

Peter John Myler

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

227
papers

9,867
citations

47
h-index

94
g-index

236
ext. papers

11,137
ext. citations

5.5
avg, IF

5.25
L-index

#	Paper	IF	Citations
227	Crystal structure of a short-chain dehydrogenase/reductase from Burkholderia phymatum in complex with NAD.. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022 , 78, 52-58	1.1	0
226	Crystal structures of FolM alternative dihydrofolate reductase 1 from Brucella suis and Brucella canis.. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022 , 78, 31-38	1.1	
225	Crystal structure of a hypothetical protein from Giardia lamblia.. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022 , 78, 59-65	1.1	0
224	Crystal structure of betaine aldehyde dehydrogenase from Burkholderia pseudomallei.. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022 , 78, 45-51	1.1	
223	Crystal structure of a putative short-chain dehydrogenase/reductase from Paraburkholderia xenovorans.. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022 , 78, 25-30	1.1	1
222	Crystal structure of an inorganic pyrophosphatase from Chlamydia trachomatis D/UW-3/Cx.. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022 , 78, 135-142	1.1	
221	The transcriptome of Balamuthia mandrillaris trophozoites for structure-guided drug design. <i>Scientific Reports</i> , 2021 , 11, 21664	4.9	2
220	Naegleria fowleri: Protein structures to facilitate drug discovery for the deadly, pathogenic free-living amoeba. <i>PLoS ONE</i> , 2021 , 16, e0241738	3.7	4
219	Exploring TERRA during Leishmania major developmental cycle and continuous in vitro passages. <i>International Journal of Biological Macromolecules</i> , 2021 , 174, 573-586	7.9	3
218	Identification of P218 as a potent inhibitor of DHFR. <i>RSC Medicinal Chemistry</i> , 2021 , 12, 103-109	3.5	0
217	Backbone chemical shift assignments for the SARS-CoV-2 non-structural protein Nsp9: intermediate (ms - μ s) dynamics in the C-terminal helix at the dimer interface. <i>Biomolecular NMR Assignments</i> , 2021 , 15, 107-116	0.7	5
216	Crystal structure of acetoacetyl-CoA reductase from Rickettsia felis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021 , 77, 54-60	1.1	
215	Chromatin-Associated Protein Complexes Link DNA Base J and Transcription Termination in. <i>MSphere</i> , 2021 , 6,	5	5
214	Turnover of Variant Surface Glycoprotein in Trypanosoma brucei Is a Bimodal Process. <i>MBio</i> , 2021 , 12, e0172521	7.8	2
213	Genome Assemblies across the Diverse Evolutionary Spectrum of Protozoan Parasites. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0054521	1.3	0
212	Arginine sensing in intracellular parasitism of Leishmania. <i>Current Opinion in Microbiology</i> , 2021 , 64, 41-46	6.9	1
211	Discovery of a Natural Product That Binds to the Protein Rv1466 Using Native Mass Spectrometry. <i>Molecules</i> , 2020 , 25,	4.8	12

210	A Phenotarget Approach for Identifying an Alkaloid Interacting with the Tuberculosis Protein Rv1466. <i>Marine Drugs</i> , 2020 , 18,	6	7
209	Structures of glyceraldehyde 3-phosphate dehydrogenase in <i>Neisseria gonorrhoeae</i> and <i>Chlamydia trachomatis</i> . <i>Protein Science</i> , 2020 , 29, 768-778	6.3	6
208	Structural diversity in the Mycobacteria DUF3349 superfamily. <i>Protein Science</i> , 2020 , 29, 670-685	6.3	1
207	Solution structure for an Encephalitozoon cuniculi adrenodoxin-like protein in the oxidized state. <i>Protein Science</i> , 2020 , 29, 809-817	6.3	2
206	Identification of Selective Inhibitors of N-Myristoyltransferase by High-Throughput Screening. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 591-600	8.3	8
205	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	3.4	1
204	Sensing Host Arginine Is Essential for Parasites Intracellular Development. <i>MBio</i> , 2020 , 11,	7.8	9
203	Structural characterization of Eukaryotic ACP synthase I bound to platencin and fragment screening molecules at two substrate binding sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 47-56	4.2	2
202	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	4.8	9
201	Structure-Guided Identification of Resistance Breaking Antimalarial N-Myristoyltransferase Inhibitors. <i>Cell Chemical Biology</i> , 2019 , 26, 991-1000.e7	8.2	15
200	Functional genomics in sand fly-derived <i>Leishmania</i> promastigotes. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007288	4.8	10
199	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	11.5	50
198	Quantitative RNA Analysis Using RNA-Seq. <i>Methods in Molecular Biology</i> , 2019 , 1971, 95-108	1.4	3
197	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	4.8	7
196	Dynamic colocalization of 2 simultaneously active expression sites within a single expression-site body in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16561-16570	11.5	11
195	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	2.1	3
194	Crystal structure of chorismate mutase from <i>Burkholderia thailandensis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018 , 74, 294-299	1.1	1
193	Crystal structure of chorismate mutase from <i>Burkholderia phymatum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018 , 74, 187-192	1.1	2

192	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	2.9	2
191	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	6.3	11
190	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	1.1	1
189	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	1.1	1
188	<i>Mycobacterium tuberculosis</i> Rv3651 is a triple sensor-domain protein. <i>Protein Science</i> , 2018 , 27, 568-572	6.3	1
187	Ab initio structure solution of a proteolytic fragment using ARCIMBOLDO. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018 , 74, 530-535	1.1	
186	Multiplexed Spliced-Leader Sequencing: A high-throughput, selective method for RNA-seq in Trypanosomatids. <i>Scientific Reports</i> , 2017 , 7, 3725	4.9	18
185	Ligand co-crystallization of aminoacyl-tRNA synthetases from infectious disease organisms. <i>Scientific Reports</i> , 2017 , 7, 223	4.9	3
184	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	0.7	6
183	<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	3.4	5
182	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	3.2	4
181	Membrane skeletal association and post-translational allosteric regulation of <i>Toxoplasma gondii</i> GAPDH1. <i>Molecular Microbiology</i> , 2017 , 103, 618-634	4.1	9
180	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	5.5	28
179	Disclosing 3QTR cis-elements and putative partners involved in gene expression regulation in <i>Leishmania</i> spp. <i>PLoS ONE</i> , 2017 , 12, e0183401	3.7	1
178	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	1.1	5
177	The <i>Rickettsia</i> type IV secretion system: unrealized complexity mired by gene family expansion. <i>Pathogens and Disease</i> , 2016 , 74,	4.2	27
176	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	4.5	28
175	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	1.1	3

174	An Arginine Deprivation Response Pathway Is Induced in Leishmania during Macrophage Invasion. <i>PLoS Pathogens</i> , 2016 , 12, e1005494	7.6	56
173	Illuminating Parasite Protein Production by Ribosome Profiling. <i>Trends in Parasitology</i> , 2016 , 32, 446-457	6.4	14
172	Defining the sequence requirements for the positioning of base J in DNA using SMRT sequencing. <i>Nucleic Acids Research</i> , 2015 , 43, 2102-15	20.1	19
171	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, 566-71	1.1	3
170	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, 594-9	1.1	20
169	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, 572-6	1.1	2
168	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	4.8	92
167	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, 514-21	1.1	4
166	Crystal structures of Mycobacterial MeaB and MMAA-like GTPases. <i>Journal of Structural and Functional Genomics</i> , 2015 , 16, 91-9		6
165	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	4.5	86
164	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, 615-21	1.1	13
163	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, 522-30	1.1	0
162	Advancing <i>Trypanosoma brucei</i> genome annotation through ribosome profiling and spliced leader mapping. <i>Molecular and Biochemical Parasitology</i> , 2015 , 202, 1-10	1.9	13
161	Recent contributions of structure-based drug design to the development of antibacterial compounds. <i>Current Opinion in Microbiology</i> , 2015 , 27, 133-8	7.9	13
160	Synthesis and biological evaluation of pyrazolopyrimidines as potential antibacterial agents. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2015 , 25, 5699-704	2.9	5
159	Backbone chemical shift assignments for the sensor domain of the <i>Burkholderia pseudomallei</i> histidine kinase RisS: "missing" resonances at the dimer interface. <i>Biomolecular NMR Assignments</i> , 2015 , 9, 381-5	0.7	3
158	Structural Insight into How Bacteria Prevent Interference between Multiple Divergent Type IV Secretion Systems. <i>MBio</i> , 2015 , 6, e01867-15	7.8	25
157	Increasing the structural coverage of tuberculosis drug targets. <i>Tuberculosis</i> , 2015 , 95, 142-8	2.6	80

156	RNA-seq approaches for determining mRNA abundance in Leishmania. <i>Methods in Molecular Biology</i> , 2015 , 1201, 207-19	1.4	12
155	Structural Genomics Support for Infectious Disease Drug Design. <i>ACS Infectious Diseases</i> , 2015 , 1, 127-129	5.5	2
154	Structural analysis of H1N1 and H7N9 influenza A virus PA in the absence of PB1. <i>Scientific Reports</i> , 2014 , 4, 5944	4.9	6
153	Mycobacterium tuberculosis Rv2179c protein establishes a new exoribonuclease family with broad phylogenetic distribution. <i>Journal of Biological Chemistry</i> , 2014 , 289, 2139-47	5.4	9
152	Tb927.10.6900 encodes the glucosyltransferase involved in synthesis of base J in Trypanosoma brucei. <i>Molecular and Biochemical Parasitology</i> , 2014 , 196, 9-11	1.9	18
151	Regulation dynamics of Leishmania differentiation: deconvoluting signals and identifying phosphorylation trends. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1787-99	7.6	51
150	The putative Leishmania telomerase RNA (LeishTER) undergoes trans-splicing and contains a conserved template sequence. <i>PLoS ONE</i> , 2014 , 9, e112061	3.7	7
149	Extensive stage-regulation of translation revealed by ribosome profiling of Trypanosoma brucei. <i>BMC Genomics</i> , 2014 , 15, 911	4.5	80
148	Metabolic reprogramming during purine stress in the protozoan pathogen Leishmania donovani. <i>PLoS Pathogens</i> , 2014 , 10, e1003938	7.6	50
147	Genetic analysis of Leishmania donovani tropism using a naturally attenuated cutaneous strain. <i>PLoS Pathogens</i> , 2014 , 10, e1004244	7.6	67
146	Tyrosine aminotransferase from Leishmania infantum: A new drug target candidate. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2014 , 4, 347-54	4	20
145	A structural biology approach enables the development of antimicrobials targeting bacterial immunophilins. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 1458-67	5.9	13
144	Crystal structure and putative substrate identification for the Entamoeba histolytica low molecular weight tyrosine phosphatase. <i>Molecular and Biochemical Parasitology</i> , 2014 , 193, 33-44	1.9	6
143	Selecting targets from eukaryotic parasites for structural genomics and drug discovery. <i>Methods in Molecular Biology</i> , 2014 , 1140, 53-9	1.4	5
142	Genome-wide approaches to dissecting Leishmania differentiation (232.4). <i>FASEB Journal</i> , 2014 , 28, 232.4.9		
141	Crystal structure of a macrophage migration inhibitory factor from Giardia lamblia. <i>Journal of Structural and Functional Genomics</i> , 2013 , 14, 47-57		10
140	Cytidine derivatives as IspF inhibitors of Burkholderia pseudomallei. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013 , 23, 6860-3	2.9	11
139	Kinetoplastid-specific histone variant functions are conserved in Leishmania major. <i>Molecular and Biochemical Parasitology</i> , 2013 , 191, 53-7	1.9	19

138	Solution structure of a putative FKBP-type peptidyl-propyl cis-trans isomerase from <i>Giardia lamblia</i> . <i>Journal of Biomolecular NMR</i> , 2013 , 57, 369-74	3	1
137	Discovery of Inhibitors of Methionine Aminopeptidase with Antibacterial Activity. <i>ACS Medicinal Chemistry Letters</i> , 2013 , 4,	4.3	15
136	Iron uptake controls the generation of <i>Leishmania</i> infective forms through regulation of ROS levels. <i>Journal of Experimental Medicine</i> , 2013 , 210, 401-16	16.6	95
135	Combining functional and structural genomics to sample the essential <i>Burkholderia</i> structome. <i>PLoS ONE</i> , 2013 , 8, e53851	3.7	93
134	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	3.4	1
133	Glucosylated hydroxymethyluracil, DNA base J, prevents transcriptional readthrough in <i>Leishmania</i> . <i>Cell</i> , 2012 , 150, 909-21	56.2	109
132	A new drug for an old bug. <i>Chemistry and Biology</i> , 2012 , 19, 1499-500		5
131	Learning virulent proteins from integrated query networks. <i>BMC Bioinformatics</i> , 2012 , 13, 321	3.6	2
130	<i>Mycobacterium thermoresistibile</i> as a source of thermostable orthologs of <i>Mycobacterium tuberculosis</i> proteins. <i>Protein Science</i> , 2012 , 21, 1093-6	6.3	13
129	Chemical shift assignments for Rv0577, a putative glyoxylase associated with virulence from <i>Mycobacterium tuberculosis</i> . <i>Biomolecular NMR Assignments</i> , 2012 , 6, 43-6	0.7	4
128	GeneDB--an annotation database for pathogens. <i>Nucleic Acids Research</i> , 2012 , 40, D98-108	20.1	186
127	Fragment screening of infectious disease targets in a structural genomics environment. <i>Methods in Enzymology</i> , 2011 , 493, 533-56	1.7	5
126	Inaugural structure from the DUF3349 superfamily of proteins, <i>Mycobacterium tuberculosis</i> Rv0543c. <i>Archives of Biochemistry and Biophysics</i> , 2011 , 506, 150-6	4.1	6
125	Identity crisis? The need for systematic gene IDs. <i>Trends in Parasitology</i> , 2011 , 27, 183-4	6.4	2
124	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	2.7	6
123	SAD phasing using iodide ions in a high-throughput structural genomics environment. <i>Journal of Structural and Functional Genomics</i> , 2011 , 12, 83-95		61
122	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		19
121	Structures of phosphopantetheine adenylyltransferase from <i>Burkholderia pseudomallei</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 1032-7		11

120	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, 1129-36		5
119	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, 1148-53		8
118	Structures of a putative β -class glutathione S-transferase from the pathogenic fungus <i>Coccidioides immitis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 1038-43		4
117	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, 1106-12		4
116	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, 1078-83		4
115	Comparative analysis of glutaredoxin domains from bacterial opportunistic pathogens. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 1141-7		7
114	Probing conformational states of glutaryl-CoA dehydrogenase by fragment screening. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 1060-9		7
113	Structure of triosephosphate isomerase from <i>Cryptosporidium parvum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 1095-9		1
112	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, 1123-8		3
111	Inhibitor-bound complexes of dihydrofolate reductase-thymidylate synthase from <i>Babesia bovis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 1070-7		11
110	Structural genomics of infectious disease drug targets: the SSGCID. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 979-84		47
109	Structure of the cystathionine β -synthase MetB from <i>Mycobacterium ulcerans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 1154-8		9
108	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, 1044-50		15
107	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, 1118-22		9
106	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, 1027-31		18
105	Design and initial characterization of the SC-200 proteomics standard mixture. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 73-82	3.8	6
104	Structural basis of the substrate specificity of bifunctional isocitrate dehydrogenase kinase/phosphatase. <i>Biochemistry</i> , 2011 , 50, 8103-6	3.2	11
103	Crystal structure of <i>Toxoplasma gondii</i> porphobilinogen synthase: insights on octameric structure and porphobilinogen formation. <i>Journal of Biological Chemistry</i> , 2011 , 286, 15298-307	5.4	20

102	Multiple levels of gene regulation mediate differentiation of the intracellular pathogen Leishmania. <i>FASEB Journal</i> , 2011 , 25, 515-25	0.9	116
101	Structure of a Burkholderia pseudomallei trimeric autotransporter adhesin head. <i>PLoS ONE</i> , 2010 , 5, e12803	3.7	31
100	TriTrypDB: a functional genomic resource for the Trypanosomatidae. <i>Nucleic Acids Research</i> , 2010 , 38, D457-62	20.1	625
99	Biological and structural characterization of a host-adapting amino acid in influenza virus. <i>PLoS Pathogens</i> , 2010 , 6, e1001034	7.6	245
98	Structural characterization of Burkholderia pseudomallei adenylate kinase (Adk): profound asymmetry in the crystal structure of the Open State. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 394, 1012-7	3.4	2
97	X-ray structure determination of the glycine cleavage system protein H of Mycobacterium tuberculosis using an inverse Compton synchrotron X-ray source. <i>Journal of Structural and Functional Genomics</i> , 2010 , 11, 91-100		19
96	Solution structure of Rv2377c-founding member of the MbtH-like protein family. <i>Tuberculosis</i> , 2010 , 90, 245-51	2.6	27
95	Nanovolume optimization of protein crystal growth using the microcapillary protein crystallization system. <i>Journal of Applied Crystallography</i> , 2010 , 43, 1078-1083	3.8	14
94	The role of medical structural genomics in discovering new drugs for infectious diseases. <i>PLoS Computational Biology</i> , 2009 , 5, e1000530	5	29
93	Histone acetylations mark origins of polycistronic transcription in Leishmania major. <i>BMC Genomics</i> , 2009 , 10, 152	4.5	97
92	Gene organization and sequence analyses of transfer RNA genes in Trypanosomatid parasites. <i>BMC Genomics</i> , 2009 , 10, 232	4.5	21
91	Widespread variation in transcript abundance within and across developmental stages of Trypanosoma brucei. <i>BMC Genomics</i> , 2009 , 10, 482	4.5	116
90	Backbone and side chain (1)H, (13)C, and (15)N NMR assignments for the organic hydroperoxide resistance protein (Ohr) from Burkholderia pseudomallei. <i>Biomolecular NMR Assignments</i> , 2009 , 3, 163-6 ^{0.7}		1
89	A comprehensive analysis of Trypanosoma brucei mitochondrial proteome. <i>Proteomics</i> , 2009 , 9, 434-50	4.8	138
88	On the Reachability of Trustworthy Information from Integrated Exploratory Biological Queries. <i>Lecture Notes in Computer Science</i> , 2009 , 55-70	0.9	
87	Searching the TriTryp genomes for drug targets. <i>Advances in Experimental Medicine and Biology</i> , 2008 , 625, 133-40	3.6	27
86	Trypanosoma brucei mitochondrial ribosomes: affinity purification and component identification by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1286-96	7.6	86
85	Mitochondrial complexes in Trypanosoma brucei: a novel complex and a unique oxidoreductase complex. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 534-45	7.6	112

84	Post-translational modification of cellular proteins during <i>Leishmania donovani</i> differentiation. <i>Proteomics</i> , 2008 , 8, 1843-50	4.8	92
83	Structural genomics of pathogenic protozoa: an overview. <i>Methods in Molecular Biology</i> , 2008 , 426, 497-513		34
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5	In silico detection of SARS-CoV-2 specific B-cell epitopes and validation in ELISA for serological diagnosis of COVID-19		4
4	The transcriptome of <i>Balamuthia mandrillaris</i> trophozoites for structure-based drug design		1
3	<i>Naegleria fowleri</i> : protein structures to facilitate drug discovery for the deadly, pathogenic free-living amoeba		1
2	A divergent protein kinase A in the human pathogen <i>Leishmania</i> is associated with developmental morphogenesis		
1	Genome instability drives epistatic adaptation in the human pathogen <i>Leishmania</i>		2