

# Martin Zoltner

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2497274/publications.pdf>

Version: 2024-02-01

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  | 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. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 10162-10180. | 3.5 | 2         |
| 2  | CRISPR/Cas9-based precision tagging of essential genes in bloodstream form African trypanosomes. <i>Molecular and Biochemical Parasitology</i> , 2022, 249, 111476.   | 1.1 | 7         |
| 3  | A novel membrane complex is required for docking and regulated exocytosis of lysosome-related organelles in <i>Tetrahymena thermophila</i> . <i>PLoS Genetics</i> , 2022, 18, e1010194.   | 3.5 | 6         |
| 4  | Designing and development of phthalimides as potent anti-tubulin hybrid molecules against malaria. <i>European Journal of Medicinal Chemistry</i> , 2022, 239, 114534.  | 5.5 | 7         |
| 5  | Evolving Differentiation in African Trypanosomes. <i>Trends in Parasitology</i> , 2021, 37, 296-303.  | 3.3 | 33        |
| 6  | A hub-and-spoke nuclear lamina architecture in trypanosomes. <i>Journal of Cell Science</i> , 2021, 134, .  | 2.0 | 4         |
| 7  | The distinctive flagellar proteome of <i>Euglena gracilis</i> illuminates the complexities of protistan flagella adaptation. <i>New Phytologist</i> , 2021, 232, 1323-1336.   | 7.3 | 14        |
| 8  | 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        |
| 9  | 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        |
| 10 | 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        |
| 11 | Development of a High-Throughput Screening Assay to Identify Inhibitors of the Major M17-Leucyl Aminopeptidase from <i>Trypanosoma cruzi</i> Using RapidFire Mass Spectrometry. <i>SLAS Discovery</i> , 2020, 25, 1064-1071.  | 2.7 | 10        |
| 12 | A Uniquely Complex Mitochondrial Proteome from <i>Euglena gracilis</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2173-2191.  | 8.9 | 22        |
| 13 | $\langle scp \rangle$ EIF2 $\hat{1}\pm$ $\langle /scp \rangle$ phosphorylation is regulated in intracellular amastigotes for the generation of infective <i>Trypanosoma cruzi</i> trypomastigote forms. <i>Cellular Microbiology</i> , 2020, 22, e13243.  | 2.1 | 5         |
| 14 | Diversification of CORVET tethers facilitates transport complexity in <i>Tetrahymena thermophila</i> . <i>Journal of Cell Science</i> , 2020, 133, .  | 2.0 | 16        |
| 15 | Sorting the Muck from the Brass: Analysis of Protein Complexes and Cell Lysates. <i>Methods in Molecular Biology</i> , 2020, 2116, 645-653.   | 0.9 | 6         |
| 16 | High-Level Expression in <i>Escherichia coli</i> , Purification and Kinetic Characterization of LAPTc, a <i>Trypanosoma cruzi</i> M17-Aminopeptidase. <i>Protein Journal</i> , 2019, 38, 167-180.   | 1.6 | 10        |
| 17 | Transcriptome, proteome and draft genome of <i>Euglena gracilis</i> . <i>BMC Biology</i> , 2019, 17, 11.  | 3.8 | 98        |
| 18 | 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        |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | 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        |
| 20 | Evolution of protein trafficking in kinetoplastid parasites: Complexity and pathogenesis. <i>Traffic</i> , 2018, 19, 803-812.   | 2.7 | 8         |
| 21 | Host-parasite co-metabolic activation of antitrypanosomal aminomethyl-benzoxaboroles. <i>PLoS Pathogens</i> , 2018, 14, e1006850.   | 4.7 | 26        |
| 22 | Haem-iron plays a key role in the regulation of the Ess/type VII secretion system of <i>Staphylococcus aureus</i> RN6390. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1839-1850.  | 1.8 | 25        |
| 23 | Functional analysis of the EsaB component of the <i>Staphylococcus aureus</i> Type VII secretion system. <i>Microbiology (United Kingdom)</i> , 2017, 163, 1851-1863.   | 1.8 | 19        |
| 24 | Exploiting the Achilles™ heel of membrane trafficking in trypanosomes. <i>Current Opinion in Microbiology</i> , 2016, 34, 97-103.   | 5.1 | 28        |
| 25 | 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        |
| 26 | Membrane interactions and self-association of components of the Ess/Type VII secretion system of <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2016, 590, 349-357.   | 2.8 | 27        |
| 27 | Structures of <i>Pseudomonas aeruginosa</i> 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. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1020-1026. | 0.8 | 4         |
| 28 | Modulation of the Surface Proteome through Multiple Ubiquitylation Pathways in African Trypanosomes. <i>PLoS Pathogens</i> , 2015, 11, e1005236.  | 4.7 | 34        |
| 29 | Structures of bacterial kynurenine formamidase reveal a crowded binuclear zinc catalytic site primed to generate a potent nucleophile. <i>Biochemical Journal</i> , 2014, 462, 581-589.   | 3.7 | 9         |
| 30 | 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        |
| 31 | 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        |
| 32 | The Architecture of EssB, an Integral Membrane Component of the Type VII Secretion System. <i>Structure</i> , 2013, 21, 595-603.  | 3.3 | 19        |
| 33 | 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        |