

# Mario Tyago Murakami

## List of Publications by Year in descending order

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Version: 2024-02-01

158  
papers

4,129  
citations

101496

36  
h-index

175177

52  
g-index

161  
all docs

161  
docs citations

161  
times ranked

4862  
citing authors

| #  | ARTICLE                                                                                                                                                                                                                                          | IF  | CITATIONS |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 1  | Enzymatic toxins from snake venom: structural characterization and mechanism of catalysis. FEBS Journal, 2011, 278, 4544-4576.                                                                                                                   | 2.2 | 233       |
| 2  | Recent advances in the understanding of brown spider venoms: From the biology of spiders to the molecular mechanisms of toxins. Toxicon, 2014, 83, 91-120.                                                                                       | 0.8 | 116       |
| 3  | Structural basis for glucose tolerance in GH1 $\beta$ -glucosidases. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1631-1639.                                                                                          | 2.5 | 115       |
| 4  | Inhibition of Myotoxic Activity of <i>Bothrops asper</i> Myotoxin II by the Anti-trypanosomal Drug Suramin. Journal of Molecular Biology, 2005, 350, 416-426.                                                                                    | 2.0 | 106       |
| 5  | Structural Basis for Metal Ion Coordination and the Catalytic Mechanism of Sphingomyelinases D. Journal of Biological Chemistry, 2005, 280, 13658-13664.                                                                                         | 1.6 | 90        |
| 6  | Batroxase, a new metalloproteinase from <i>B. atrox</i> snake venom with strong fibrinolytic activity. Toxicon, 2012, 60, 70-82.                                                                                                                 | 0.8 | 85        |
| 7  | Dissecting structure-function-stability relationships of a thermostable GH5-CBM3 cellulase from <i>Bacillus subtilis</i> 168. Biochemical Journal, 2012, 441, 95-104.                                                                            | 1.7 | 81        |
| 8  | Plant Pathogenic Bacteria Utilize Biofilm Growth-associated Repressor (BigR), a Novel Winged-helix Redox Switch, to Control Hydrogen Sulfide Detoxification under Hypoxia. Journal of Biological Chemistry, 2011, 286, 26148-26157.              | 1.6 | 73        |
| 9  | The <i>Penicillium echinulatum</i> Secretome on Sugar Cane Bagasse. PLoS ONE, 2012, 7, e50571.                                                                                                                                                   | 1.1 | 70        |
| 10 | Rational engineering of the <i>Trichoderma reesei</i> RUT-C30 strain into an industrially relevant platform for cellulase production. Biotechnology for Biofuels, 2020, 13, 93.                                                                  | 6.2 | 68        |
| 11 | Structural insights into the catalytic mechanism of sphingomyelinases D and evolutionary relationship to glycerophosphodiester phosphodiesterases. Biochemical and Biophysical Research Communications, 2006, 342, 323-329.                      | 1.0 | 63        |
| 12 | Structure and Function of a Novel Cellulase 5 from Sugarcane Soil Metagenome. PLoS ONE, 2013, 8, e83635.                                                                                                                                         | 1.1 | 59        |
| 13 | Interfacial surface charge and free accessibility to the PLA2-active site-like region are essential requirements for the activity of Lys49 PLA2 homologues. Toxicon, 2007, 49, 378-387.                                                          | 0.8 | 58        |
| 14 | Molecular Mechanisms Associated with Xylan Degradation by <i>Xanthomonas</i> Plant Pathogens. Journal of Biological Chemistry, 2014, 289, 32186-32200.                                                                                           | 1.6 | 57        |
| 15 | Oligomerization as a strategy for cold adaptation: Structure and dynamics of the GH1 $\beta$ -glucosidase from <i>Exiguobacterium antarcticum</i> B7. Scientific Reports, 2016, 6, 23776.                                                        | 1.6 | 57        |
| 16 | Crystal structure of the platelet activator convulxin, a disulfide-linked $\beta$ -4 $\beta$ 24 cyclic tetramer from the venom of <i>Crotalus durissus terrificus</i> . Biochemical and Biophysical Research Communications, 2003, 310, 478-482. | 1.0 | 55        |
| 17 | Biochemical and structural characterization of a $\beta$ -1,3 $\alpha$ -1,4-glucanase from <i>Bacillus subtilis</i> 168. Process Biochemistry, 2011, 46, 1202-1206.                                                                              | 1.8 | 55        |
| 18 | A novel cold-adapted and glucose-tolerant GH1 $\beta$ -glucosidase from <i>Exiguobacterium antarcticum</i> B7. International Journal of Biological Macromolecules, 2016, 82, 375-380.                                                            | 3.6 | 55        |

| #  | ARTICLE                                                                                                                                                                                                                                                                                               | IF  | CITATIONS |
|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 19 | Structural basis for branching enzyme activity of glycoside hydrolase family 57: Structure and stability studies of a novel branching enzyme from the hyperthermophilic archaeon <i>Thermococcus kodakaraensis</i> KOD1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 547-557. | 1.5 | 54        |
| 20 | Engineering Bifunctional Laccase-Xylanase Chimeras for Improved Catalytic Performance. <i>Journal of Biological Chemistry</i> , 2011, 286, 43026-43038.                                                                                                                                               | 1.6 | 52        |
| 21 | Structure of a novel class II phospholipase D: Catalytic cleft is modified by a disulphide bridge. <i>Biochemical and Biophysical Research Communications</i> , 2011, 409, 622-627.                                                                                                                   | 1.0 | 49        |
| 22 | Correlation of temperature induced conformation change with optimum catalytic activity in the recombinant G/11 xylanase A from <i>Bacillus subtilis</i> strain 168 (1A1). <i>FEBS Letters</i> , 2005, 579, 6505-6510.                                                                                 | 1.3 | 46        |
| 23 | Isolation, characterization and biological activity of acidic phospholipase A2 isoforms from <i>Bothrops jararacussu</i> snake venom. <i>Biochimie</i> , 2003, 85, 983-991.                                                                                                                           | 1.3 | 45        |
| 24 | Functional characterization and oligomerization of a recombinant xyloglucan-specific endo- $\beta$ -1,4-glucanase (GH12) from <i>Aspergillus niger</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 461-467.                                                        | 1.1 | 45        |
| 25 | Crystal structure and biochemical characterization of the recombinant ThBgl, a GH1 $\beta$ -glucosidase overexpressed in <i>Trichoderma harzianum</i> under biomass degradation conditions. <i>Biotechnology for Biofuels</i> , 2016, 9, 71.                                                          | 6.2 | 45        |
| 26 | Thrombomodulin-independent Activation of Protein C and Specificity of Hemostatically Active Snake Venom Serine Proteinases. <i>Journal of Biological Chemistry</i> , 2005, 280, 39309-39315.                                                                                                          | 1.6 | 43        |
| 27 | Mode of operation and low-resolution structure of a multi-domain and hyperthermophilic endo- $\beta$ -1,3-glucanase from <i>Thermotoga petrophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2011, 406, 590-594.                                                              | 1.0 | 43        |
| 28 | How pH Modulates the Dimer-Decamer Interconversion of 2-Cys Peroxiredoxins from the Prx1 Subfamily. <i>Journal of Biological Chemistry</i> , 2015, 290, 8582-8590.                                                                                                                                    | 1.6 | 43        |
| 29 | Crystal structure of mature 2S albumin from <i>Moringa oleifera</i> seeds. <i>Biochemical and Biophysical Research Communications</i> , 2015, 468, 365-371.                                                                                                                                           | 1.0 | 43        |
| 30 | Molecular insights into substrate specificity and thermal stability of a bacterial GH5-CBM27 endo- $\beta$ -1,4-d-mannanase. <i>Journal of Structural Biology</i> , 2012, 177, 469-476.                                                                                                               | 1.3 | 42        |
| 31 | Effects of the linker region on the structure and function of modular GH5 cellulases. <i>Scientific Reports</i> , 2016, 6, 28504.                                                                                                                                                                     | 1.6 | 40        |
| 32 | The repeat domain of the type III effector protein PthA shows a TPR-like structure and undergoes conformational changes upon DNA interaction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3386-3395.                                                                          | 1.5 | 39        |
| 33 | A structure based model for liposome disruption and the role of catalytic activity in myotoxic phospholipase A2s. <i>Toxicon</i> , 2003, 42, 903-913.                                                                                                                                                 | 0.8 | 38        |
| 34 | SMase II, a new sphingomyelinase D from <i>Loxosceles laeta</i> venom gland: Molecular cloning, expression, function and structural analysis. <i>Toxicon</i> , 2009, 53, 743-753.                                                                                                                     | 0.8 | 38        |
| 35 | Molecular characterization of an acidic phospholipase A2 from <i>Bothrops pirajai</i> snake venom: synthetic C-terminal peptide identifies its antiplatelet region. <i>Archives of Toxicology</i> , 2011, 85, 1219-1233.                                                                              | 1.9 | 38        |
| 36 | Structural studies of BmooMP1-L, a non-hemorrhagic metalloproteinase from <i>Bothrops moojeni</i> venom. <i>Toxicon</i> , 2010, 55, 361-368.                                                                                                                                                          | 0.8 | 37        |

| #  | ARTICLE                                                                                                                                                                                                                                                                                                                                                          | IF  | CITATIONS |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | Structure of the polypeptide crotamine from the Brazilian rattlesnake <i>Crotalus durissus terrificus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1958-1964.                                                                                                                                                           | 2.5 | 37        |
| 38 | Purification, characterization and crystallization of Jararacussin-I, a fibrinogen-clotting enzyme isolated from the venom of <i>Bothrops jararacussu</i> . <i>Toxicon</i> , 2002, 40, 1307-1312.                                                                                                                                                                | 0.8 | 36        |
| 39 | Intermolecular Interactions and Characterization of the Novel Factor Xa Exosite Involved in Macromolecular Recognition and Inhibition: Crystal Structure of Human Gla-domainless Factor Xa Complexed with the Anticoagulant Protein NAPc2 from the Hematophagous Nematode <i>Ancylostoma caninum</i> . <i>Journal of Molecular Biology</i> , 2007, 366, 602-610. | 2.0 | 36        |
| 40 | Thermal-induced conformational changes in the product release area drive the enzymatic activity of xylanases 10B: Crystal structure, conformational stability and functional characterization of the xylanase 10B from <i>Thermotoga petrophila</i> RKU-1. <i>Biochemical and Biophysical Research Communications</i> , 2010, 403, 214-219.                      | 1.0 | 36        |
| 41 | Molecular adaptability of nucleoside diphosphate kinase b from trypanosomatid parasites: stability, oligomerization and structural determinants of nucleotide binding. <i>Molecular BioSystems</i> , 2011, 7, 2189.                                                                                                                                              | 2.9 | 36        |
| 42 | An engineered GH1 $\beta$ -glucosidase displays enhanced glucose tolerance and increased sugar release from lignocellulosic materials. <i>Scientific Reports</i> , 2019, 9, 4903.                                                                                                                                                                                | 1.6 | 36        |
| 43 | Gene cloning, expression and biochemical characterization of a glucose- and xylose-stimulated $\beta$ -glucosidase from <i>Humicola insolens</i> RP86. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2014, 106, 1-10.                                                                                                                                     | 1.8 | 33        |
| 44 | The molecular motor Myosin Va interacts with the cilia-centrosomal protein RPGRIP1L. <i>Scientific Reports</i> , 2017, 7, 43692.                                                                                                                                                                                                                                 | 1.6 | 33        |
| 45 | Assembling a xylanase-lichenase chimera through all-atom molecular dynamics simulations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1492-1500.                                                                                                                                                                                 | 1.1 | 32        |
| 46 | Cloning, heterologous expression and biochemical characterization of a non-specific endoglucanase family 12 from <i>Aspergillus terreus</i> NIH2624. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 395-403.                                                                                                                       | 1.1 | 32        |
| 47 | An actinobacteria lytic polysaccharide monooxygenase acts on both cellulose and xylan to boost biomass saccharification. <i>Biotechnology for Biofuels</i> , 2019, 12, 117.                                                                                                                                                                                      | 6.2 | 31        |
| 48 | Crystal structure of an acidic platelet aggregation inhibitor and hypotensive phospholipase A2 in the monomeric and dimeric states: insights into its oligomeric state. <i>Biochemical and Biophysical Research Communications</i> , 2004, 323, 24-31.                                                                                                           | 1.0 | 30        |
| 49 | Structural Insights into Functional Overlapping and Differentiation among Myosin V Motors. <i>Journal of Biological Chemistry</i> , 2013, 288, 34131-34145.                                                                                                                                                                                                      | 1.6 | 29        |
| 50 | Development of a chimeric hemicellulase to enhance the xylose production and thermotolerance. <i>Enzyme and Microbial Technology</i> , 2015, 69, 31-37.                                                                                                                                                                                                          | 1.6 | 29        |
| 51 | Active site mapping of <i>Loxosceles</i> phospholipases D: Biochemical and biological features. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2016, 1861, 970-979.                                                                                                                                                               | 1.2 | 29        |
| 52 | The mechanism by which a distinguishing arabinofuranosidase can cope with internal di-substitutions in arabinoxylans. <i>Biotechnology for Biofuels</i> , 2018, 11, 223.                                                                                                                                                                                         | 6.2 | 29        |
| 53 | Development and Biotechnological Application of a Novel Endoxylanase Family GH10 Identified from Sugarcane Soil Metagenome. <i>PLoS ONE</i> , 2013, 8, e70014.                                                                                                                                                                                                   | 1.1 | 28        |
| 54 | The structure of a native <i>Vipera ammodytes</i> amino acid oxidase, the major component of the <i>Vipera ammodytes</i> venom, reveals dynamic active site and quaternary structure stabilization by divalent ions. <i>Molecular BioSystems</i> , 2011, 7, 379-384.                                                                                             | 2.9 | 27        |



| #  | ARTICLE                                                                                                                                                                                                                                                                         | IF  | CITATIONS |
|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 73 | Crystal structure of $\beta$ -galactosidase from <i>Bifidobacterium bifidum</i> S17: trimeric architecture, molecular determinants of the enzymatic activity and its inhibition by $\beta$ -galactose. <i>FEBS Journal</i> , 2016, 283, 4097-4112.                              | 2.2 | 22        |
| 74 | Crystal Structure and Regulation of the Citrus Pol III Repressor MAF1 by Auxin and Phosphorylation. <i>Structure</i> , 2017, 25, 1360-1370.e4.                                                                                                                                  | 1.6 | 22        |
| 75 | Functional characterization and comparative analysis of two heterologous endoglucanases from diverging subfamilies of glycosyl hydrolase family 45. <i>Enzyme and Microbial Technology</i> , 2019, 120, 23-35.                                                                  | 1.6 | 22        |
| 76 | Functional and structural analysis of two fibrinogen-activating enzymes isolated from the venoms of <i>Crotalus durissus terrificus</i> and <i>Crotalus durissus collilineatus</i> . <i>Acta Biochimica Et Biophysica Sinica</i> , 2009, 41, 21-29.                             | 0.9 | 21        |
| 77 | Molecular cloning and biochemical characterization of a myotoxin inhibitor from <i>Bothrops alternatus</i> snake plasma. <i>Biochimie</i> , 2011, 93, 583-592.                                                                                                                  | 1.3 | 21        |
| 78 | Mechanistic Strategies for Catalysis Adopted by Evolutionary Distinct Family 43 Arabinanases. <i>Journal of Biological Chemistry</i> , 2014, 289, 7362-7373.                                                                                                                    | 1.6 | 21        |
| 79 | Kinetic and mechanistic characterization of the Sphingomyelinases D from <i>Loxosceles intermedia</i> spider venom. <i>Toxicon</i> , 2006, 47, 380-386.                                                                                                                         | 0.8 | 19        |
| 80 | Functional and biophysical characterization of a hyperthermostable GH51 $\beta$ -l-arabinofuranosidase from <i>Thermotoga petrophila</i> . <i>Biotechnology Letters</i> , 2011, 33, 131-137.                                                                                    | 1.1 | 19        |
| 81 | Crystal structure of Jararacussin: The highly negatively charged catalytic interface contributes to macromolecular selectivity in snake venom thrombin-like enzymes. <i>Protein Science</i> , 2013, 22, 128-132.                                                                | 3.1 | 19        |
| 82 | Structural insights into $\beta$ -1,3-glucan cleavage by a glycoside hydrolase family. <i>Nature Chemical Biology</i> , 2020, 16, 920-929.                                                                                                                                      | 3.9 | 19        |
| 83 | Structural studies of the <i>Trypanosoma cruzi</i> Old Yellow Enzyme: Insights into enzyme dynamics and specificity. <i>Biophysical Chemistry</i> , 2013, 184, 44-53.                                                                                                           | 1.5 | 18        |
| 84 | Effect of dynamic high pressure on functional and structural properties of bovine serum albumin. <i>Food Research International</i> , 2017, 99, 748-754.                                                                                                                        | 2.9 | 18        |
| 85 | N-glycan Utilization by <i>Bifidobacterium</i> Gut Symbionts Involves a Specialist $\beta$ -Mannosidase. <i>Journal of Molecular Biology</i> , 2019, 431, 732-747.                                                                                                              | 2.0 | 18        |
| 86 | Reduction of sulfenic acids by ascorbate in proteins, connecting thiol-dependent to alternative redox pathways. <i>Free Radical Biology and Medicine</i> , 2020, 156, 207-216.                                                                                                  | 1.3 | 18        |
| 87 | Crystallographic portrayal of different conformational states of a Lys49 phospholipase A2 homologue: Insights into structural determinants for myotoxicity and dimeric configuration. <i>International Journal of Biological Macromolecules</i> , 2012, 51, 209-214.            | 3.6 | 17        |
| 88 | P-I class metalloproteinase from <i>Bothrops moojeni</i> venom is a post-proline cleaving peptidase with kininogenase activity: Insights into substrate selectivity and kinetic behavior. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 545-552. | 1.1 | 17        |
| 89 | Crystal structure of a novel myotoxic Arg49 phospholipase A2 homolog (zhaoermiatoxin) from <i>Zhaoermia mangshanensis</i> snake venom: Insights into Arg49 coordination and the role of Lys122 in the polarization of the C-terminus. <i>Toxicon</i> , 2008, 51, 723-735.       | 0.8 | 16        |
| 90 | Adaptive evolution in the toxicity of a spider's venom enzymes. <i>BMC Evolutionary Biology</i> , 2015, 15, 290.                                                                                                                                                                | 3.2 | 16        |

| #   | ARTICLE                                                                                                                                                                                                                                                                           | IF  | CITATIONS |
|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 91  | Structural basis of exo- $\beta$ -mannanase activity in the GH2 family. <i>Journal of Biological Chemistry</i> , 2018, 293, 13636-13649.                                                                                                                                          | 1.6 | 16        |
| 92  | Targeting <i>Loxosceles</i> spider Sphingomyelinase D with small-molecule inhibitors as a potential therapeutic approach for loxoscelism. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2019, 34, 310-321.                                                        | 2.5 | 16        |
| 93  | Structural Insights into Substrate Binding of Brown Spider Venom Class II Phospholipases D. <i>Current Protein and Peptide Science</i> , 2015, 16, 768-774.                                                                                                                       | 0.7 | 16        |
| 94  | Structure-guided design combined with evolutionary diversity led to the discovery of the xylose-releasing exo-xylanase activity in the glycoside hydrolase family 43. <i>Biotechnology and Bioengineering</i> , 2019, 116, 734-744.                                               | 1.7 | 15        |
| 95  | Purification, Biochemical and Functional Characterization of Miliin, a New Thiol-Dependent Serine Protease Isolated from the Latex of <i>Euphorbia milii</i> . <i>Protein and Peptide Letters</i> , 2008, 15, 724-730.                                                            | 0.4 | 14        |
| 96  | How high pressure pre-treatments affect the function and structure of hen egg-white lysozyme. <i>Innovative Food Science and Emerging Technologies</i> , 2018, 47, 195-203.                                                                                                       | 2.7 | 14        |
| 97  | Biochemical and Structural Investigations of Bothropstoxin-II, a Myotoxic Asp49 Phospholipase A2 from <i>Bothrops jararacussu</i> Venom. <i>Protein and Peptide Letters</i> , 2008, 15, 1002-1008.                                                                                | 0.4 | 13        |
| 98  | Crystallization and preliminary X-ray diffraction analysis of a class II phospholipase D from <i>Loxosceles intermedia</i> venom. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 234-236.                                                 | 0.7 | 13        |
| 99  | Expression, purification and spectroscopic analysis of an HdrC: An iron-sulfur cluster-containing protein from <i>Acidithiobacillus ferrooxidans</i> . <i>Process Biochemistry</i> , 2011, 46, 1335-1341.                                                                         | 1.8 | 13        |
| 100 | Crystal structure of <i>Staphylococcus aureus</i> exfoliative toxin D-like protein: Structural basis for the high specificity of exfoliative toxins. <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 171-177.                                             | 1.0 | 13        |
| 101 | A Novel Fungal Lipase With Methanol Tolerance and Preference for Macaw Palm Oil. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 304.                                                                                                                             | 2.0 | 13        |
| 102 | Characterization of a Hexameric Exo-Acting GH51 $\beta$ -D-Arabinofuranosidase from the Mesophilic <i>Bacillus subtilis</i> . <i>Molecular Biotechnology</i> , 2013, 55, 260-267.                                                                                                 | 1.3 | 12        |
| 103 | Correlation between catalysis and tertiary structure arrangement in an archaeal halophilic subtilase. <i>Biochimie</i> , 2012, 94, 798-805.                                                                                                                                       | 1.3 | 11        |
| 104 | A novel $\beta$ -glucosidase isolated from the microbial metagenome of Lake Poraquã (Amazon, Brazil). <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 569-579.                                                                                       | 1.1 | 11        |
| 105 | Luciferase isozymes from the Brazilian <i>Aspisoma lineatum</i> (Lampyridae) firefly: origin of efficient pH-sensitive lantern luciferases from fat body pH-insensitive ancestors. <i>Photochemical and Photobiological Sciences</i> , 2020, 19, 1750-1764.                       | 1.6 | 11        |
| 106 | Exploring the Molecular Basis for Substrate Affinity and Structural Stability in Bacterial GH39 $\beta$ -Xylosidases. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 419.                                                                                        | 2.0 | 11        |
| 107 | Structure of myotoxin II, a catalytically inactive Lys49 phospholipase A2 homologue from <i>Atropoides nummifer</i> venom. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 423-426.                                                        | 0.7 | 10        |
| 108 | Expression, purification, crystallization and preliminary crystallographic analysis of an endo-1,5- $\alpha$ -L-arabinanase from hyperthermophilic <i>Thermotoga petrophila</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 902-905. | 0.7 | 10        |

| #   | ARTICLE                                                                                                                                                                                                                                                                                                               | IF  | CITATIONS |
|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 109 | Insights into Phosphate Cooperativity and Influence of Substrate Modifications on Binding and Catalysis of Hexameric Purine Nucleoside Phosphorylases. <i>PLoS ONE</i> , 2012, 7, e44282.                                                                                                                             | 1.1 | 10        |
| 110 | Pyrrrole-indolinone SU11652 targets the nucleoside diphosphate kinase from <i>Leishmania</i> parasites. <i>Biochemical and Biophysical Research Communications</i> , 2017, 488, 461-465.                                                                                                                              | 1.0 | 10        |
| 111 | Calcium and magnesium ions modulate the oligomeric state and function of mitochondrial 2-Cys peroxiredoxins in <i>Leishmania</i> parasites. <i>Journal of Biological Chemistry</i> , 2017, 292, 7023-7039.                                                                                                            | 1.6 | 10        |
| 112 | Crystallization and preliminary X-ray crystallographic analysis of the heterodimeric crotoxin complex and the isolated subunits crotopotin and phospholipase A2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 287-290.                                                      | 0.7 | 9         |
| 113 | Spatially remote motifs cooperatively affect substrate preference of a ruminal GH26-type endo- $\beta$ -1,4-mannanase. <i>Journal of Biological Chemistry</i> , 2020, 295, 5012-5021.                                                                                                                                 | 1.6 | 9         |
| 114 | Identification of a cold-adapted and metal-stimulated $\beta$ -1,4-glucanase with potential use in the extraction of bioactive compounds from plants. <i>International Journal of Biological Macromolecules</i> , 2021, 166, 190-199.                                                                                 | 3.6 | 9         |
| 115 | Cloning, expression, purification, crystallization and preliminary X-ray diffraction studies of the catalytic domain of a hyperthermostable endo-1,4- $\beta$ -D-mannanase from <i>Thermotoga petrophila</i> RKU-1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1078-1081. | 0.7 | 8         |
| 116 | The small heat shock proteins from <i>Acidithiobacillus ferrooxidans</i> : gene expression, phylogenetic analysis, and structural modeling. <i>BMC Microbiology</i> , 2011, 11, 259.                                                                                                                                  | 1.3 | 8         |
| 117 | Crystallization and preliminary X-ray diffraction analysis of an L-amino-acid oxidase from <i>Bothrops jararacussu</i> venom. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 211-213.                                                                                         | 0.7 | 8         |
| 118 | Crystallization and preliminary X-ray diffraction studies of an L-amino-acid oxidase from <i>Lachesis muta</i> venom. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1556-1559.                                                                                               | 0.4 | 8         |
| 119 | Crystallization and preliminary X-ray diffraction analysis of a novel sphingomyelinase D from <i>Loxosceles gaucho</i> venom. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1418-1420.                                                                                       | 0.4 | 8         |
| 120 | Adenosine Kinase couples sensing of cellular potassium depletion to purine metabolism. <i>Scientific Reports</i> , 2018, 8, 11988.                                                                                                                                                                                    | 1.6 | 8         |
| 121 | Crystal Structure of Bucain, a Three-Fingered Toxin from the Venom of the Malayan Krait ( <i>Bungarus</i> ) Tj ETQq1 1 0.784314 rgBT /Over 0,4                                                                                                                                                                        |     |           |
| 122 | The Water Effect on the Kinetics of the Bovine Liver Catalase. <i>Protein and Peptide Letters</i> , 2011, 18, 879-885.                                                                                                                                                                                                | 0.4 | 7         |
| 123 | Crystal structure and biophysical characterization of the nucleoside diphosphate kinase from <i>Leishmania braziliensis</i> . <i>BMC Structural Biology</i> , 2015, 15, 2.                                                                                                                                            | 2.3 | 7         |
| 124 | New contributions for industrial n-butanol fermentation: An optimized <i>Clostridium</i> strain and the use of xylooligosaccharides as a fermentation additive. <i>Biomass and Bioenergy</i> , 2018, 119, 304-313.                                                                                                    | 2.9 | 7         |
| 125 | Unveiling the interaction between the molecular motor Myosin Vc and the small GTPase Rab3A. <i>Journal of Proteomics</i> , 2020, 212, 103549.                                                                                                                                                                         | 1.2 | 7         |
| 126 | Voices of chemical biology. <i>Nature Chemical Biology</i> , 2021, 17, 1-4.                                                                                                                                                                                                                                           | 3.9 | 7         |

| #   | ARTICLE                                                                                                                                                                                                                                                                                                   | IF  | CITATIONS |
|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 127 | Crystallization and preliminary X-ray diffraction analysis of suramin, a highly charged polysulfonated naphthylurea, complexed with a myotoxic PLA2 from <i>Bothrops asper</i> venom. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1703, 83-85.                                 | 1.1 | 6         |
| 128 | Purification, crystallization and preliminary X-ray diffraction analysis of a class P-III metalloproteinase (BmMP-III) from the venom of <i>Bothrops moojeni</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1222-1225.                                      | 0.7 | 6         |
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