Acinetobacter Species. Molecular and Cellular Proteomics, 2014, 13, 2354-2370.	3.8	64

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19	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
20	Protein O-fucosylation in Plasmodium falciparum ensures efficient infection of mosquito and vertebrate hosts. Nature Communications, 2017, 8, 561.	12.8	63
21	Structure of human ST8SiaIII sialyltransferase provides insight into cell-surface polysialylation. Nature Structural and Molecular Biology, 2015, 22, 627-635.	8.2	62
22	Glycoproteomics. Nature Reviews Methods Primers, 2022, 2, .	21.2	61
23	A platform for glycoengineering a polyvalent pneumococcal bioconjugate vaccine using E. coli as a host. Nature Communications, 2019, 10, 891.	12.8	60
24	An atlas of protein-protein interactions across mouse tissues. Cell, 2021, 184, 4073-4089.e17.	28.9	59
25	Surface Exposure and Packing of Lipoproteins into Outer Membrane Vesicles Are Coupled Processes in <i>Bacteroides</i> . MSphere, 2018, 3, .	2.9	57
26	A general protein <scp> <i>O</i> </scp> â€glycosylation system within the <scp> <i>B</i> </scp> <i>urkholderia cepacia</i> complex is involved in motility and virulence. Molecular Microbiology, 2014, 92, 116-137.	2.5	56
27	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
28	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). BMC Bioinformatics, 2017, 18, 457.	2.6	54
29	Profiling the Escherichia coli membrane protein interactome captured in Peptidisc libraries. ELife, 2019, 8, .	6.0	54
30	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
31	Interactome disassembly during apoptosis occurs independent of caspase cleavage. Molecular Systems Biology, 2017, 13, 906.	7.2	49
32	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
33	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
34	SUGAR-seq enables simultaneous detection of glycans, epitopes, and the transcriptome in single cells. Science Advances, 2021, 7, .	10.3	46
35	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
36	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

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37	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
38	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
39	Rewiring of the Human Mitochondrial Interactome during Neuronal Reprogramming Reveals Regulators of the Respirasome and Neurogenesis. IScience, 2019, 19, 1114-1132.	4.1	38
40	Low pH Exposure During Immunoglobulin G Purification Methods Results in Aggregates That Avidly Bind Fcl ³ Receptors: Implications for Measuring Fc Dependent Antibody Functions. Frontiers in Immunology, 2019, 10, 2415.	4.8	35
41	Trefoil factors share a lectin activity that defines their role in mucus. Nature Communications, 2020, 11, 2265.	12.8	34
42	Glycoproteomics: growing up fast. Current Opinion in Structural Biology, 2021, 68, 18-25.	5.7	33
43	Protein O-linked glycosylation in the plant pathogen <i>Ralstonia solanacearum</i> . Glycobiology, 2016, 26, cwv098.	2.5	32
44	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
45	The Glycoprotease CpaA Secreted by Medically Relevant Acinetobacter Species Targets Multiple <i>O</i> -Linked Host Glycoproteins. MBio, 2020, 11, .	4.1	31
46	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
47	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
48	An intra-bacterial activity for a T3SS effector. Scientific Reports, 2020, 10, 1073.	3.3	30
49	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
50	Proteomics of the oxidative stress response induced by hydrogen peroxide and paraquat reveals a novel AhpCâ€like protein in <i>Pseudomonas aeruginosa</i> . Proteomics, 2011, 11, 3056-3069.	2.2	27
51	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
52	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
53	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
54	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

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55	Modern Acinetobacter baumannii clinical isolates replicate inside spacious vacuoles and egress from macrophages. PLoS Pathogens, 2021, 17, e1009802.	4.7	21
56	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
57	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
58	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
59	The Phenylacetic Acid Catabolic Pathway Regulates Antibiotic and Oxidative Stress Responses in Acinetobacter. MBio, 2022, 13, e0186321.	4.1	18
60	Post-translational Mechanisms of Host Subversion by Bacterial Effectors. Trends in Molecular Medicine, 2017, 23, 1088-1102.	6.7	17
61	Yeast- and antibody-based tools for studying tryptophan C-mannosylation. Nature Chemical Biology, 2021, 17, 428-437.	8.0	17
62	<i>Campylobacter</i> proteomics: guidelines, challenges and future perspectives. Expert Review of Proteomics, 2009, 6, 61-74.	3.0	16
63	The Salmonella Effector SseK3 Targets Small Rab GTPases. Frontiers in Cellular and Infection Microbiology, 2020, 10, 419.	3.9	16
64	Characterization of the <i>Citrobacter rodentium</i> Cpx regulon and its role in host infection. Molecular Microbiology, 2019, 111, 700-716.	2.5	15
65	TLR2-mediated activation of innate responses in the upper airways confers antiviral protection of the lungs. JCI Insight, 2021, 6, .	5.0	15
66	A Sulfoglycolytic Entner-Doudoroff Pathway in Rhizobium leguminosarum bv. trifolii SRDI565. Applied and Environmental Microbiology, 2020, 86, .	3.1	14
67	High-Frequency Variation of Purine Biosynthesis Genes Is a Mechanism of Success in Campylobacter jejuni. MBio, 2015, 6, e00612-15.	4.1	13
68	The Type III Effector NIeD from Enteropathogenic Escherichia coli Differentiates between Host Substrates p38 and JNK. Infection and Immunity, 2017, 85, .	2.2	13
69	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
70	Enrichment and Identification of Bacterial Glycopeptides by Mass Spectrometry. Methods in Molecular Biology, 2015, 1295, 355-368.	0.9	13
71	Peptidyl-Prolyl Isomerase <i>ppiB</i> Is Essential for Proteome Homeostasis and Virulence in Burkholderia pseudomallei. Infection and Immunity, 2019, 87, .	2.2	12
72	Loss of <i>O</i> -Linked Protein Glycosylation in Burkholderia cenocepacia Impairs Biofilm Formation and Siderophore Activity and Alters Transcriptional Regulators. MSphere, 2019, 4, .	2.9	12

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73	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
74	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
75	Clinical implications of glycoproteomics for <i>Acinetobacter baumannii</i> . Expert Review of Proteomics, 2015, 12, 1-3.	3.0	11
76	Characterization of the O-Glycoproteome of Porphyromonas gingivalis. Microbiology Spectrum, 2022, 10, e0150221.	3.0	11
77	InvL, an Invasin-Like Adhesin, Is a Type II Secretion System Substrate Required for Acinetobacter baumannii Uropathogenesis. MBio, 2022, 13, .	4.1	11
78	Arginine glycosylation enhances methylglyoxal detoxification. Scientific Reports, 2021, 11, 3834.	3.3	10
79	NleB2 from enteropathogenic Escherichia coli is a novel arginine-glucose transferase effector. PLoS Pathogens, 2021, 17, e1009658.	4.7	9
80	Transmission of Cricket paralysis virus via exosome-like vesicles during infection of Drosophila cells. Scientific Reports, 2018, 8, 17353.	3.3	8
81	An Atlas of Protein-Protein Interactions Across Mammalian Tissues. SSRN Electronic Journal, 0, , .	0.4	8
82	Influence of Protein Glycosylation on Campylobacter fetus Physiology. Frontiers in Microbiology, 2020, 11, 1191.	3.5	7
83	Development and Immunogenicity of a Prototype Multivalent Group B <i>Streptococcus</i> Bioconjugate Vaccine. ACS Infectious Diseases, 2021, 7, 3111-3123.	3.8	7
84	Arginine glycosylation regulates UDP-GlcNAc biosynthesis in Salmonella enterica. Scientific Reports, 2022, 12, 5293.	3.3	7
85	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
86	BonA from <i>Acinetobacter baumannii</i> Forms a Divisome-Localized Decamer That Supports Outer Envelope Function. MBio, 2021, 12, e0148021.	4.1	5
87	Characterization of the O-Glycoproteome of Tannerella forsythia. MSphere, 2021, 6, e0064921.	2.9	5
88	Burkholderia PglL enzymes are Serine preferring oligosaccharyltransferases which target conserved proteins across the Burkholderia genus. Communications Biology, 2021, 4, 1045.	4.4	4
89	The role of mass spectrometry analysis in bacterial effector characterization. Biochemical Journal, 2017, 474, 2779-2784.	3.7	2
90	Expanding our understanding of the role of microbial glycoproteomes through high-throughput mass spectrometry approaches. Glycoconjugate Journal, 2019, 36, 259-266.	2.7	2

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91	The Application of Open Searching-based Approaches for the Identification of Acinetobacter baumannii O-linked Glycopeptides. Journal of Visualized Experiments, 2021, , .	0.3	2
92	Getting more out of FLAC-Tag co-immunoprecipitation mass spectrometry experiments using FAIMS. Journal of Proteomics, 2022, 254, 104473.	2.4	2
93	Sculpting the Bacterial <i>O</i> -Glycoproteome: Functional Analyses of Orthologous Oligosaccharyltransferases with Diverse Targeting Specificities. MBio, 2022, 13, e0379721.	4.1	2
94	Characterizing Glycoproteins by Mass Spectrometry in Campylobacter jejuni. Methods in Molecular Biology, 2017, 1512, 211-232.	0.9	1
95	Editorial overview: Systems biology and the rise and rise of omics approaches. Current Opinion in Chemical Biology, 2021, 60, A1-A3.	6.1	1
96	2020 FASEB Science Research Conference on Microbial Glycobiology, July 13â€14, 2020. FASEB Journal, 2020, 34, 14069-14072.	0.5	0