

Martin Zoltner

List of Publications by Year in descending order

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33
papers

789
citations

516710

16
h-index

580821

25
g-index

33
all docs

33
docs citations

33
times ranked

983
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome, proteome and draft genome of <i>Euglena gracilis</i> . <i>BMC Biology</i> , 2019, 17, 11.	3.8	98
2	Heterogeneity in <i>Ess</i> transcriptional organization and variable contribution of the <i>Ess</i> /Type VII protein secretion system to virulence across closely related <i>Staphylococcus aureus</i> strains. <i>Molecular Microbiology</i> , 2014, 93, 928-943.	2.5	84
3	Metabolic quirks and the colourful history of the <i>Euglena gracilis</i> secondary plastid. <i>New Phytologist</i> , 2020, 225, 1578-1592.	7.3	65
4	EssC: domain structures inform on the elusive translocation channel in the Type VII secretion system. <i>Biochemical Journal</i> , 2016, 473, 1941-1952.	3.7	48
5	Modulation of the Surface Proteome through Multiple Ubiquitylation Pathways in African Trypanosomes. <i>PLoS Pathogens</i> , 2015, 11, e1005236.	4.7	34
6	Evolving Differentiation in African Trypanosomes. <i>Trends in Parasitology</i> , 2021, 37, 296-303.	3.3	33
7	Suramin exposure alters cellular metabolism and mitochondrial energy production in African trypanosomes. <i>Journal of Biological Chemistry</i> , 2020, 295, 8331-8347.	3.4	32
8	Exploiting the Achilles' heel of membrane trafficking in trypanosomes. <i>Current Opinion in Microbiology</i> , 2016, 34, 97-103.	5.1	28
9	Membrane interactions and self-association of components of the <i>Ess</i> /Type VII secretion system of <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2016, 590, 349-357.	2.8	27
10	The <i>Plasmodium falciparum</i> Artemisinin Susceptibility-Associated AP-2 Adaptin $\frac{1}{4}$ Subunit is Clathrin Independent and Essential for Schizont Maturation. <i>MBio</i> , 2020, 11, .	4.1	27
11	Comparative proteomics of the two <i>T. brucei</i> PABPs suggests that PABP2 controls bulk mRNA. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006679.	3.0	26
12	Host-parasite co-metabolic activation of antitrypanosomal aminomethyl-benzoxaboroles. <i>PLoS Pathogens</i> , 2018, 14, e1006850.	4.7	26
13	Characterization of <i>Staphylococcus aureus</i> EssB, an integral membrane component of the Type VII secretion system: atomic resolution crystal structure of the cytoplasmic segment. <i>Biochemical Journal</i> , 2013, 449, 469-477.	3.7	25
14	Haem-iron plays a key role in the regulation of the <i>Ess</i> /type VII secretion system of <i>Staphylococcus aureus</i> RN6390. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1839-1850.	1.8	25
15	A chemical-genetics approach to study the role of atypical protein kinase C in <i>Drosophila</i> . <i>Development (Cambridge)</i> , 2019, 146, .	2.5	22
16	A Uniquely Complex Mitochondrial Proteome from <i>Euglena gracilis</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2173-2191.	8.9	22
17	Sulfate Acts as Phosphate Analog on the Monomeric Catalytic Fragment of the CPx-ATPase CopB from <i>Sulfolobus solfataricus</i> . <i>Journal of Molecular Biology</i> , 2007, 369, 368-385.	4.2	21
18	The Architecture of EssB, an Integral Membrane Component of the Type VII Secretion System. <i>Structure</i> , 2013, 21, 595-603.	3.3	19

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19	Functional analysis of the EsaB component of the Staphylococcus aureus Type VII secretion system. Microbiology (United Kingdom), 2017, 163, 1851-1863.	1.8	19
20	Diversification of CORVET tethers facilitates transport complexity in <i>Tetrahymena thermophila</i> . Journal of Cell Science, 2020, 133, .	2.0	16
21	The distinctive flagellar proteome of <i>Euglena gracilis</i> illuminates the complexities of protistan flagella adaptation. New Phytologist, 2021, 232, 1323-1336.	7.3	14
22	High-Level Expression in Escherichia coli, Purification and Kinetic Characterization of LAPTc, a Trypanosoma cruzi M17-Aminopeptidase. Protein Journal, 2019, 38, 167-180.	1.6	10
23	Development of a High-Throughput Screening Assay to Identify Inhibitors of the Major M17-Leucyl Aminopeptidase from Trypanosoma cruzi Using RapidFire Mass Spectrometry. SLAS Discovery, 2020, 25, 1064-1071.	2.7	10
24	Structures of bacterial kynurenine formamidase reveal a crowded binuclear zinc catalytic site primed to generate a potent nucleophile. Biochemical Journal, 2014, 462, 581-589.	3.7	9
25	Evolution of protein trafficking in kinetoplastid parasites: Complexity and pathogenesis. Traffic, 2018, 19, 803-812.	2.7	8
26	CRISPR/Cas9-based precision tagging of essential genes in bloodstream form African trypanosomes. Molecular and Biochemical Parasitology, 2022, 249, 111476.	1.1	7
27	Designing and development of phthalimides as potent anti-tubulin hybrid molecules against malaria. European Journal of Medicinal Chemistry, 2022, 239, 114534.	5.5	7
28	Sorting the Muck from the Brass: Analysis of Protein Complexes and Cell Lysates. Methods in Molecular Biology, 2020, 2116, 645-653.	0.9	6
29	A novel membrane complex is required for docking and regulated exocytosis of lysosome-related organelles in Tetrahymena thermophila. PLoS Genetics, 2022, 18, e1010194.	3.5	6
30	EIF2 $\hat{\pm}$ phosphorylation is regulated in intracellular amastigotes for the generation of infective <i>Trypanosoma cruzi</i> trypomastigote forms. Cellular Microbiology, 2020, 22, e13243.	2.1	5
31	Structures of <i>Pseudomonas aeruginosa</i> $\hat{2}$ -ketoacyl-(acyl-carrier-protein) synthase II (FabF) and a C164Q mutant provide templates for antibacterial drug discovery and identify a buried potassium ion and a ligand-binding site that is an artefact of the crystal form. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1020-1026.	0.8	4
32	A hub-and-spoke nuclear lamina architecture in trypanosomes. Journal of Cell Science, 2021, 134, .	2.0	4
33	Computational study of novel inhibitory molecule, 1-(4-((2 <i>S</i> ,3 <i>S</i>)-3-amino-2-hydroxy-4-phenylbutyl)piperazin-1-yl)-3-phenylurea, with high potential to competitively block ATP binding to the RNA dependent RNA polymerase of SARS-CoV-2 virus. Journal of Biomolecular Structure and Dynamics, 2022, 40, 10162-10180.	3.5	2