

Peter John Myler

List of Publications by Year in descending order

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222
papers

11,810
citations

41258

49
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31759

101
g-index

236
all docs

236
docs citations

236
times ranked

10057
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. <i>Science</i> , 2005, 309, 409-415. | 6.0 | 1,273 |
| 2 | The Genome of the Kinetoplastid Parasite, <i>Leishmania major</i> . <i>Science</i> , 2005, 309, 436-442. | 6.0 | 1,237 |
| 3 | TriTrypDB: a functional genomic resource for the Trypanosomatidae. <i>Nucleic Acids Research</i> , 2010, 38, D457-D462. | 6.5 | 847 |
| 4 | Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409. | 6.0 | 713 |
| 5 | Biological and Structural Characterization of a Host-Adapting Amino Acid in Influenza Virus. <i>PLoS Pathogens</i> , 2010, 6, e1001034. | 2.1 | 299 |
| 6 | Transcription of <i>Leishmania major</i> Friedlin Chromosome 1 Initiates in Both Directions within a Single Region. <i>Molecular Cell</i> , 2003, 11, 1291-1299. | 4.5 | 231 |
| 7 | <i>Leishmania major</i> Friedlin chromosome 1 has an unusual distribution of protein-coding genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 2902-2906. | 3.3 | 225 |
| 8 | GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D98-D108. | 6.5 | 217 |
| 9 | Heterologous expression of proteins from <i>Plasmodium falciparum</i> : Results from 1000 genes. <i>Molecular and Biochemical Parasitology</i> , 2006, 148, 144-160. | 0.5 | 173 |
| 10 | A comprehensive analysis of <i>Trypanosoma brucei</i> mitochondrial proteome. <i>Proteomics</i> , 2009, 9, 434-450. | 1.3 | 162 |
| 11 | Patterns of gene recombination shape var gene repertoires in <i>Plasmodium falciparum</i> : comparisons of geographically diverse isolates. <i>BMC Genomics</i> , 2007, 8, 45. | 1.2 | 161 |
| 12 | Analysis of the <i>Leishmania donovani</i> transcriptome reveals an ordered progression of transient and permanent changes in gene expression during differentiation. <i>Molecular and Biochemical Parasitology</i> , 2007, 152, 53-65. | 0.5 | 149 |
| 13 | Multiple levels of gene regulation mediate differentiation of the intracellular pathogen <i>Leishmania</i> . <i>FASEB Journal</i> , 2011, 25, 515-525. | 0.2 | 143 |
| 14 | Glucosylated Hydroxymethyluracil, DNA Base J, Prevents Transcriptional Readthrough in <i>Leishmania</i> . <i>Cell</i> , 2012, 150, 909-921. | 13.5 | 138 |
| 15 | Small RNAs derived from tRNAs and rRNAs are highly enriched in exosomes from both old and new world <i>Leishmania</i> providing evidence for conserved exosomal RNA Packaging. <i>BMC Genomics</i> , 2015, 16, 151. | 1.2 | 136 |
| 16 | Transcription Initiation and Termination on <i>Leishmania major</i> Chromosome 3. <i>Eukaryotic Cell</i> , 2004, 3, 506-517. | 3.4 | 135 |
| 17 | Mitochondrial Complexes in <i>Trypanosoma brucei</i> . <i>Molecular and Cellular Proteomics</i> , 2008, 7, 534-545. | 2.5 | 133 |
| 18 | Widespread variation in transcript abundance within and across developmental stages of <i>Trypanosoma brucei</i> . <i>BMC Genomics</i> , 2009, 10, 482. | 1.2 | 126 |

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|----|---|------|-----------|
| 19 | Genome and Phylogenetic Analyses of <i>Trypanosoma evansi</i> Reveal Extensive Similarity to <i>T. brucei</i> and Multiple Independent Origins for Dyskinetoplasty. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e3404. | 1.3 | 124 |
| 20 | Extensive stage-regulation of translation revealed by ribosome profiling of <i>Trypanosoma brucei</i> . <i>BMC Genomics</i> , 2014, 15, 911. | 1.2 | 121 |
| 21 | Histone acetylations mark origins of polycistronic transcription in <i>Leishmania major</i> . <i>BMC Genomics</i> , 2009, 10, 152. | 1.2 | 118 |
| 22 | Iron uptake controls the generation of <i>Leishmania</i> infective forms through regulation of ROS levels. <i>Journal of Experimental Medicine</i> , 2013, 210, 401-416. | 4.2 | 114 |
| 23 | Combining Functional and Structural Genomics to Sample the Essential <i>Burkholderia</i> Structome. <i>PLoS ONE</i> , 2013, 8, e53851. | 1.1 | 113 |
| 24 | Post-translational modification of cellular proteins during <i>Leishmania donovani</i> differentiation. <i>Proteomics</i> , 2008, 8, 1843-1850. | 1.3 | 111 |
| 25 | Increasing the structural coverage of tuberculosis drug targets. <i>Tuberculosis</i> , 2015, 95, 142-148. | 0.8 | 103 |
| 26 | Comparison of the A2 Gene Locus in <i>Leishmania donovani</i> and <i>Leishmania major</i> and Its Control over Cutaneous Infection. <i>Journal of Biological Chemistry</i> , 2003, 278, 35508-35515. | 1.6 | 99 |
| 27 | Genetic Analysis of <i>Leishmania donovani</i> Tropism Using a Naturally Attenuated Cutaneous Strain. <i>PLoS Pathogens</i> , 2014, 10, e1004244. | 2.1 | 97 |
| 28 | Lysyl-tRNA synthetase as a drug target in malaria and cryptosporidiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7015-7020. | 3.3 | 94 |
| 29 | Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191. | 0.5 | 92 |
| 30 | <i>Trypanosoma brucei</i> Mitochondrial Ribosomes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1286-1296. | 2.5 | 92 |
| 31 | An Arginine Deprivation Response Pathway Is Induced in <i>Leishmania</i> during Macrophage Invasion. <i>PLoS Pathogens</i> , 2016, 12, e1005494. | 2.1 | 86 |
| 32 | Two mechanisms of expression of a predominant variant antigen gene of <i>Trypanosoma brucei</i> . <i>Nature</i> , 1984, 309, 282-284. | 13.7 | 83 |
| 33 | Genetic nomenclature for <i>Trypanosoma</i> and <i>Leishmania</i> . <i>Molecular and Biochemical Parasitology</i> , 1998, 97, 221-224. | 0.5 | 83 |
| 34 | Evaluation of differential gene expression in <i>Leishmania major</i> Friedlin procyclics and metacyclics using DNA microarray analysis. <i>Molecular and Biochemical Parasitology</i> , 2003, 129, 103-114. | 0.5 | 81 |
| 35 | A Novel Active DNA Topoisomerase I in <i>Leishmania donovani</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 3521-3526. | 1.6 | 76 |
| 36 | Metabolic Reprogramming during Purine Stress in the Protozoan Pathogen <i>Leishmania donovani</i> . <i>PLoS Pathogens</i> , 2014, 10, e1003938. | 2.1 | 74 |

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|----|---|-----|-----------|
| 37 | Trypanosoma brucei minicircles encode multiple guide RNAs which can direct editing of extensively overlapping sequences. <i>Nucleic Acids Research</i> , 1993, 21, 4313-4320. | 6.5 | 73 |
| 38 | Regulation Dynamics of Leishmania Differentiation: Deconvoluting Signals and Identifying Phosphorylation Trends. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1787-1799. | 2.5 | 72 |
| 39 | SAD phasing using iodide ions in a high-throughput structural genomics environment. <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 83-95. | 1.2 | 68 |
| 40 | The Leishmania donovani LD1 locus gene ORFG encodes a biopterin transporter (BT1). <i>Molecular and Biochemical Parasitology</i> , 1999, 104, 93-105. | 0.5 | 67 |
| 41 | Using Fragment Cocktail Crystallography To Assist Inhibitor Design of Trypanosoma brucei Nucleoside 2-Deoxyribosyltransferase. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 5939-5946. | 2.9 | 66 |
| 42 | Leishmania major chromosome 3 contains two long convergent polycistronic gene clusters separated by a tRNA gene. <i>Nucleic Acids Research</i> , 2003, 31, 4201-4210. | 6.5 | 65 |
| 43 | (TAA)n within sequences flanking several intrachromosomal variant surface glycoprotein genes in Trypanosoma brucei. <i>Nucleic Acids Research</i> , 1985, 13, 3161-3177. | 6.5 | 62 |
| 44 | Association of Guide RNA Binding Protein gBP21 with Active RNA Editing Complexes in Trypanosoma brucei. <i>Molecular and Cellular Biology</i> , 1998, 18, 6014-6022. | 1.1 | 56 |
| 45 | Structural genomics of infectious disease drug targets: the SSGCID. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 979-984. | 0.7 | 55 |
| 46 | Structural organization of the maxicircle variable region of Trypanosoma brucei: identification of potential replication origins and topoisomerase II binding sites. <i>Nucleic Acids Research</i> , 1993, 21, 687-694. | 6.5 | 53 |
| 47 | Cloning, heterologous expression, and substrate specificities of protein farnesyltransferases from Trypanosoma cruzi and Leishmania major. <i>Molecular and Biochemical Parasitology</i> , 2002, 122, 181-188. | 0.5 | 53 |
| 48 | Genomic organization and functional characterization of the Leishmania major Friedlin ribosomal RNA gene locus. <i>Molecular and Biochemical Parasitology</i> , 2001, 116, 147-157. | 0.5 | 52 |
| 49 | Editing of Trypanosoma brucei maxicircle CR5 mRNA generates variable carboxy terminal predicted protein sequences. <i>Nucleic Acids Research</i> , 1994, 22, 1489-1495. | 6.5 | 51 |
| 50 | Trypanosoma brucei mitochondrial CR4 gene encodes an extensively edited mRNA with completely edited sequence only in bloodstream forms. <i>Molecular and Biochemical Parasitology</i> , 1994, 64, 65-74. | 0.5 | 50 |
| 51 | Integrative analysis of the Trypanosoma brucei gene expression cascade predicts differential regulation of mRNA processing and unusual control of ribosomal protein expression. <i>BMC Genomics</i> , 2016, 17, 306. | 1.2 | 50 |
| 52 | Distribution and sequence divergence of LRV1 viruses among different Leishmania species. <i>Molecular and Biochemical Parasitology</i> , 1992, 54, 101-104. | 0.5 | 49 |
| 53 | Recent developments from the Leishmania genome project. <i>Current Opinion in Microbiology</i> , 2000, 3, 412-416. | 2.3 | 49 |
| 54 | Xanthine Phosphoribosyltransferase from Leishmania donovani. <i>Journal of Biological Chemistry</i> , 1999, 274, 34403-34410. | 1.6 | 47 |

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|----|--|-----|-----------|
| 55 | Telomere and subtelomere of <i>Trypanosoma cruzi</i> chromosomes are enriched in (pseudo)genes of retrotransposon hot spot and trans-sialidase-like gene families: the origins of <i>T. cruzi</i> telomeres. <i>Gene</i> , 2005, 346, 153-161. | 1.0 | 47 |
| 56 | A DNA sequence (LD1) which occurs in several genomic organizations in <i>Leishmania</i> . <i>Molecular and Biochemical Parasitology</i> , 1991, 47, 151-160. | 0.5 | 46 |
| 57 | Cathepsin B-like cysteine proteases and <i>Caenorhabditis elegans</i> homologues dominate gene products expressed in adult <i>Haemonchus contortus</i> intestine. <i>Molecular and Biochemical Parasitology</i> , 2001, 116, 159-169. | 0.5 | 45 |
| 58 | The <i>Rickettsia</i> type IV secretion system: unrealized complexity mired by gene family expansion. <i>Pathogens and Disease</i> , 2016, 74, ftw058. | 0.8 | 45 |
| 59 | Biochemical and Structural Characterization of Selective Allosteric Inhibitors of the <i>Plasmodium falciparum</i> Drug Target, Prolyl-tRNA-synthetase. <i>ACS Infectious Diseases</i> , 2017, 3, 34-44. | 1.8 | 45 |
| 60 | The size difference between <i>Leishmania major</i> Friedlin chromosome one homologues is localized to sub-telomeric repeats at one chromosomal end. <i>Molecular and Biochemical Parasitology</i> , 2000, 109, 1-15. | 0.5 | 44 |
| 61 | Shotgun optical mapping of the entire <i>Leishmania major</i> Friedlin genome. <i>Molecular and Biochemical Parasitology</i> , 2004, 138, 97-106. | 0.5 | 41 |
| 62 | Glyoxalase I from <i>Leishmania donovani</i> : A potential target for anti-parasite drug. <i>Biochemical and Biophysical Research Communications</i> , 2005, 337, 1237-1248. | 1.0 | 40 |
| 63 | The two ATPase 6 mRNAs of <i>Leishmania tarentolae</i> differ at their 3' ends. <i>Molecular and Biochemical Parasitology</i> , 1991, 48, 139-149. | 0.5 | 39 |
| 64 | Structural Genomics of Pathogenic Protozoa: an Overview. <i>Methods in Molecular Biology</i> , 2008, 426, 497-513. | 0.4 | 38 |
| 65 | Immunization with recombinant LD1 antigens protects against experimental leishmaniasis. <i>Vaccine</i> , 2000, 19, 423-430. | 1.7 | 37 |
| 66 | Tetracycline regulated gene expression in <i>Leishmania donovani</i> . <i>Molecular and Biochemical Parasitology</i> , 2001, 112, 61-69. | 0.5 | 37 |
| 67 | Solution structure of Rv2377c-founding member of the Mbth-like protein family. <i>Tuberculosis</i> , 2010, 90, 245-251. | 0.8 | 37 |
| 68 | Kinetoplastid-specific histone variant functions are conserved in <i>Leishmania major</i> . <i>Molecular and Biochemical Parasitology</i> , 2013, 191, 53-57. | 0.5 | 37 |
| 69 | The <i>Leishmania</i> genome project: new insights into gene organization and function. <i>Medical Microbiology and Immunology</i> , 2001, 190, 9-12. | 2.6 | 36 |
| 70 | Quantitation of RNA editing substrates, products and potential intermediates: implications for developmental regulation. <i>Nucleic Acids Research</i> , 1995, 23, 708-712. | 6.5 | 35 |
| 71 | Characterization of the RNA polymerase II and III complexes in <i>Leishmania major</i> . <i>International Journal for Parasitology</i> , 2007, 37, 491-502. | 1.3 | 35 |
| 72 | Crystal structure of glyceraldehyde-3-phosphate dehydrogenase from <i>Plasmodium falciparum</i> at 2.25 Å... resolution reveals intriguing extra electron density in the active site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 570-577. | 1.5 | 34 |

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|----|---|-----|-----------|
| 73 | Searching the Tritryp Genomes for Drug Targets. <i>Advances in Experimental Medicine and Biology</i> , 2008, 625, 133-140. | 0.8 | 34 |
| 74 | The Role of Medical Structural Genomics in Discovering New Drugs for Infectious Diseases. <i>PLoS Computational Biology</i> , 2009, 5, e1000530. | 1.5 | 34 |
| 75 | A multicopy, extrachromosomal DNA in <i>Leishmania infantum</i> contains two inverted repeats of the 27.5-kilobase LD1 sequence and encodes numerous transcripts. <i>Molecular and Biochemical Parasitology</i> , 1992, 55, 39-50. | 0.5 | 33 |
| 76 | Cloning and Characterization of <i>Leishmania donovani</i> Telomeres. <i>Experimental Parasitology</i> , 2000, 94, 248-258. | 0.5 | 33 |
| 77 | Structural Insight into How Bacteria Prevent Interference between Multiple Divergent Type IV Secretion Systems. <i>MBio</i> , 2015, 6, e01867-15. | 1.8 | 33 |
| 78 | Characterization of the <i>Leishmania donovani</i> ribosomal RNA promoter. <i>Molecular and Biochemical Parasitology</i> , 1999, 103, 197-210. | 0.5 | 32 |
| 79 | Ploidy changes associated with disruption of two adjacent genes on <i>Leishmania major</i> chromosome 1. <i>International Journal for Parasitology</i> , 2005, 35, 419-429. | 1.3 | 32 |
| 80 | An amplified DNA element in <i>Leishmania</i> encodes potential integral membrane and nucleotide-binding proteins. <i>Molecular and Biochemical Parasitology</i> , 1994, 66, 11-20. | 0.5 | 31 |
| 81 | Structure of a <i>Burkholderia pseudomallei</i> Trimeric Autotransporter Adhesin Head. <i>PLoS ONE</i> , 2010, 5, e12803. | 1.1 | 31 |
| 82 | Early Expression of a <i>Trypanosoma brucei</i> VSG Gene Duplicated from an Incomplete Basic Copy. <i>Journal of Eukaryotic Microbiology</i> , 1994, 41, 71-78. | 0.8 | 29 |
| 83 | Gene organization and sequence analyses of transfer RNA genes in Trypanosomatid parasites. <i>BMC Genomics</i> , 2009, 10, 232. | 1.2 | 29 |
| 84 | Tyrosine aminotransferase from <i>Leishmania infantum</i> : A new drug target candidate. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2014, 4, 347-354. | 1.4 | 29 |
| 85 | Genomic organization and expression of the expanded SCG/L/R gene family of <i>Leishmania major</i> : Internal clusters and telomeric localization of SCGs mediating species-specific LPG modifications. <i>Molecular and Biochemical Parasitology</i> , 2006, 146, 231-241. | 0.5 | 28 |
| 86 | A frequently amplified region in <i>Leishmania</i> contains a gene conserved in prokaryotes and eukaryotes. <i>Gene</i> , 1994, 148, 187-193. | 1.0 | 27 |
| 87 | Structure of an ADP-ribosylation factor, ARF1, from <i>Entamoeba histolytica</i> bound to Mg ²⁺ -GDP. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 594-599. | 0.4 | 27 |
| 88 | A simple method for cloning blunt ended DNA fragments. <i>Nucleic Acids Research</i> , 1991, 19, 398-398. | 6.5 | 26 |
| 89 | Structure-Guided Identification of Resistance Breaking Antimalarial N-Myristoyltransferase Inhibitors. <i>Cell Chemical Biology</i> , 2019, 26, 991-1000.e7. | 2.5 | 26 |
| 90 | A low-background inducible promoter system in <i>Leishmania donovani</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 119, 217-223. | 0.5 | 25 |

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|-----|---|-----|-----------|
| 91 | Genomic organization and gene expression in a chromosomal region of <i>Leishmania major</i> . <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 233-243. | 0.5 | 25 |
| 92 | Tb927.10.6900 encodes the glucosyltransferase involved in synthesis of base J in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 2014, 196, 9-11. | 0.5 | 25 |
| 93 | Defining the sequence requirements for the positioning of base J in DNA using SMRT sequencing. <i>Nucleic Acids Research</i> , 2015, 43, 2102-2115. | 6.5 | 25 |
| 94 | Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in <i>Trypanosomatids</i> . <i>Scientific Reports</i> , 2017, 7, 3725. | 1.6 | 24 |
| 95 | X-ray structure determination of the glycine cleavage system protein H of <i>Mycobacterium tuberculosis</i> using an inverse Compton synchrotron X-ray source. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 91-100. | 1.2 | 23 |
| 96 | Crystal structures and proposed structural/functional classification of three protozoan proteins from the isochorismatase superfamily. <i>Protein Science</i> , 2005, 14, 2887-2894. | 3.1 | 21 |
| 97 | Wheat germ cell-free expression system as a pathway to improve protein yield and solubility for the SSGCID pipeline. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1027-1031. | 0.7 | 21 |
| 98 | Crystal Structure of <i>Toxoplasma gondii</i> Porphobilinogen Synthase. <i>Journal of Biological Chemistry</i> , 2011, 286, 15298-15307. | 1.6 | 21 |
| 99 | Discovery of Inhibitors of <i>Burkholderia pseudomallei</i> Methionine Aminopeptidase with Antibacterial Activity. <i>ACS Medicinal Chemistry Letters</i> , 2013, 4, 699-703. | 1.3 | 21 |
| 100 | A survey of <i>Leishmania braziliensis</i> genome by shotgun sequencing. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 81-86. | 0.5 | 20 |
| 101 | Structure of a ribulose 5-phosphate 3-epimerase from <i>Plasmodium falciparum</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 338-342. | 1.5 | 20 |
| 102 | Advancing <i>Trypanosoma brucei</i> genome annotation through ribosome profiling and spliced leader mapping. <i>Molecular and Biochemical Parasitology</i> , 2015, 202, 1-10. | 0.5 | 20 |
| 103 | Comparative transcriptomics in <i>Leishmania braziliensis</i> : disclosing differential gene expression of coding and putative noncoding RNAs across developmental stages. <i>RNA Biology</i> , 2019, 16, 639-660. | 1.5 | 20 |
| 104 | Leveraging structure determination with fragment screening for infectious disease drug targets: MECP synthase from <i>Burkholderia pseudomallei</i> . <i>Journal of Structural and Functional Genomics</i> , 2011, 12, 63-76. | 1.2 | 19 |
| 105 | Structure of Lmaj006129AAA, a hypothetical protein from <i>Leishmania major</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 175-179. | 0.7 | 18 |
| 106 | An ensemble of structures of <i>Burkholderia pseudomallei</i> 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1044-1050. | 0.7 | 18 |
| 107 | A Structural Biology Approach Enables the Development of Antimicrobials Targeting Bacterial Immunophilins. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 1458-1467. | 1.4 | 18 |
| 108 | RNA-Seq Approaches for Determining mRNA Abundance in <i>Leishmania</i> . <i>Methods in Molecular Biology</i> , 2015, 1201, 207-219. | 0.4 | 18 |

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|-----|--|-----|-----------|
| 109 | Iron superoxide dismutases in eukaryotic pathogens: new insights from Apicomplexa and Trypanosoma structures. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 615-621. | 0.4 | 18 |
| 110 | Recent contributions of structure-based drug design to the development of antibacterial compounds. <i>Current Opinion in Microbiology</i> , 2015, 27, 133-138. | 2.3 | 18 |
| 111 | Membrane skeletal association and post-translational allosteric regulation of <i>Toxoplasma gondii</i> GAPDH1. <i>Molecular Microbiology</i> , 2017, 103, 618-634. | 1.2 | 18 |
| 112 | Dramatic changes in gene expression in different forms of <i>Crithidia fasciculata</i> reveal potential mechanisms for insect-specific adhesion in kinetoplastid parasites. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007570. | 1.3 | 18 |
| 113 | Discovery of a Natural Product That Binds to the Mycobacterium tuberculosis Protein Rv1466 Using Native Mass Spectrometry. <i>Molecules</i> , 2020, 25, 2384. | 1.7 | 18 |
| 114 | The LD1 amplified element from <i>Leishmania infantum</i> encodes a homolog of ribosomal protein L37. <i>Molecular and Biochemical Parasitology</i> , 1993, 62, 147-151. | 0.5 | 17 |
| 115 | <i>Leishmania donovani</i> : Characterization and Expression of ORFF, a Gene Amplified from the LDI Locus. <i>Experimental Parasitology</i> , 1999, 93, 225-230. | 0.5 | 17 |
| 116 | Functional genomics in sand fly-derived <i>Leishmania</i> promastigotes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007288. | 1.3 | 17 |
| 117 | Identification of Selective Inhibitors of <i>Plasmodium</i> N-Myristoyltransferase by High-Throughput Screening. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 591-600. | 2.9 | 17 |
| 118 | Sensing Host Arginine Is Essential for <i>Leishmania</i> Parasites' Intracellular Development. <i>MBio</i> , 2020, 11, . | 1.8 | 17 |
| 119 | Molecular variation in trypanosomes. <i>Acta Tropica</i> , 1993, 53, 205-225. | 0.9 | 16 |
| 120 | Sense and antisense transcripts in the histone H1 (HIS-1) locus of <i>Leishmania major</i> . <i>International Journal for Parasitology</i> , 2003, 33, 965-975. | 1.3 | 16 |
| 121 | Trypanosomatid flagellum biogenesis: ARL-3A is involved in several species. <i>Experimental Parasitology</i> , 2004, 108, 126-133. | 0.5 | 16 |
| 122 | Nanovolume optimization of protein crystal growth using the microcapillary protein crystallization system. <i>Journal of Applied Crystallography</i> , 2010, 43, 1078-1083. | 1.9 | 16 |
| 123 | Inhibitor-bound complexes of dihydrofolate reductase-thymidylate synthase from <i>Babesia bovis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1070-1077. | 0.7 | 16 |
| 124 | New <i>Trypanosoma cruzi</i> Repeated Element That Shows Site Specificity for Insertion. <i>Eukaryotic Cell</i> , 2007, 6, 1228-1238. | 3.4 | 15 |
| 125 | <i>Mycobacterium thermoresistibile</i> as a source of thermostable orthologs of <i>Mycobacterium tuberculosis</i> proteins. <i>Protein Science</i> , 2012, 21, 1093-1096. | 3.1 | 15 |
| 126 | Dynamic colocalization of 2 simultaneously active <i>VSG</i> expression sites within a single expression-site body in <i>Trypanosoma brucei</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16561-16570. | 3.3 | 15 |

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|-----|---|-----|-----------|
| 127 | Backbone chemical shift assignments for the SARS-CoV-2 non-structural protein Nsp9: intermediate (ms $\hat{=}$ $\hat{1}/4$ s) dynamics in the C-terminal helix at the dimer interface. <i>Biomolecular NMR Assignments</i> , 2021, 15, 107-116. | 0.4 | 15 |
| 128 | Illuminating Parasite Protein Production by Ribosome Profiling. <i>Trends in Parasitology</i> , 2016, 32, 446-457. | 1.5 | 14 |
| 129 | Cytosolic expression, solution structures, and molecular dynamics simulation of genetically encodable disulfide-rich <i><i>de novo</i></i> designed peptides. <i>Protein Science</i> , 2018, 27, 1611-1623. | 3.1 | 14 |
| 130 | A novel telomeric gene conversion in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 1989, 35, 11-19. | 0.5 | 13 |
| 131 | Importing statistical measures into Artemis enhances gene identification in the <i>Leishmania</i> genome project. <i>BMC Bioinformatics</i> , 2003, 4, 23. | 1.2 | 13 |
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