## Michael L Barta

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11949737/publications.pdf Version: 2024-02-01



Μιςμλει Ι. Βλατλ

#	Article	IF	CITATIONS
1	Composition and Biophysical Properties of the Sorting Platform Pods in the Shigella Type III Secretion System. Frontiers in Cellular and Infection Microbiology, 2021, 11, 682635.	3.9	9
2	The Tip Complex: From Host Cell Sensing to Translocon Formation. Current Topics in Microbiology and Immunology, 2019, 427, 173-199.	1.1	6
3	The cytoplasmic domain of MxiG interacts with MxiK and directs assembly of the sorting platform in the Shigella type III secretion system. Journal of Biological Chemistry, 2019, 294, 19184-19196.	3.4	20
4	Using disruptive insertional mutagenesis to identify the <i>in situ</i> structureâ€function landscape of the <i>Shigella</i> translocator protein IpaB. Protein Science, 2018, 27, 1392-1406.	7.6	13
5	The Loss of Expression of a Single Type 3 Effector (CT622) Strongly Reduces Chlamydia trachomatis Infectivity and Growth. Frontiers in Cellular and Infection Microbiology, 2018, 8, 145.	3.9	21
6	Single-domain antibodies pinpoint potential targets within Shigella invasion plasmid antigen D of the needle tip complex for inhibition of type III secretion. Journal of Biological Chemistry, 2017, 292, 16677-16687.	3.4	16
7	Evaluation of lumazine synthase from <i>Bacillus anthracis</i> as a presentation platform for polyvalent antigen display. Protein Science, 2017, 26, 2059-2072.	7.6	10
8	Characterization of Type Three Secretion System Translocator Interactions with Phospholipid Membranes. Methods in Molecular Biology, 2017, 1531, 81-91.	0.9	3
9	Recombinant Expression and Purification of the Shigella Translocator IpaB. Methods in Molecular Biology, 2017, 1531, 173-181.	0.9	4
10	Computational modeling of TC0583 as a putative component of the Chlamydia muridarum V-type ATP synthase complex and assessment of its protective capabilities as a vaccine antigen. Microbes and Infection, 2016, 18, 245-253.	1.9	6
11	Hypothetical protein <scp>CT</scp> 398 ( <scp>C</scp> ds <scp>Z</scp> ) interacts with σ <sup>54</sup> ( <scp>R</scp> po <scp>N</scp> )â€holoenzyme and the type III secretion export apparatus in <i>Chlamydia trachomatis</i> . Protein Science, 2015, 24, 1617-1632.	7.6	23
12	Structural and Biochemical Characterization of Chlamydia trachomatis Hypothetical Protein CT263 Supports That Menaquinone Synthesis Occurs through the Futalosine Pathway. Journal of Biological Chemistry, 2014, 289, 32214-32229.	3.4	23
13	Structure of CT584 fromChlamydia trachomatisrefined to 3.05â€Ã resolution. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1196-1201.	0.7	8
14	Studies of the conformational stability of invasion plasmid antigen B from <i>Shigella</i> . Protein Science, 2013, 22, 666-670.	7.6	8
15	Structural Basis for Nucleotide Binding and Reaction Catalysis in Mevalonate Diphosphate Decarboxylase. Biochemistry, 2012, 51, 5611-5621.	2.5	23
16	The Structures of Coiled-Coil Domains from Type III Secretion System Translocators Reveal Homology to Pore-Forming Toxins. Journal of Molecular Biology, 2012, 417, 395-405.	4.2	63
17	Identification of the bile salt binding site on ipad from <i>Shigella flexneri</i> and the influence of ligand binding on IpaD structure. Proteins: Structure, Function and Bioinformatics, 2012, 80, 935-945.	2.6	51
18	Biochemical and Structural Basis for Inhibition of <i>Enterococcus faecalis</i> Hydroxymethylglutaryl-CoA Synthase, mvaS, by Hymeglusin. Biochemistry, 2012, 51, 4713-4722.	2.5	29

#	Article	IF	CITATIONS
19	Crystal Structures of Staphylococcus epidermidis Mevalonate Diphosphate Decarboxylase Bound to Inhibitory Analogs Reveal New Insight into Substrate Binding and Catalysis. Journal of Biological Chemistry, 2011, 286, 23900-23910.	3.4	29
20	Evidence for alternative quaternary structure in a bacterial Type III secretion system chaperone. BMC Structural Biology, 2010, 10, 21.	2.3	18