

# Stuart J Cordwell

## List of Publications by Year in descending order

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121  
papers

7,501  
citations

50276

46  
h-index

56724

83  
g-index

122  
all docs

122  
docs citations

122  
times ranked

8902  
citing authors

#	ARTICLE	IF	CITATIONS
1	Progress with geneâ€product mapping of the Mollicutes: <i>Mycoplasma genitalium</i> . Electrophoresis, 1995, 16, 1090-1094.	2.4	892
2	Therapeutic Inflammatory Monocyte Modulation Using Immune-Modifying Microparticles. Science Translational Medicine, 2014, 6, 219ra7.	12.4	284
3	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
4	Proteome research: Complementarity and limitations with respect to the RNA and DNA worlds. Electrophoresis, 1997, 18, 1217-1242.	2.4	232
5	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
6	Complementing genomics with proteomics: The membrane subproteome of Pseudomonas aeruginosa PAO1. Electrophoresis, 2000, 21, 3797-3809.	2.4	193
7	A Cortactin-CD2-associated Protein (CD2AP) Complex Provides a Novel Link between Epidermal Growth Factor Receptor Endocytosis and the Actin Cytoskeleton. Journal of Biological Chemistry, 2003, 278, 21805-21813.	3.4	192
8	Global Analysis of Outer Membrane Proteins from Leptospira interrogans Serovar Lai. Infection and Immunity, 2002, 70, 2311-2318.	2.2	176
9	Beyond gene expression: The impact of protein post-translational modifications in bacteria. Journal of Proteomics, 2014, 97, 265-286.	2.4	176
10	Site-Specific Glycan-Peptide Analysis for Determination of <i>N</i> -Glycoproteome Heterogeneity. Journal of Proteome Research, 2013, 12, 5791-5800.	3.7	153
11	Subproteomics based upon protein cellular location and relative solubilities in conjunction with composite two-dimensional electrophoresis gels. Electrophoresis, 2000, 21, 1094-1103.	2.4	144
12	Proteome analysis of extracellular proteins regulated by the las and rhl quorum sensing systems in Pseudomonas aeruginosa PAO1. Microbiology (United Kingdom), 2003, 149, 1311-1322.	1.8	141
13	Cross-species identification of proteins separated by two-dimensional gel electrophoresis using matrix-assisted laser desorption/ionisation/time-of-flight mass spectrometry and amino acid composition. Electrophoresis, 1995, 16, 438-443.	2.4	136
14	Graphite powder as an alternative or supplement to reversed-phase material for desalting and concentration of peptide mixtures prior to matrix-assisted laser desorption/ionization-mass spectrometry. Proteomics, 2002, 2, 1277-1287.	2.2	129
15	A Novel Method for the Simultaneous Enrichment, Identification, and Quantification of Phosphopeptides and Sialylated Glycopeptides Applied to a Temporal Profile of Mouse Brain Development. Molecular and Cellular Proteomics, 2012, 11, 1191-1202.	3.8	121
16	Proteolytic Processing of the Mycoplasma hyopneumoniae Cilium Adhesin. Infection and Immunity, 2004, 72, 2791-2802.	2.2	101
17	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
18	Comparative proteomics of bacterial pathogens. Proteomics, 2001, 1, 461-472.	2.2	99

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19	Surface Analyses and Immune Reactivities of Major Cell Wall-Associated Proteins of Group A Streptococcus. <i>Infection and Immunity</i> , 2005, 73, 3137-3146.	2.2	99
20	Functions of the CckA histidine kinase in Caulobacter cell cycle control. <i>Molecular Microbiology</i> , 2003, 47, 1279-1290.	2.5	96
21	Technologies for plasma membrane proteomics. <i>Proteomics</i> , 2010, 10, 611-627.	2.2	94
22	Proteomics of ischemia/reperfusion injury in rabbit myocardium reveals alterations to proteins of essential functional systems. <i>Proteomics</i> , 2005, 5, 1395-1410.	2.2	91
23	Technologies for bacterial surface proteomics. <i>Current Opinion in Microbiology</i> , 2006, 9, 320-329.	5.1	91
24	Identification of type II and type III pyoverdine receptors from <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2003, 149, 821-831.	1.8	90
25	P159 is a proteolytically processed, surface adhesin of <i>Mycoplasma hyopneumoniae</i> : defined domains of P159 bind heparin and promote adherence to eukaryote cells. <i>Molecular Microbiology</i> , 2006, 60, 669-686.	2.5	89
26	Comparative proteomics of <i>Staphylococcus aureus</i> and the response of methicillin-resistant and methicillin-sensitive strains to Triton X-100. The identifications for the spots shown in Fig. 1 F1 can be found as supplementary data in <i>Microbiology Online</i> ( <a href="http://mic.sgmjournals.org">http://mic.sgmjournals.org</a> ). <i>Microbiology (United Kingdom)</i> , 2002, 148, 2765-2781.	1.8	89
27	Proteomic comparison of membrane and extracellular proteins from invasive (PAO1) and cytotoxic (6206) strains of <i>Pseudomonas aeruginosa</i> . <i>Proteomics</i> , 2002, 2, 1325-1346.	2.2	87
28	Identification of membrane-associated proteins from <i>Campylobacter jejuni</i> strains using complementary proteomics technologies. <i>Proteomics</i> , 2008, 8, 122-139.	2.2	87
29	Improved accuracy of cell surface shaving proteomics in <i>Staphylococcus aureus</i> using a false-positive control. <i>Proteomics</i> , 2010, 10, 2037-2049.	2.2	86
30	Functional decorations: post-translational modifications and heart disease delineated by targeted proteomics. <i>Genome Medicine</i> , 2013, 5, 20.	8.2	85
31	Diversity in the Protein N-Glycosylation Pathways Within the <i>Campylobacter</i> Genus. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1203-1219.	3.8	84
32	Abnormal pathways in the genu of the corpus callosum in schizophrenia pathogenesis: a proteome study. <i>Proteomics - Clinical Applications</i> , 2007, 1, 1291-1305.	1.6	80
33	Proteomics Reveals Multiple Phenotypes Associated with N-linked Glycosylation in <i>Campylobacter jejuni</i> . <i>Molecular and Cellular Proteomics</i> , 2019, 18, 715-734.	3.8	70
34	Current methodologies for proteomics of bacterial surface-exposed and cell envelope proteins. <i>Proteomics</i> , 2011, 11, 3169-3189.	2.2	69
35	Strategies for the enrichment and identification of basic proteins in proteome projects. <i>Proteomics</i> , 2003, 3, 569-579.	2.2	68
36	The Role of Proteomics in Clinical Cardiovascular Biomarker Discovery. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1824-1837.	3.8	63

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37	Modification of the <i>Campylobacter jejuni</i> N-Linked Glycan by EptC Protein-mediated Addition of Phosphoethanolamine. <i>Journal of Biological Chemistry</i> , 2012, 287, 29384-29396.	3.4	63
38	Mhp493 (P216) is a proteolytically processed, cilium and heparin binding protein of <i>Mycoplasma hyopneumoniae</i> . <i>Molecular Microbiology</i> , 2009, 71, 566-582.	2.5	62
39	Proteomics of <i>Staphylococcus aureus</i> —current state and future challenges. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2003, 787, 179-195.	2.3	58
40	Diverse Peptide Hormones Affecting Root Growth Identified in the <i>Medicago truncatula</i> Secreted Peptidome. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 160-174.	3.8	57
41	Comparative Transcriptional and Translational Analysis of <i>Leptospiral</i> Outer Membrane Protein Expression in Response to Temperature. <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e560.	3.0	55
42	Proteome analysis of <i>Spiroplasma melliferum</i> (A56) and protein characterisation across species boundaries. <i>Electrophoresis</i> , 1997, 18, 1335-1346.	2.4	52
43	Cellular and extracellular proteome analysis of <i>Streptococcus mutans</i> grown in a chemostat. <i>Proteomics</i> , 2003, 3, 627-646.	2.2	52
44	Conserved anchorless surface proteins as group A streptococcal vaccine candidates. <i>Journal of Molecular Medicine</i> , 2012, 90, 1197-1207.	3.9	49
45	Characterization of reaction conditions providing rapid and specific cysteine alkylation for peptide-based mass spectrometry. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 372-379.	2.3	48
46	Comparative Proteomics and Glycoproteomics Reveal Increased N-Linked Glycosylation and Relaxed Sequon Specificity in <i>Campylobacter jejuni</i> NCTC11168 O. <i>Journal of Proteome Research</i> , 2014, 13, 5136-5150.	3.7	48
47	Structural Basis for Phosphorylation and Lysine Acetylation Cross-talk in a Kinase Motif Associated with Myocardial Ischemia and Cardioprotection. <i>Journal of Biological Chemistry</i> , 2014, 289, 25890-25906.	3.4	48
48	Proteomic identification of putative plasmodesmatal proteins from <i>Chara corallina</i> . <i>Proteomics</i> , 2005, 5, 2866-2875.	2.2	47
49	Sequence TTKF†QE Defines the Site of Proteolytic Cleavage in Mhp683 Protein, a Novel Glycosaminoglycan and Cilium Adhesin of <i>Mycoplasma hyopneumoniae</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 41217-41229.	3.4	47
50	Comparison of Predicted and Observed Properties of Proteins Encoded in the Genome of <i>Mycobacterium Tuberculosis</i> H37Rv. <i>Biochemical and Biophysical Research Communications</i> , 1998, 253, 70-79.	2.1	45
51	Purification and Identification of O-GlcNAc-Modified Peptides Using Phosphate-Based Alkyne CLICK Chemistry in Combination with Titanium Dioxide Chromatography and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 1449-1458.	3.7	45
52	Proteomics of <i>Pseudomonas aeruginosa</i> Australian Epidemic Strain 1 (AES-1) Cultured under Conditions Mimicking the Cystic Fibrosis Lung Reveals Increased Iron Acquisition via the Siderophore Pyochelin. <i>Journal of Proteome Research</i> , 2012, 11, 776-795.	3.7	45
53	Proteomic profiling of <i>Pseudomonas aeruginosa</i> AES-1R, PAO1 and PA14 reveals potential virulence determinants associated with a transmissible cystic fibrosis-associated strain. <i>BMC Microbiology</i> , 2012, 12, 16.	3.3	43
54	Modifications of myosin-regulatory light chain correlate with function of stunned myocardium. <i>Journal of Molecular and Cellular Cardiology</i> , 2003, 35, 833-840.	1.9	42

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55	Role of group A <i>Streptococcus</i> HtrA in the maturation of SpeB protease. <i>Proteomics</i> , 2007, 7, 4488-4498.	2.2	42
56	Mass Spectrometric Characterization of the Surface-Associated 42 kDa Lipoprotein JlpA as a Glycosylated Antigen in Strains of <i>Campylobacter jejuni</i> . <i>Journal of Proteome Research</i> , 2009, 8, 4654-4664.	3.7	41
57	<i>Staphylococcus aureus</i> Surface Proteins Involved in Adaptation to Oxacillin Identified Using a Novel Cell Shaving Approach. <i>Journal of Proteome Research</i> , 2014, 13, 2954-2972.	3.7	41
58	Malate/lactate dehydrogenase in mollicutes: evidence for a multienzyme protein. <i>Gene</i> , 1997, 195, 113-120.	2.2	40
59	Therapeutic Inhibition of Acid-Sensing Ion Channel 1a Recovers Heart Function After Ischemia-Induced Reperfusion Injury. <i>Circulation</i> , 2021, 144, 947-960.	1.6	40
60	Altered proteins of the anterior cingulate cortex white matter proteome in schizophrenia. <i>Proteomics - Clinical Applications</i> , 2007, 1, 157-166.	1.6	39
61	Immunoproteomics To Examine Cystic Fibrosis Host Interactions with Extracellular <i>Pseudomonas aeruginosa</i> Proteins. <i>Infection and Immunity</i> , 2008, 76, 4624-4632.	2.2	39
62	Proteomic Identification of Putative MicroRNA394 Target Genes in <i>Arabidopsis thaliana</i> Identifies Major Latex Protein Family Members Critical for Normal Development. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2033-2047.	3.8	39
63	Ischemia-specific phosphorylation and myofilament translocation of heat shock protein 27 precedes alpha B-crystallin and occurs independently of reactive oxygen species in rabbit myocardium. <i>Journal of Molecular and Cellular Cardiology</i> , 2006, 40, 761-774.	1.9	37
64	Characterisation of basic proteins from <i>Spiroplasma melliferum</i> using novel immobilised pH gradients. <i>Electrophoresis</i> , 1997, 18, 1393-1398.	2.4	36
65	A proteomic approach to the identification and characterisation of protein composition in wheat germ. <i>Functional and Integrative Genomics</i> , 2006, 6, 322-337.	3.5	35
66	Anti-tropomyosin antibodies co-localise with actin microfilaments and label plasmodesmata. <i>European Journal of Cell Biology</i> , 2009, 88, 357-369.	3.6	34
67	Global Analysis of Myocardial Peptides Containing Cysteines With Irreversible Sulfinic and Sulfonic Acid Post-Translational Modifications. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 609-620.	3.8	34
68	Proteome analysis of <i>Helicobacter pylori</i> : major proteins of type strain NCTC 11637. <i>Pathology</i> , 2001, 33, 365-374.	0.6	33
69	Large-Scale Capture of Peptides Containing Reversibly Oxidized Cysteines by Thiol-Disulfide Exchange Applied to the Myocardial Redox Proteome. <i>Analytical Chemistry</i> , 2013, 85, 3774-3780.	6.5	33
70	Cellular targets of the myeloperoxidase-derived oxidant hypothiocyanous acid (HOSCN) and its role in the inhibition of glycolysis in macrophages. <i>Free Radical Biology and Medicine</i> , 2016, 94, 88-98.	2.9	33
71	Characterization of disulfide (cystine) oxidation by HOCl in a model peptide: Evidence for oxygen addition, disulfide bond cleavage and adduct formation with thiols. <i>Free Radical Biology and Medicine</i> , 2020, 154, 62-74.	2.9	32
72	Proteomics of ischemia and reperfusion injuries in rabbit myocardium with and without intervention by an oxygen-free radical scavenger. <i>Proteomics</i> , 2006, 6, 6221-6233.	2.2	31

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73	<i>Pseudomonas aeruginosa</i> AES-1 Exhibits Increased Virulence Gene Expression during Chronic Infection of Cystic Fibrosis Lung. <i>PLoS ONE</i> , 2011, 6, e24526.	2.5	31
74	Effects of chronic risperidone treatment on the striatal protein profiles in rats. <i>Brain Research</i> , 2006, 1113, 24-32.	2.2	30
75	Mass spectrometric characterization of the <i>Campylobacter jejuni</i> adherence factor CadF reveals post-translational processing that removes immunogenicity while retaining fibronectin binding. <i>Proteomics</i> , 2010, 10, 277-288.	2.2	30
76	Construction and evaluation of a plasmid vector for the expression of recombinant lipoproteins in <i>Escherichia coli</i> . <i>Plasmid</i> , 2003, 49, 18-29.	1.4	29
77	A proteome analysis of the dorsolateral prefrontal cortex in human alcoholic patients. <i>Proteomics - Clinical Applications</i> , 2007, 1, 62-72.	1.6	29
78	A Global Profile of Reversible and Irreversible Cysteine Redox Post-Translational Modifications During Myocardial Ischemia/Reperfusion Injury and Antioxidant Intervention. <i>Antioxidants and Redox Signaling</i> , 2021, 34, 11-31.	5.4	28
79	Proteomics of the oxidative stress response induced by hydrogen peroxide and paraquat reveals a novel AhpC-like protein in <i>Pseudomonas aeruginosa</i> . <i>Proteomics</i> , 2011, 11, 3056-3069.	2.2	27
80	Conserved Motifs as the Basis for Recognition of Homologous Proteins Across Species Boundaries Using Peptide-mass Fingerprinting. , 1997, 32, 370-378.		26
81	Evaluation of algorithms used for cross-species proteome characterisation. <i>Electrophoresis</i> , 1997, 18, 1410-1417.	2.4	25
82	Mitochondria: A mirror into cellular dysfunction in heart disease. <i>Proteomics - Clinical Applications</i> , 2008, 2, 845-861.	1.6	23
83	Release of Tissue-specific Proteins into Coronary Perfusate as a Model for Biomarker Discovery in Myocardial Ischemia/Reperfusion Injury. <i>Journal of Proteome Research</i> , 2012, 11, 2114-2126.	3.7	23
84	The nuclear proteome and DNA-binding fraction of human Raji lymphoma cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 413-432.	2.3	22
85	Phosphorylation of KrÄppel-like Factor 3 (KLF3/BKLF) and C-terminal Binding Protein 2 (CtBP2) by Homeodomain-interacting Protein Kinase 2 (HIPK2) Modulates KLF3 DNA Binding and Activity. <i>Journal of Biological Chemistry</i> , 2015, 290, 8591-8605.	3.4	22
86	Sequential Extraction of Proteins by Chemical Reagents. <i>Methods in Molecular Biology</i> , 2008, 424, 139-146.	0.9	21
87	Identifying the targets and functions of N-linked protein glycosylation in <i>Campylobacter jejuni</i> . <i>Molecular Omics</i> , 2020, 16, 287-304.	2.8	21
88	Acquisition and archiving of information for bacterial proteomics: From sample preparation to database. <i>Methods in Enzymology</i> , 2002, 358, 207-227.	1.0	20
89	Modulation of gene expression by <i>Pseudomonas aeruginosa</i> during chronic infection in the adult cystic fibrosis lung. <i>Microbiology (United Kingdom)</i> , 2013, 159, 2354-2363.	1.8	19
90	Secretome of Transmissible <i>Pseudomonas aeruginosa</i> AES-1R Grown in a Cystic Fibrosis Lung-Like Environment. <i>Journal of Proteome Research</i> , 2013, 12, 5357-5369.	3.7	18

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91	The microbial proteome database – an automated laboratory catalogue for monitoring protein expression in bacteria. <i>Electrophoresis</i> , 1999, 20, 3580-3588.	2.4	17
92	Human macrophage cathepsin B-mediated C-terminal cleavage of apolipoprotein B at Ser <sup>228</sup> severely impairs antiatherogenic capacity. <i>FASEB Journal</i> , 2016, 30, 4239-4255.	0.5	17
93	Comparative analysis of <i>Staphylococcus epidermidis</i> strains utilizing quantitative and cell surface shaving proteomics. <i>Journal of Proteomics</i> , 2016, 130, 190-199.	2.4	17
94	Functional analysis of the <i>Helicobacter pullorum</i> N-linked protein glycosylation system. <i>Glycobiology</i> , 2018, 28, 233-244.	2.5	17
95	<i>Campylobacter</i> proteomics: guidelines, challenges and future perspectives. <i>Expert Review of Proteomics</i> , 2009, 6, 61-74.	3.0	16
96	Characterization of a locus encoding four paralogous outer membrane lipoproteins of <i>Brachyspira hyodysenteriae</i> . <i>Microbes and Infection</i> , 2003, 5, 275-283.	1.9	15
97	Enhancing the stability of adalimumab by engineering additional glycosylation motifs. <i>International Journal of Biological Macromolecules</i> , 2020, 158, 189-196.	7.5	13
98	Enrichment and Identification of Bacterial Glycopeptides by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2015, 1295, 355-368.	0.9	13
99	Proteomics of bacterial pathogens: <i>Pseudomonas aeruginosa</i> infections in cystic fibrosis – A case study. <i>Proteomics - Clinical Applications</i> , 2010, 4, 228-248.	1.6	12
100	Phosphoproteomic Profiling of the Myocyte. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 575-575.	5.1	12
101	Proteomics of <i>Campylobacter jejuni</i> Growth in Deoxycholate Reveals Cj0025c as a Cystine Transport Protein Required for Wild-type Human Infection Phenotypes. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1263-1280.	3.8	12
102	Assigning a role for chemosensory signal transduction in <i>Campylobacter jejuni</i> biofilms using a combined omics approach. <i>Scientific Reports</i> , 2020, 10, 6829.	3.3	11
103	When does a fingerprint constitute a diagnostic?. <i>Lancet, The</i> , 2006, 368, 971-973.	13.7	9
104	The major surface Vsp proteins of <i>Brachyspira hyodysenteriae</i> form antigenic protein complexes. <i>Veterinary Microbiology</i> , 2011, 149, 157-162.	1.9	8
105	Exploring and Exploiting Bacterial Proteomes. , 2004, 266, 115-135.		7
106	Homogentisate 1-2-Dioxygenase Downregulation in the Chronic Persistence of <i>Pseudomonas aeruginosa</i> Australian Epidemic Strain-1 in the CF Lung. <i>PLoS ONE</i> , 2015, 10, e0134229.	2.5	7
107	Targeted Proteomics for Determining Phosphorylation Site-Specific Associations in Cardiovascular Disease. <i>Circulation</i> , 2012, 126, 1803-1807.	1.6	6
108	A novel phosphoproteomic landscape evoked in response to type I interferon in the brain and in glial cells. <i>Journal of Neuroinflammation</i> , 2021, 18, 237.	7.2	6

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109	Cell Shaving and False-Positive Control Strategies Coupled to Novel Statistical Tools to Profile Gram-Positive Bacterial Surface Proteomes. <i>Methods in Molecular Biology</i> , 2016, 1440, 47-55.	0.9	4
110	Optimal Preparation of Formalin Fixed Samples for Peptide Based Matrix Assisted Laser Desorption/Ionization Mass Spectrometry Imaging Workflows. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	4
111	Multi-omics of a pre-clinical model of diabetic cardiomyopathy reveals increased fatty acid supply impacts mitochondrial metabolic selectivity. <i>Journal of Molecular and Cellular Cardiology</i> , 2022, 164, 92-109.	1.9	4
112	Application of Proteomics to <i>Pseudomonas aeruginosa</i> . <i>Advances in Biochemical Engineering/Biotechnology</i> , 2003, 83, 117-140.	1.1	3
113	Subproteomics based upon protein cellular location and relative solubilities in conjunction with composite two-dimensional electrophoresis gels. <i>Electrophoresis</i> , 2000, 21, 1094-1103.	2.4	3
114	Statistical Analysis of Image Data Provided by Two-Dimensional Gel Electrophoresis for Discovery Proteomics. <i>Methods in Molecular Medicine</i> , 2008, 141, 271-286.	0.8	3
115	Integrated mass spectrometry-based multi-omics for elucidating mechanisms of bacterial virulence. <i>Biochemical Society Transactions</i> , 2021, 49, 1905-1926.	3.4	2
116	Glycan Profile Analysis of Engineered Trastuzumab with Rationally Added Glycosylation Sequons Presents Significantly Increased Glycan Complexity. <i>Pharmaceutics</i> , 2021, 13, 1747.	4.5	2
117	11 Isoelectric focusing and proteomics. <i>Separation Science and Technology</i> , 2005, , 247-264.	0.2	1
118	Reportsites - A Computational Method to Extract Positional and Physico-Chemical Information from Large-Scale Proteomic Post-Translational Modification Datasets. <i>Journal of Proteomics and Bioinformatics</i> , 2012, 05, .	0.4	1
119	Exploiting <i>pglB</i> Oligosaccharyltransferase-Positive and -Negative <i>Campylobacter jejuni</i> and a Multiprotease Digestion Strategy to Identify Novel Sites Modified by N-Linked Protein Glycosylation. <i>Journal of Proteome Research</i> , 2021, 20, 4995-5009.	3.7	1
120	Proteome Analysis of Outer Membrane and Extracellular Proteins from <i>Pseudomonas aeruginosa</i> for Vaccine Discovery. , 2005, , 285-304.		0
121	Structural basis for phosphorylation and lysine acetylation cross-talk in a kinase motif associated with myocardial ischemia and cardioprotection.. <i>Journal of Biological Chemistry</i> , 2014, 289, 33875.	3.4	0