Matthew Champion

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	C-Terminal Signal Sequence Promotes Virulence Factor Secretion in Mycobacterium tuberculosis. Science, 2006, 313, 1632-1636.	6.0	200
2	ESXâ€∃ secreted virulence factors are recognized by multiple cytosolic AAA ATPases in pathogenic mycobacteria. Molecular Microbiology, 2009, 73, 950-962.	1.2	140
3	Quantitative proteomics of Xenopus laevis embryos: expression kinetics of nearly 4000 proteins during early development. Scientific Reports, 2014, 4, 4365.	1.6	93
4	Validation of Matrix Metalloproteinase-9 (MMP-9) as a Novel Target for Treatment of Diabetic Foot Ulcers in Humans and Discovery of a Potent and Selective Small-Molecule MMP-9 Inhibitor That Accelerates Healing. Journal of Medicinal Chemistry, 2018, 61, 8825-8837.	2.9	82
5	Correlation of Phenotypic Profiles Using Targeted Proteomics Identifies Mycobacterial Esx-1 Substrates. Journal of Proteome Research, 2014, 13, 5151-5164.	1.8	55
6	Activation of BlaR1 Protein of Methicillin-resistant Staphylococcus aureus, Its Proteolytic Processing, and Recovery from Induction of Resistance. Journal of Biological Chemistry, 2011, 286, 38148-38158.	1.6	52
7	Coupling Capillary Zone Electrophoresis with Electron Transfer Dissociation and Activated Ion Electron Transfer Dissociation for Top-Down Proteomics. Analytical Chemistry, 2015, 87, 5422-5429.	3.2	51
8	A Novel ESX-1 Locus Reveals that Surface-Associated ESX-1 Substrates Mediate Virulence in Mycobacterium marinum. Journal of Bacteriology, 2014, 196, 1877-1888.	1.0	42
9	WhiB6 regulation of ESX-1 gene expression is controlled by a negative feedback loop in <i>Mycobacterium marinum</i> . Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10772-E10781.	3.3	39
10	Direct Detection of Bacterial Protein Secretion Using Whole Colony Proteomics. Molecular and Cellular Proteomics, 2012, 11, 596-604.	2.5	37
11	Inhibitors of the protein disulfide isomerase family for the treatment of multiple myeloma. Leukemia, 2019, 33, 1011-1022.	3.3	37
12	Capillary zone electrophoresis for bottomâ€up analysis of complex proteomes. Proteomics, 2016, 16, 188-196.	1.3	33
13	Proteome analysis of Escherichia coli K-12 by two-dimensional native-state chromatography and MALDI-MS. Molecular Microbiology, 2003, 47, 383-396.	1.2	30
14	A Practical Guide to Small Protein Discovery and Characterization Using Mass Spectrometry. Journal of Bacteriology, 2022, 204, JB0035321.	1.0	30
15	Capillary zone electrophoresis-electrospray ionization-tandem mass spectrometry for quantitative parallel reaction monitoring of peptide abundance and single-shot proteomic analysis of a human cell line. Journal of Chromatography A, 2014, 1359, 303-308.	1.8	29
16	Homeostasis of N-α-Terminal Acetylation of EsxA Correlates with Virulence in Mycobacterium marinum. Infection and Immunity, 2014, 82, 4572-4586.	1.0	29
17	A New ESX-1 Substrate in Mycobacterium marinum That Is Required for Hemolysis but Not Host Cell Lysis. Journal of Bacteriology, 2019, 201, .	1.0	27
18	Inhibiting host-protein deposition on urinary catheters reduces associated urinary tract infections. ELife, 2022, 11, .	2.8	26

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19	Genomewide Dam Methylation in Escherichia coli during Long-Term Stationary Phase. MSystems, 2016, 1, .	1.7	25
20	Pervasive translation in Mycobacterium tuberculosis. ELife, 2022, 11, .	2.8	25
21	Phosphorylation Dynamics Dominate the Regulated Proteome during Early Xenopus Development. Scientific Reports, 2017, 7, 15647.	1.6	24
22	Proteo-genetic analysis reveals clear hierarchy of ESX-1 secretion in <i>Mycobacterium marinum</i> . Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	23
23	Polycysteineâ€encoding leaderless short ORFs function as cysteineâ€responsive attenuators of operonic gene expression in mycobacteria. Molecular Microbiology, 2020, 114, 93-108.	1.2	21
24	EspM Is a Conserved Transcription Factor That Regulates Gene Expression in Response to the ESX-1 System. MBio, 2020, 11, .	1.8	21
25	A Nonsense Mutation in Mycobacterium marinum That Is Suppressible by a Novel Mechanism. Infection and Immunity, 2017, 85, .	1.0	20
26	Quantitative N-Terminal Footprinting of Pathogenic Mycobacteria Reveals Differential Protein Acetylation. Journal of Proteome Research, 2018, 17, 3246-3258.	1.8	18
27	Hyperbaric oxygen therapy accelerates wound healing in diabetic mice by decreasing active matrix metalloproteinaseâ€9. Wound Repair and Regeneration, 2020, 28, 194-201.	1.5	15
28	DegP Chaperone Suppresses Toxic Inner Membrane Translocation Intermediates. PLoS ONE, 2016, 11, e0162922.	1.1	14
29	Minimal deuterium isotope effects in quantitation of dimethylâ€labeled complex proteomes analyzed with capillary zone electrophoresis/mass spectrometry. Electrophoresis, 2020, 41, 1374-1378.	1.3	12
30	Expression of active matrix metalloproteinase-9 as a likely contributor to the clinical failure of aclerastide in treatment of diabetic foot ulcers. European Journal of Pharmacology, 2018, 834, 77-83.	1.7	11
31	Capillary zone electrophoresis as a tool for bottom-up protein analysis. Bioanalysis, 2016, 8, 89-92.	0.6	10
32	Rational engineering of a virulence gene from Mycobacterium tuberculosis facilitates proteomic analysis of a natural protein N-terminus. Scientific Reports, 2016, 6, 33265.	1.6	6
33	Quantitative capillary zone electrophoresis-mass spectrometry reveals the <i>N</i> -glycome developmental plan during vertebrate embryogenesis. Molecular Omics, 2020, 16, 210-220.	1.4	5
34	Remnants of the Balbiani body are required for formation of RNA transport granules in Xenopus oocytes. IScience, 2022, 25, 103878.	1.9	5
35	Proteomics ofXenopusdevelopment. Molecular Human Reproduction, 2016, 22, 193-199.	1.3	4
36	The genetic proteome: Using genetics to inform the proteome of mycobacterial pathogens. PLoS Pathogens, 2021, 17, e1009124.	2.1	4

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37	Electroblotting through a tryptic membrane for LC-MS/MS analysis of proteins separated in electrophoretic gels. Analyst, The, 2020, 145, 7724-7735.	1.7	3
38	3-D printed injection system for capillary electrophoresis. Analytical Methods, 2022, 14, 1163-1168.	1.3	2