

Peter John Myler

List of Publications by Year in descending order

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222
papers

11,810
citations

41258

49
h-index

31759

101
g-index

236
all docs

236
docs citations

236
times ranked

10057
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of a putative short-chain dehydrogenase/reductase from <i>Paraburkholderia xenovorans</i> . Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 25-30.	0.4	2
2	Crystal structure of a short-chain dehydrogenase/reductase from <i>Burkholderia phymatum</i> in complex with NAD. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 52-58.	0.4	1
3	Crystal structures of FolM alternative dihydrofolate reductase 1 from <i>Brucella suis</i> and <i>Brucella canis</i> . Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 31-38.	0.4	0
4	Crystal structure of a hypothetical protein from <i>Giardia lamblia</i> . Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 59-65.	0.4	2
5	Crystal structure of betaine aldehyde dehydrogenase from <i>Burkholderia pseudomallei</i> . Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 45-51.	0.4	1
6	Crystal structure of an inorganic pyrophosphatase from <i>Chlamydia trachomatis</i> D/UW-3/Cx. Acta Crystallographica Section F, Structural Biology Communications, 2022, 78, 135-142.	0.4	0
7	Broad-spectrum <i>in vitro</i> activity of macrophage infectivity potentiator inhibitors against Gram-negative bacteria and <i>Leishmania major</i> . Journal of Antimicrobial Chemotherapy, 2022, 77, 1625-1634.	1.3	5
8	Identification of P218 as a potent inhibitor of <i>Mycobacterium ulcerans</i> DHFR. RSC Medicinal Chemistry, 2021, 12, 103-109.	1.7	4
9	Backbone chemical shift assignments for the SARS-CoV-2 non-structural protein Nsp9: intermediate (ms $\hat{\epsilon}$ $\hat{1}/4$ s) dynamics in the C-terminal helix at the dimer interface. Biomolecular NMR Assignments, 2021, 15, 107-116.	0.4	15
10	Crystal structure of acetoacetyl-CoA reductase from <i>Rickettsia felis</i> . Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 54-60.	0.4	1
11	Chromatin-Associated Protein Complexes Link DNA Base J and Transcription Termination in <i>Leishmania</i> . MSphere, 2021, 6, .	1.3	12
12	<i>Naegleria fowleri</i> : Protein structures to facilitate drug discovery for the deadly, pathogenic free-living amoeba. PLoS ONE, 2021, 16, e0241738.	1.1	12
13	Exploring TERRA during <i>Leishmania major</i> developmental cycle and continuous <i>in vitro</i> passages. International Journal of Biological Macromolecules, 2021, 174, 573-586.	3.6	9
14	Turnover of Variant Surface Glycoprotein in <i>Trypanosoma brucei</i> Is a Bimodal Process. MBio, 2021, 12, e0172521.	1.8	10
15	Genome Assemblies across the Diverse Evolutionary Spectrum of <i>Leishmania</i> Protozoan Parasites. Microbiology Resource Announcements, 2021, 10, e0054521.	0.3	8
16	Arginine sensing in intracellular parasitism of <i>Leishmania</i> . Current Opinion in Microbiology, 2021, 64, 41-46.	2.3	1
17	The transcriptome of <i>Balamuthia mandrillaris</i> trophozoites for structure-guided drug design. Scientific Reports, 2021, 11, 21664.	1.6	7
18	Structural characterization of $\hat{2}$ ketoacyl ACP synthase I bound to platencin and fragment screening molecules at two substrate binding sites. Proteins: Structure, Function and Bioinformatics, 2020, 88, 47-56.	1.5	3

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19	Structural diversity in the Mycobacteria DUF3349 superfamily. <i>Protein Science</i> , 2020, 29, 670-685.	3.1	1
20	Solution structure for an Encephalitozoon cuniculi adrenodoxin-like protein in the oxidized state. <i>Protein Science</i> , 2020, 29, 809-817.	3.1	2
21	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
22	Structural analysis of CACHE domain of the McpA chemoreceptor from <i>Leptospira interrogans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 1323-1329.	1.0	2
23	Sensing Host Arginine Is Essential for <i>Leishmania</i> Parasites' Intracellular Development. <i>MBio</i> , 2020, 11, .	1.8	17
24	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
25	A Phenotarget Approach for Identifying an Alkaloid Interacting with the Tuberculosis Protein Rv1466. <i>Marine Drugs</i> , 2020, 18, 149.	2.2	11
26	Structures of glyceraldehyde 3-phosphate dehydrogenase in <i>Neisseria gonorrhoeae</i> and <i>Chlamydia trachomatis</i> . <i>Protein Science</i> , 2020, 29, 768-778.	3.1	10
27	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
28	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
29	Structure-Guided Identification of Resistance Breaking Antimalarial N-Myristoyltransferase Inhibitors. <i>Cell Chemical Biology</i> , 2019, 26, 991-1000.e7.	2.5	26
30	Functional genomics in sand fly-derived <i>Leishmania</i> promastigotes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007288.	1.3	17
31	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
32	Quantitative RNA Analysis Using RNA-Seq. <i>Methods in Molecular Biology</i> , 2019, 1971, 95-108.	0.4	4
33	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
34	RNA-seq analysis reveals differences in transcript abundance between cultured and sand fly-derived <i>Leishmania infantum</i> promastigotes. <i>Parasitology International</i> , 2018, 67, 476-480.	0.6	4
35	Crystal structure of chorismate mutase from <i>Burkholderia thailandensis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 294-299.	0.4	1
36	Crystal structure of chorismate mutase from <i>Burkholderia phymatum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 187-192.	0.4	2

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37	The identification of inhibitory compounds of <i>Rickettsia prowazekii</i> methionine aminopeptidase for antibacterial applications. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2018, 28, 1376-1380.	1.0	4
38	<i>Mycobacterium tuberculosis</i> Rv3651 is a triple sensor domain protein. <i>Protein Science</i> , 2018, 27, 568-572.	3.1	1
39	Ab initio structure solution of a proteolytic fragment using ARCIMBOLDO. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 530-535.	0.4	1
40	Cytosolic expression, solution structures, and molecular dynamics simulation of genetically encodable disulfide-rich de novo designed peptides. <i>Protein Science</i> , 2018, 27, 1611-1623.	3.1	14
41	Structure and analysis of nucleoside diphosphate kinase from <i>Borrelia burgdorferi</i> prepared in a transition-state complex with ADP and vanadate moieties. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 373-384.	0.4	1
42	Solution NMR structures of oxidized and reduced <i>Ehrlichia chaffeensis</i> thioredoxin: NMR-invisible structure owing to backbone dynamics. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 46-56.	0.4	3
43	Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in Trypanosomatids. <i>Scientific Reports</i> , 2017, 7, 3725.	1.6	24
44	Ligand co-crystallization of aminoacyl-tRNA synthetases from infectious disease organisms. <i>Scientific Reports</i> , 2017, 7, 223.	1.6	6
45	Backbone chemical shift assignments and secondary structure analysis of the U1 protein from the Bas-Congo virus. <i>Biomolecular NMR Assignments</i> , 2017, 11, 51-56.	0.4	11
46	<i>Rickettsia prowazekii</i> methionine aminopeptidase as a promising target for the development of antibacterial agents. <i>Bioorganic and Medicinal Chemistry</i> , 2017, 25, 813-824.	1.4	10
47	Structural and Biophysical Characterization of the <i>Mycobacterium tuberculosis</i> Protein Rv0577, a Protein Associated with Neutral Red Staining of Virulent Tuberculosis Strains and Homologue of the <i>Streptomyces coelicolor</i> Protein KbpA. <i>Biochemistry</i> , 2017, 56, 4015-4027.	1.2	4
48	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
49	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
50	Disclosing 3' UTR cis-elements and putative partners involved in gene expression regulation in <i>Leishmania</i> spp.. <i>PLoS ONE</i> , 2017, 12, e0183401.	1.1	2
51	Cloning, expression, purification, crystallization and X-ray diffraction analysis of dihydrodipicolinate synthase from the human pathogenic bacterium <i>Bartonella henselae</i> strain Houston-1 at 2.1 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 2-9.	0.4	5
52	An Arginine Deprivation Response Pathway Is Induced in <i>Leishmania</i> during Macrophage Invasion. <i>PLoS Pathogens</i> , 2016, 12, e1005494.	2.1	86
53	Illuminating Parasite Protein Production by Ribosome Profiling. <i>Trends in Parasitology</i> , 2016, 32, 446-457.	1.5	14
54	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

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55	Integrative analysis of the <i>Trypanosoma brucei</i> 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
56	The crystal structure of dihydrodipicolinate reductase from the human-pathogenic bacterium <i>Bartonella henselae</i> strain Houston-1 at 2.3 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 885-891.	0.4	4
57	Backbone chemical shift assignments for the sensor domain of the <i>Burkholderia pseudomallei</i> histidine kinase RisS: α -resonances at the dimer interface. <i>Biomolecular NMR Assignments</i> , 2015, 9, 381-385.	0.4	3
58	Structural Insight into How Bacteria Prevent Interference between Multiple Divergent Type IV Secretion Systems. <i>MBio</i> , 2015, 6, e01867-15.	1.8	33
59	Increasing the structural coverage of tuberculosis drug targets. <i>Tuberculosis</i> , 2015, 95, 142-148.	0.8	103
60	RNA-Seq Approaches for Determining mRNA Abundance in <i>Leishmania</i> . <i>Methods in Molecular Biology</i> , 2015, 1201, 207-219.	0.4	18
61	Structural Genomics Support for Infectious Disease Drug Design. <i>ACS Infectious Diseases</i> , 2015, 1, 127-129.	1.8	2
62	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
63	Structures of aspartate aminotransferases from <i>Trypanosoma brucei</i> , <i>Leishmania major</i> and <i>Giardia lamblia</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 566-571.	0.4	5
64	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
65	Structures of a histidine triad family protein from <i>Entamoeba histolytica</i> bound to sulfate, AMP and GMP. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 572-576.	0.4	3
66	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
67	Solution-state NMR structure of the putative morphogene protein BolA (PFE0790c) from <i>Plasmodium falciparum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 514-521.	0.4	4
68	Crystal structures of Mycobacterial MeaB and MMAA-like GTPases. <i>Journal of Structural and Functional Genomics</i> , 2015, 16, 91-99.	1.2	7
69	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
70	Iron superoxide dismutases in eukaryotic pathogens: new insights from Apicomplexa and <i>Trypanosoma</i> structures. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 615-621.	0.4	18
71	Structure of a CutA1 divalent-cation tolerance protein from <i>Cryptosporidium parvum</i> , the protozoal parasite responsible for cryptosporidiosis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 522-530.	0.4	1
72	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

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73	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
74	Synthesis and biological evaluation of pyrazolopyrimidines as potential antibacterial agents. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015, 25, 5699-5704.	1.0	7
75	The Putative <i>Leishmania</i> Telomerase RNA (LeishTER) Undergoes Trans-Splicing and Contains a Conserved Template Sequence. <i>PLoS ONE</i> , 2014, 9, e112061.	1.1	13
76	Extensive stage-regulation of translation revealed by ribosome profiling of <i>Trypanosoma brucei</i> . <i>BMC Genomics</i> , 2014, 15, 911.	1.2	121
77	Metabolic Reprogramming during Purine Stress in the Protozoan Pathogen <i>Leishmania donovani</i> . <i>PLoS Pathogens</i> , 2014, 10, e1003938.	2.1	74
78	Genetic Analysis of <i>Leishmania donovani</i> Tropism Using a Naturally Attenuated Cutaneous Strain. <i>PLoS Pathogens</i> , 2014, 10, e1004244.	2.1	97
79	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
80	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
81	Crystal structure and putative substrate identification for the <i>Entamoeba histolytica</i> low molecular weight tyrosine phosphatase. <i>Molecular and Biochemical Parasitology</i> , 2014, 193, 33-44.	0.5	7
82	<i>Mycobacterium tuberculosis</i> Rv2179c Protein Establishes a New Exoribonuclease Family with Broad Phylogenetic Distribution. <i>Journal of Biological Chemistry</i> , 2014, 289, 2139-2147.	1.6	13
83	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
84	Regulation Dynamics of <i>Leishmania</i> Differentiation: Deconvoluting Signals and Identifying Phosphorylation Trends. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1787-1799.	2.5	72
85	Structural analysis of H1N1 and H7N9 influenza A virus PA in the absence of PB1. <i>Scientific Reports</i> , 2014, 4, 5944.	1.6	10
86	Selecting Targets from Eukaryotic Parasites for Structural Genomics and Drug Discovery. <i>Methods in Molecular Biology</i> , 2014, 1140, 53-59.	0.4	5
87	Genome-wide approaches to dissecting <i>Leishmania</i> differentiation (232.4). <i>FASEB Journal</i> , 2014, 28, 232.4.	0.2	0
88	Crystal structure of a macrophage migration inhibitory factor from <i>Giardia lamblia</i> . <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 47-57.	1.2	13
89	Cytidine derivatives as IspF inhibitors of <i>Burkholderia pseudomallei</i> . <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013, 23, 6860-6863.	1.0	11
90	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

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91	Solution structure of a putative FKBP-type peptidyl-propyl cisâ€“trans isomerase from <i>Giardia lamblia</i> . <i>Journal of Biomolecular NMR</i> , 2013, 57, 369-374.	1.6	1
92	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
93	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
94	Combining Functional and Structural Genomics to Sample the Essential <i>Burkholderia</i> Structome. <i>PLoS ONE</i> , 2013, 8, e53851.	1.1	113
95	Iron uptake controls the generation of <i>Leishmania</i> infective forms through regulation of ROS levels. <i>Journal of General Physiology</i> , 2013, 141, i7-i7.	0.9	1
96	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012, 40, D98-D108.	6.5	217
97	Glucosylated Hydroxymethyluracil, DNA Base J, Prevents Transcriptional Readthrough in <i>Leishmania</i> . <i>Cell</i> , 2012, 150, 909-921.	13.5	138
98	A New Drug for an Old Bug. <i>Chemistry and Biology</i> , 2012, 19, 1499-1500.	6.2	5
99	Learning virulent proteins from integrated query networks. <i>BMC Bioinformatics</i> , 2012, 13, 321.	1.2	2
100	<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
101	Chemical shift assignments for Rv0577, a putative glyoxylase associated with virulence from <i>Mycobacterium tuberculosis</i> . <i>Biomolecular NMR Assignments</i> , 2012, 6, 43-46.	0.4	5
102	Design and Initial Characterization of the SC-200 Proteomics Standard Mixture. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 73-82.	1.0	6
103	Structural Basis of the Substrate Specificity of Bifunctional Isocitrate Dehydrogenase Kinase/Phosphatase. <i>Biochemistry</i> , 2011, 50, 8103-8106.	1.2	12
104	Fragment Screening of Infectious Disease Targets in a Structural Genomics Environment. <i>Methods in Enzymology</i> , 2011, 493, 533-556.	0.4	5
105	Inaugural structure from the DUF3349 superfamily of proteins, <i>Mycobacterium tuberculosis</i> Rv0543c. <i>Archives of Biochemistry and Biophysics</i> , 2011, 506, 150-156.	1.4	6
106	Identity crisis? The need for systematic gene IDs. <i>Trends in Parasitology</i> , 2011, 27, 183-184.	1.5	2
107	Structural characterization of a ribose-5-phosphate isomerase B from the pathogenic fungus <i>Coccidioides immitis</i> . <i>BMC Structural Biology</i> , 2011, 11, 39.	2.3	7
108	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

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109	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
110	Structures of phosphopantetheine adenylyltransferase from <i>Burkholderia pseudomallei</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1032-1037.	0.7	13
111	Solution structure of an arsenate reductase-related protein, YffB, from <i>Brucella melitensis</i> , the etiological agent responsible for brucellosis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1129-1136.	0.7	5
112	Solution-state NMR structure and biophysical characterization of zinc-substituted rubredoxin B (Rv3250c) from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1148-1153.	0.7	9
113	Structures of a putative Γ -class glutathione S-transferase from the pathogenic fungus <i>Coccidioides immitis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1038-1043.	0.7	5
114	BrAbA.11339.a: anomalous diffraction and ligand binding guide towards the elucidation of the function of a 'putative β -lactamase-like protein' from <i>Brucella melitensis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1106-1112.	0.7	5
115	Structure of a Nudix hydrolase (MutT) in the Mg ²⁺ -bound state from <i>Bartonella henselae</i> , the bacterium responsible for cat scratch fever. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1078-1083.	0.7	4
116	Comparative analysis of glutaredoxin domains from bacterial opportunistic pathogens. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1141-1147.	0.7	7
117	Probing conformational states of glutaryl-CoA dehydrogenase by fragment screening. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1060-1069.	0.7	8
118	Structure of triosephosphate isomerase from <i>Cryptosporidium parvum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1095-1099.	0.7	3
119	Structure of fumarate hydratase from <i>Rickettsia prowazekii</i> , the agent of typhus and suspected relative of the mitochondria. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1123-1128.	0.7	3
120	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
121	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
122	Structure of the cystathionine β -synthase MetB from <i>Mycobacterium ulcerans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1154-1158.	0.7	13
123	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
124	Structure of 3-ketoacyl-(acyl-carrier-protein) reductase from <i>Rickettsia prowazekii</i> at 2.25 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1118-1122.	0.7	10
125	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
126	Crystal Structure of <i>Toxoplasma gondii</i> Porphobilinogen Synthase. <i>Journal of Biological Chemistry</i> , 2011, 286, 15298-15307.	1.6	21

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127	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
128	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
129	Solution structure of Rv2377c-founding member of the MbtH-like protein family. <i>Tuberculosis</i> , 2010, 90, 245-251.	0.8	37
130	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
131	Structure of a <i>Burkholderia pseudomallei</i> Trimeric Autotransporter Adhesin Head. <i>PLoS ONE</i> , 2010, 5, e12803.	1.1	31
132	TriTrypDB: a functional genomic resource for the Trypanosomatidae. <i>Nucleic Acids Research</i> , 2010, 38, D457-D462.	6.5	847
133	Biological and Structural Characterization of a Host-Adapting Amino Acid in Influenza Virus. <i>PLoS Pathogens</i> , 2010, 6, e1001034.	2.1	299
134	Structural characterization of <i>Burkholderia pseudomallei</i> adenylate kinase (Adk): Profound asymmetry in the crystal structure of the "open" state. <i>Biochemical and Biophysical Research Communications</i> , 2010, 394, 1012-1017.	1.0	3
135	The Role of Medical Structural Genomics in Discovering New Drugs for Infectious Diseases. <i>PLoS Computational Biology</i> , 2009, 5, e1000530.	1.5	34
136	Histone acetylations mark origins of polycistronic transcription in <i>Leishmania major</i> . <i>BMC Genomics</i> , 2009, 10, 152.	1.2	118
137	Gene organization and sequence analyses of transfer RNA genes in Trypanosomatid parasites. <i>BMC Genomics</i> , 2009, 10, 232.	1.2	29
138	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
139	Backbone and side chain ¹ H, ¹³ C, and ¹⁵ N NMR assignments for the organic hydroperoxide resistance protein (Ohr) from <i>Burkholderia pseudomallei</i> . <i>Biomolecular NMR Assignments</i> , 2009, 3, 163-166.	0.4	1
140	A comprehensive analysis of <i>Trypanosoma brucei</i> mitochondrial proteome. <i>Proteomics</i> , 2009, 9, 434-450.	1.3	162
141	On the Reachability of Trustworthy Information from Integrated Exploratory Biological Queries. <i>Lecture Notes in Computer Science</i> , 2009, , 55-70.	1.0	1
142	Post-translational modification of cellular proteins during <i>Leishmania donovani</i> differentiation. <i>Proteomics</i> , 2008, 8, 1843-1850.	1.3	111
143	Searching the TriTryp Genomes for Drug Targets. <i>Advances in Experimental Medicine and Biology</i> , 2008, 625, 133-140.	0.8	34
144	<i>Trypanosoma brucei</i> Mitochondrial Ribosomes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1286-1296.	2.5	92

#	ARTICLE	IF	CITATIONS
145	Mitochondrial Complexes in <i>Trypanosoma brucei</i> . <i>Molecular and Cellular Proteomics</i> , 2008, 7, 534-545.	2.5	133
146	Structural Genomics of Pathogenic Protozoa: an Overview. <i>Methods in Molecular Biology</i> , 2008, 426, 497-513.	0.4	38
147	Learning pathogenic proteins across fractured and heterogeneous data. <i>AMIA ... Annual Symposium proceedings</i> , 2008, , 889.	0.2	1
148	New <i>Trypanosoma cruzi</i> Repeated Element That Shows Site Specificity for Insertion. <i>Eukaryotic Cell</i> , 2007, 6, 1228-1238.	3.4	15
149	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
150	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
151	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
152	Biomediator data integration and inference for functional annotation of anonymous sequences. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2007, , 343-54.	0.7	9
153	Using Fragment Cocktail Crystallography To Assist Inhibitor Design of <i>Trypanosoma brucei</i> Nucleoside 2-Deoxyribosyltransferase. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 5939-5946.	2.9	66
154	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
155	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
156	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
157	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
158	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
159	Protozoan genomes: gene identification and annotation. <i>International Journal for Parasitology</i> , 2005, 35, 495-512.	1.3	13
160	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
161	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
162	The Genome Sequence of <i>Trypanosoma cruzi</i> , Etiologic Agent of Chagas Disease. <i>Science</i> , 2005, 309, 409-415.	6.0	1,273

#	ARTICLE	IF	CITATIONS
163	The Genome of the Kinetoplastid Parasite, <i>Leishmania major</i> . <i>Science</i> , 2005, 309, 436-442.	6.0	1,237
164	Comparative Genomics of Trypanosomatid Parasitic Protozoa. <i>Science</i> , 2005, 309, 404-409.	6.0	713
165	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
166	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
167	<i>Leishmania major</i> chromosome 3 contains two long convergent polycistronic gene clusters separated by a tRNA gene. <i>Nucleic Acids Research</i> , 2004, 32, 6716-6716.	6.5	0
168	Transcription Initiation and Termination on <i>Leishmania major</i> Chromosome 3. <i>Eukaryotic Cell</i> , 2004, 3, 506-517.	3.4	135
169	Gene synteny and evolution of genome architecture in trypanosomatids. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 183-191.	0.5	92
170	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
171	A survey of <i>Leishmania braziliensis</i> genome by shotgun sequencing. <i>Molecular and Biochemical Parasitology</i> , 2004, 137, 81-86.	0.5	20
172	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
173	Trypanosomatid flagellum biogenesis: ARL-3A is involved in several species. <i>Experimental Parasitology</i> , 2004, 108, 126-133.	0.5	16
174	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
175	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
176	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
177	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
178	<i>Leishmania major</i> 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
179	A Novel Active DNA Topoisomerase I in <i>Leishmania donovani</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 3521-3526.	1.6	76
180	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

#	ARTICLE	IF	CITATIONS
181	A low-background inducible promoter system in <i>Leishmania donovani</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 119, 217-223.	0.5	25
182	Cloning, heterologous expression, and substrate specificities of protein farnesyltransferases from <i>Trypanosoma cruzi</i> and <i>Leishmania major</i> . <i>Molecular and Biochemical Parasitology</i> , 2002, 122, 181-188.	0.5	53
183	Expression of bioppterin transporter (BT1) protein in <i>Leishmania</i> . <i>FEMS Microbiology Letters</i> , 2002, 208, 89-91.	0.7	11
184	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
185	Tetracycline regulated gene expression in <i>Leishmania donovani</i> . <i>Molecular and Biochemical Parasitology</i> , 2001, 112, 61-69.	0.5	37
186	Conservation of the LD1 region in <i>Leishmania</i> includes DNA implicated in LD1 amplification. <i>Molecular and Biochemical Parasitology</i> , 2001, 113, 315-321.	0.5	10
187	Genomic organization and functional characterization of the <i>Leishmania major</i> Friedlin ribosomal RNA gene locus. <i>Molecular and Biochemical Parasitology</i> , 2001, 116, 147-157.	0.5	52
188	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
189	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
190	Cloning and Characterization of <i>Leishmania donovani</i> Telomeres. <i>Experimental Parasitology</i> , 2000, 94, 248-258.	0.5	33
191	<i>Trypanosoma brucei</i> : Four Tandemly Linked Genes for Fatty Acyl-CoA Synthetases. <i>Experimental Parasitology</i> , 2000, 96, 16-22.	0.5	7
192	Immunization with recombinant LD1 antigens protects against experimental leishmaniasis. <i>Vaccine</i> , 2000, 19, 423-430.	1.7	37
193	Recent developments from the <i>Leishmania</i> genome project. <i>Current Opinion in Microbiology</i> , 2000, 3, 412-416.	2.3	49
194	<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
195	Xanthine Phosphoribosyltransferase from <i>Leishmania donovani</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 34403-34410.	1.6	47
196	<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
197	Characterization of the <i>Leishmania donovani</i> ribosomal RNA promoter. <i>Molecular and Biochemical Parasitology</i> , 1999, 103, 197-210.	0.5	32
198	The <i>Leishmania donovani</i> LD1 locus gene ORFG encodes a bioppterin transporter (BT1). <i>Molecular and Biochemical Parasitology</i> , 1999, 104, 93-105.	0.5	67

#	ARTICLE	IF	CITATIONS
199	Genetic nomenclature for Trypanosoma and Leishmania. <i>Molecular and Biochemical Parasitology</i> , 1998, 97, 221-224.	0.5	83
200	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
201	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
202	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
203	An amplified DNA element in Leishmania encodes potential integral membrane and nucleotide-binding proteins. <i>Molecular and Biochemical Parasitology</i> , 1994, 66, 11-20.	0.5	31
204	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
205	Early Expression of a Trypanosoma brucei VSG Gene Duplicated from an Incomplete Basic Copy. <i>Journal of Eukaryotic Microbiology</i> , 1994, 41, 71-78.	0.8	29
206	A frequently amplified region in Leishmania contains a gene conserved in prokaryotes and eukaryotes. <i>Gene</i> , 1994, 148, 187-193.	1.0	27
207	Nucleotide sequence of a minicircle from Leishmania infantum. <i>Molecular and Biochemical Parasitology</i> , 1993, 62, 319-320.	0.5	1
208	The LD1 amplified element from Leishmania infantum encodes a homolog of ribosomal protein L37. <i>Molecular and Biochemical Parasitology</i> , 1993, 62, 147-151.	0.5	17
209	Molecular variation in trypanosomes. <i>Acta Tropica</i> , 1993, 53, 205-225.	0.9	16
210	The alkane-inducible Candida maltosa ALI1 gene product is an NADH:ubiquinone oxidoreductase subunit homologue. <i>Gene</i> , 1993, 137, 349-350.	1.0	3
211	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
212	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
213	Distribution and sequence divergence of LRV1 viruses among different Leishmania species. <i>Molecular and Biochemical Parasitology</i> , 1992, 54, 101-104.	0.5	49
214	A multicopy, extrachromosomal DNA in Leishmania infantum 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
215	A simple method for cloning blunt ended DNA fragments. <i>Nucleic Acids Research</i> , 1991, 19, 398-398.	6.5	26
216	The two ATPase 6 mRNAs of Leishmania tarentolae differ at their 3' ends. <i>Molecular and Biochemical Parasitology</i> , 1991, 48, 139-149.	0.5	39

#	ARTICLE	IF	CITATIONS
217	A DNA sequence (LD1) which occurs in several genomic organizations in Leishmania. <i>Molecular and Biochemical Parasitology</i> , 1991, 47, 151-160.	0.5	46
218	A retroposon in the 5' flank of a <i>Trypanosoma brucei</i> VSG gene lacks insertional terminal repeats. <i>Molecular and Biochemical Parasitology</i> , 1990, 42, 143-151.	0.5	8
219	A novel telomeric gene conversion in <i>Trypanosoma brucei</i> . <i>Molecular and Biochemical Parasitology</i> , 1989, 35, 11-19.	0.5	13
220	<i>Trypanosoma brucei</i> : Frequent loss of a telomeric variant surface glycoprotein gene. <i>Experimental Parasitology</i> , 1989, 68, 8-16.	0.5	9
221	(TAA) _n within sequences flanking several intrachromosomal variant surface glycoprotein genes in <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 1985, 13, 3161-3177.	6.5	62
222	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