

# Igor Polikarpov

## List of Publications by Year in descending order

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Version: 2024-02-01

299  
papers

10,270  
citations

41344

49  
h-index

51608

86  
g-index

305  
all docs

305  
docs citations

305  
times ranked

13188  
citing authors

| #  | ARTICLE                                                                                                                                                                                                                                                                | IF   | CITATIONS |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 1  | Bovine $\beta$ -lactoglobulin at 1.8 Å... resolution – still an enigmatic lipocalin. <i>Structure</i> , 1997, 5, 481-495.                                                                                                                                              | 3.3  | 674       |
| 2  | Average protein density is a molecular-weight-dependent function. <i>Protein Science</i> , 2009, 13, 2825-2828.                                                                                                                                                        | 7.6  | 552       |
| 3  | Determination of the molecular weight of proteins in solution from a single small-angle X-ray scattering measurement on a relative scale. <i>Journal of Applied Crystallography</i> , 2010, 43, 101-109.                                                               | 4.5  | 389       |
| 4  | Chemical and morphological characterization of sugarcane bagasse submitted to a delignification process for enhanced enzymatic digestibility. <i>Biotechnology for Biofuels</i> , 2011, 4, 54.                                                                         | 6.2  | 382       |
| 5  | Crystal structure of the extracellular region of human tissue factor. <i>Nature</i> , 1994, 370, 662-666.                                                                                                                                                              | 27.8 | 230       |
| 6  | Medium Chain Fatty Acids Are Selective Peroxisome Proliferator Activated Receptor (PPAR) $\beta$ Activators and Pan-PPAR Partial Agonists. <i>PLoS ONE</i> , 2012, 7, e36297.                                                                                          | 2.5  | 165       |
| 7  | Enzymatic hydrolysis of pretreated sugar cane bagasse using <i>Penicillium funiculosum</i> and <i>Trichoderma harzianum</i> cellulases. <i>Process Biochemistry</i> , 2011, 46, 1196-1201.                                                                             | 3.7  | 148       |
| 8  | Substrate binding is required for assembly of the active conformation of the catalytic site in Ntn amidotransferases: evidence from the 1.8 Å crystal structure of the glutaminase domain of glucosamine 6-phosphate synthase. <i>Structure</i> , 1996, 4, 801-810.    | 3.3  | 146       |
| 9  | Crystal Structure of Exo-inulinase from <i>Aspergillus awamori</i> : The Enzyme Fold and Structural Determinants of Substrate Recognition. <i>Journal of Molecular Biology</i> , 2004, 344, 471-480.                                                                   | 4.2  | 141       |
| 10 | Multi-scale structural and chemical analysis of sugarcane bagasse in the process of sequential acid–base pretreatment and ethanol production by <i>Scheffersomyces shehatae</i> and <i>Saccharomyces cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2014, 7, 63. | 6.2  | 134       |
| 11 | $\beta$ -Lactoglobulin. <i>International Dairy Journal</i> , 1998, 8, 65-72.                                                                                                                                                                                           | 3.0  | 129       |
| 12 | The High Resolution Crystal Structure of Yeast Hexokinase PII with the Correct Primary Sequence Provides New Insights into Its Mechanism of Action. <i>Journal of Biological Chemistry</i> , 2000, 275, 20814-20821.                                                   | 3.4  | 126       |
| 13 | SAXSMoW 2.0: Online calculator of the molecular weight of proteins in dilute solution from experimental SAXS data measured on a relative scale. <i>Protein Science</i> , 2019, 28, 454-463.                                                                            | 7.6  | 122       |
| 14 | Crystal Structure of Recombinant Human Interleukin-22. <i>Structure</i> , 2002, 10, 1051-1062.                                                                                                                                                                         | 3.3  | 119       |
| 15 | Efficient sugar production from sugarcane bagasse by microwave assisted acid and alkali pretreatment. <i>Biomass and Bioenergy</i> , 2016, 93, 269-278.                                                                                                                | 5.7  | 115       |
| 16 | Structural diversity of carbohydrate esterases. <i>Biotechnology Research and Innovation</i> , 2017, 1, 35-51.                                                                                                                                                         | 0.9  | 114       |
| 17 | The two types of 3-dehydroquinase have distinct structures but catalyze the same overall reaction. <i>Nature Structural Biology</i> , 1999, 6, 521-525.                                                                                                                | 9.7  | 113       |
| 18 | Effects of pretreatment on morphology, chemical composition and enzymatic digestibility of eucalyptus bark: a potentially valuable source of fermentable sugars for biofuel production – part 1. <i>Biotechnology for Biofuels</i> , 2013, 6, 75.                      | 6.2  | 108       |

| #  | ARTICLE                                                                                                                                                                                                                                       | IF   | CITATIONS |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | Structural Rearrangements in the Thyroid Hormone Receptor Hinge Domain and Their Putative Role in the Receptor Function. <i>Journal of Molecular Biology</i> , 2006, 360, 586-598.                                                            | 4.2  | 106       |
| 20 | Molecular Mechanism of Peroxisome Proliferator-Activated Receptor $\beta$ Activation by WY14643: a New Mode of Ligand Recognition and Receptor Stabilization. <i>Journal of Molecular Biology</i> , 2013, 425, 2878-2893.                     | 4.2  | 101       |
| 21 | Involvement of the C terminus in intramolecular nitrogen channeling in glucosamine 6-phosphate synthase: evidence from a 1.6 Å crystal structure of the isomerase domain. <i>Structure</i> , 1998, 6, 1047-1055.                              | 3.3  | 99        |
| 22 | Evaluating the composition and processing potential of novel sources of Brazilian biomass for sustainable biorenewables production. <i>Biotechnology for Biofuels</i> , 2014, 7, 10.                                                          | 6.2  | 87        |
| 23 | Structural Basis for Low Catalytic Activity in Lys49 Phospholipases A2A Hypothesis: The Crystal Structure of Piratoxin II Complexed to Fatty Acid. <i>Biochemistry</i> , 2001, 40, 28-36.                                                     | 2.5  | 84        |
| 24 | Mode of Peroxisome Proliferator-Activated Receptor $\beta$ Activation by Luteolin. <i>Molecular Pharmacology</i> , 2012, 81, 788-799.                                                                                                         | 2.3  | 84        |
| 25 | Structural and compositional changes in sugarcane bagasse subjected to hydrothermal and organosolv pretreatments and their impacts on enzymatic hydrolysis. <i>Industrial Crops and Products</i> , 2018, 113, 64-74.                          | 5.2  | 84        |
| 26 | Crystal Structures of $\beta$ -Galactosidase from <i>Penicillium</i> sp. and its Complex with Galactose. <i>Journal of Molecular Biology</i> , 2004, 343, 1281-1292.                                                                          | 4.2  | 83        |
| 27 | Dissecting structure–function–stability relationships of a thermostable GH5-CBM3 cellulase from <i>Bacillus subtilis</i> 168. <i>Biochemical Journal</i> , 2012, 441, 95-104.                                                                 | 3.7  | 81        |
| 28 | Stability of L-asparaginase: an enzyme used in leukemia treatment. <i>Pharmaceutica Acta Helvetiae</i> , 1999, 74, 1-9.                                                                                                                       | 1.2  | 79        |
| 29 | Crystal structure of the IL-22/IL-22R1 complex and its implications for the IL-22 signaling mechanism. <i>FEBS Letters</i> , 2008, 582, 2985-2992.                                                                                            | 2.8  | 76        |
| 30 | Gaining ligand selectivity in thyroid hormone receptors via entropy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20717-20722.                                                         | 7.1  | 76        |
| 31 | Carbohydrate binding modules enhance cellulose enzymatic hydrolysis by increasing access of cellulases to the substrate. <i>Carbohydrate Polymers</i> , 2019, 211, 57-68.                                                                     | 10.2 | 75        |
| 32 | Molecular Dynamics Simulations of Ligand Dissociation from Thyroid Hormone Receptors: Evidence of the Likeliest Escape Pathway and Its Implications for the Design of Novel Ligands. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 23-26. | 6.4  | 73        |
| 33 | Nuclear receptor full-length architectures: confronting myth and illusion with high resolution. <i>Trends in Biochemical Sciences</i> , 2015, 40, 16-24.                                                                                      | 7.5  | 73        |
| 34 | Quantitative $^{13}\text{C}$ MultiCP solid-state NMR as a tool for evaluation of cellulose crystallinity index measured directly inside sugarcane biomass. <i>Biotechnology for Biofuels</i> , 2015, 8, 110.                                  | 6.2  | 72        |
| 35 | Structural features of lignin obtained at different alkaline oxidation conditions from sugarcane bagasse. <i>Industrial Crops and Products</i> , 2012, 35, 61-69.                                                                             | 5.2  | 71        |
| 36 | The MX2 macromolecular crystallography beamline: a wiggler X-ray source at the LNLS. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 69-75.                                                                                               | 2.4  | 70        |

| #  | ARTICLE                                                                                                                                                                                                                                                     | IF  | CITATIONS |
|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | Crystal Structure of $\beta$ -Galactosidase from <i>Trichoderma reesei</i> and Its Complex with Galactose: Implications for Catalytic Mechanism. <i>Journal of Molecular Biology</i> , 2004, 339, 413-422.                                                  | 4.2 | 69        |
| 38 | Molecular Dynamics Simulations Reveal Multiple Pathways of Ligand Dissociation from Thyroid Hormone Receptors. <i>Biophysical Journal</i> , 2005, 89, 2011-2023.                                                                                            | 0.5 | 66        |
| 39 | Purification, characterization, gene cloning and preliminary X-ray data of the exo-inulinase from <i>Aspergillus awamori</i> . <i>Biochemical Journal</i> , 2002, 362, 131-135.                                                                             | 3.7 | 65        |
| 40 | Mechanisms of Peroxisome Proliferator Activated Receptor $\beta$ Regulation by Non-steroidal Anti-inflammatory Drugs. <i>Nuclear Receptor Signaling</i> , 2015, 13, nrs.13004.                                                                              | 1.0 | 63        |
| 41 | Set-up and Experimental Parameters of the Protein Crystallography Beamline at the Brazilian National Synchrotron Laboratory. <i>Journal of Synchrotron Radiation</i> , 1998, 5, 72-76.                                                                      | 2.4 | 62        |
| 42 | Mapping the lignin distribution in pretreated sugarcane bagasse by confocal and fluorescence lifetime imaging microscopy. <i>Biotechnology for Biofuels</i> , 2013, 6, 43.                                                                                  | 6.2 | 61        |
| 43 | <i>Aspergillus niger</i> $\beta$ -Glucosidase Has a Cellulase-like Tadpole Molecular Shape. <i>Journal of Biological Chemistry</i> , 2013, 288, 32991-33005.                                                                                                | 3.4 | 60        |
| 44 | Sugarcane waste as a valuable source of lipophilic molecules. <i>Industrial Crops and Products</i> , 2015, 76, 95-103.                                                                                                                                      | 5.2 | 59        |
| 45 | Ajulemic Acid, a Synthetic Nonpsychoactive Cannabinoid Acid, Bound to the Ligand Binding Domain of the Human Peroxisome Proliferator-activated Receptor $\beta$ . <i>Journal of Biological Chemistry</i> , 2007, 282, 18625-18633.                          | 3.4 | 58        |
| 46 | Nutrient availability shapes the microbial community structure in sugarcane bagasse compost-derived consortia. <i>Scientific Reports</i> , 2016, 6, 38781.                                                                                                  | 3.3 | 56        |
| 47 | Divergence in macromolecular assembly: X-ray crystallographic structure analysis of lumazine synthase from <i>Brucella abortus</i> 11Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 297, 1031-1036.                                        | 4.2 | 55        |
| 48 | Ligand Dissociation from Estrogen Receptor Is Mediated by Receptor Dimerization: Evidence from Molecular Dynamics Simulations. <i>Molecular Endocrinology</i> , 2008, 22, 1565-1578.                                                                        | 3.7 | 54        |
| 49 | A review on bioprocessing of paddy straw to ethanol using simultaneous saccharification and fermentation. <i>Process Biochemistry</i> , 2019, 85, 125-134.                                                                                                  | 3.7 | 53        |
| 50 | Crystal structure of neurotoxin Ts1 from <i>Tityus serrulatus</i> provides insights into the specificity and toxicity of scorpion toxins 1 1Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 290, 175-184.                                   | 4.2 | 52        |
| 51 | Only Subtle Protein Conformational Adaptations Are Required for Ligand Binding to Thyroid Hormone Receptors: Simulations Using a Novel Multipoint Steered Molecular Dynamics Approach. <i>Journal of Physical Chemistry B</i> , 2008, 112, 10741-10751.     | 2.6 | 51        |
| 52 | Crystal structure of a soluble decoy receptor IL-22BP bound to interleukin-22. <i>FEBS Letters</i> , 2009, 583, 1072-1077.                                                                                                                                  | 2.8 | 50        |
| 53 | Energetic Contributions and Topographical Organization of Ligand Binding Residues of Tissue Factor. <i>Biochemistry</i> , 1995, 34, 6310-6315.                                                                                                              | 2.5 | 49        |
| 54 | The protein crystallography beamline at LNLS, the Brazilian National Synchrotron Light Source. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 1998, 405, 159-164. | 1.6 | 49        |

| #  | ARTICLE                                                                                                                                                                                                                                   | IF  | CITATIONS |
|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 55 | Crystal structure of the Kunitz (STI)-type inhibitor from <i>Delonix regia</i> seeds. <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 1303-1308.                                                                  | 2.1 | 49        |
| 56 | An overview on progress, advances, and future outlook for biohydrogen production technology. <i>International Journal of Hydrogen Energy</i> , 2022, 47, 37264-37281.                                                                     | 7.1 | 48        |
| 57 | Interleukin-22 Forms Dimers that are Recognized by Two Interleukin-22R1 Receptor Chains. <i>Biophysical Journal</i> , 2008, 94, 1754-1765.                                                                                                | 0.5 | 46        |
| 58 | Closed Conformation of the Active Site Loop of Rabbit Muscle Triosephosphate Isomerase in the Absence of Substrate: Evidence of Conformational Heterogeneity. <i>Journal of Molecular Biology</i> , 2003, 334, 1023-1041.                 | 4.2 | 45        |
| 59 | Structure and function of interleukin-22 and other members of the interleukin-10 family. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 2909-2935.                                                                               | 5.4 | 45        |
| 60 | High-throughput cloning, expression and purification of glycoside hydrolases using Ligation-Independent Cloning (LIC). <i>Protein Expression and Purification</i> , 2014, 99, 35-42.                                                      | 1.3 | 44        |
| 61 | Defining functional diversity for lignocellulose degradation in a microbial community using multi-omics studies. <i>Biotechnology for Biofuels</i> , 2018, 11, 166.                                                                       | 6.2 | 44        |
| 62 | Role of Halogen Bonds in Thyroid Hormone Receptor Selectivity: Pharmacophore-Based 3D-QSSR Studies. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 2606-2616.                                                            | 5.4 | 43        |
| 63 | Structural Insights into Human Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta) Selective Ligand Binding. <i>PLoS ONE</i> , 2012, 7, e33643.                                                                                 | 2.5 | 43        |
| 64 | Joint X-ray crystallographic and molecular dynamics study of cellobiohydrolase I from <i>Trichoderma harzianum</i> : deciphering the structural features of cellobiohydrolase catalytic activity. <i>FEBS Journal</i> , 2013, 280, 56-69. | 4.7 | 43        |
| 65 | Structural and chemical basis for enhanced affinity and potency for a large series of estrogen receptor ligands: 2D and 3D QSAR studies. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 26, 434-442.                          | 2.4 | 42        |
| 66 | Structural basis of GC-1 selectivity for thyroid hormone receptor isoforms. <i>BMC Structural Biology</i> , 2008, 8, 8.                                                                                                                   | 2.3 | 42        |
| 67 | Novel Zn <sup>2+</sup> -binding Sites in Human Transthyretin. <i>Journal of Biological Chemistry</i> , 2010, 285, 31731-31741.                                                                                                            | 3.4 | 42        |
| 68 | Crystal structure and statistical coupling analysis of highly glycosylated peroxidase from royal palm tree ( <i>Roystonea regia</i> ). <i>Journal of Structural Biology</i> , 2010, 169, 226-242.                                         | 2.8 | 41        |
| 69 | Mapping the Intramolecular Vibrational Energy Flow in Proteins Reveals Functionally Important Residues. <i>Journal of Physical Chemistry Letters</i> , 2011, 2, 2073-2078.                                                                | 4.6 | 41        |
| 70 | Analysis of Agonist and Antagonist Effects on Thyroid Hormone Receptor Conformation by Hydrogen/Deuterium Exchange. <i>Molecular Endocrinology</i> , 2011, 25, 15-31.                                                                     | 3.7 | 41        |
| 71 | Flavonoid interactions with human transthyretin: Combined structural and thermodynamic analysis. <i>Journal of Structural Biology</i> , 2012, 180, 143-153.                                                                               | 2.8 | 41        |
| 72 | Transcriptome Profile of <i>Trichoderma harzianum</i> IOC-3844 Induced by Sugarcane Bagasse. <i>PLoS ONE</i> , 2014, 9, e88689.                                                                                                           | 2.5 | 41        |

| #  | ARTICLE                                                                                                                                                                                                                                 | IF   | CITATIONS |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 73 | Structure-Based Approach for the Study of Estrogen Receptor Binding Affinity and Subtype Selectivity. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 2243-2253.                                                        | 5.4  | 40        |
| 74 | Amino acid sequence of piratoxin-II, a myotoxic Lys49 phospholipase A2 homologue from <i>Bothrops pirajai</i> venom. <i>Biochimie</i> , 2000, 82, 245-250.                                                                              | 2.6  | 39        |
| 75 | Purification, characterization, gene cloning and preliminary X-ray data of the exo-inulinase from <i>Aspergillus awamori</i> . <i>Biochemical Journal</i> , 2002, 362, 131.                                                             | 3.7  | 39        |
| 76 | Structural comparison of <i>Escherichia coli</i> L-asparaginase in two monoclinic space groups. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 416-422.                                                | 2.5  | 39        |
| 77 | Conformational differences between the wild type and V30M mutant transthyretin modulate its binding to genistein: Implications to tetramer stability and ligand-binding. <i>Journal of Structural Biology</i> , 2010, 170, 522-531.     | 2.8  | 39        |
| 78 | Potential of oleaginous yeast <i>Trichosporon</i> sp. , for conversion of sugarcane bagasse hydrolysate into biodiesel. <i>Bioresource Technology</i> , 2017, 242, 161-168.                                                             | 9.6  | 39        |
| 79 | Structural insights into $\beta$ -glucosidase transglycosylation based on biochemical, structural and computational analysis of two GH1 enzymes from <i>Trichoderma harzianum</i> . <i>New Biotechnology</i> , 2018, 40, 218-227.       | 4.4  | 39        |
| 80 | Structural Characterization of B and non-B Subtypes of HIV-Protease: Insights into the Natural Susceptibility to Drug Resistance Development. <i>Journal of Molecular Biology</i> , 2007, 369, 1029-1040.                               | 4.2  | 38        |
| 81 | Structural and biochemical characterization of a GH3 $\beta$ -glucosidase from the probiotic bacteria <i>Bifidobacterium adolescentis</i> . <i>Biochimie</i> , 2018, 148, 107-115.                                                      | 2.6  | 38        |
| 82 | Protein crystal structure solution by fast incorporation of negatively and positively charged anomalous scatterers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 996-1002.                           | 2.5  | 37        |
| 83 | <i>Herbaspirillum seropedicae</i> signal transduction protein PII is structurally similar to the enteric GlnK. <i>FEBS Journal</i> , 2002, 269, 3296-3303.                                                                              | 0.2  | 36        |
| 84 | Dissection of a Human Septin: Definition and Characterization of Distinct Domains within Human SEPT4. <i>Biochemistry</i> , 2006, 45, 13918-13931.                                                                                      | 2.5  | 36        |
| 85 | Functional characterization of a lytic polysaccharide monooxygenase from the thermophilic fungus <i>Myceliophthora thermophila</i> . <i>PLoS ONE</i> , 2018, 13, e0202148.                                                              | 2.5  | 36        |
| 86 | Structural analysis of <i>Tityus serrulatus</i> Ts1 neurotoxin at atomic resolution: insights into interactions with Na <sup>+</sup> channels. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 405-415. | 2.5  | 35        |
| 87 | Cellulose nanofibers production using a set of recombinant enzymes. <i>Carbohydrate Polymers</i> , 2021, 256, 117510.                                                                                                                   | 10.2 | 35        |
| 88 | Different binding and recognition modes of GL479, a dual agonist of Peroxisome Proliferator-Activated Receptor $\alpha$ and $\beta$ . <i>Journal of Structural Biology</i> , 2015, 191, 332-340.                                        | 2.8  | 34        |
| 89 | Identification of a New Hormone-Binding Site on the Surface of Thyroid Hormone Receptor. <i>Molecular Endocrinology</i> , 2014, 28, 534-545.                                                                                            | 3.7  | 33        |
| 90 | Crystal structures of bovine beta-lactoglobulin in the orthorhombic space group C2221 . Structural differences between genetic variants A and B and features of the Tanford transition. <i>FEBS Journal</i> , 2001, 268, 477-484.       | 0.2  | 33        |

| #   | ARTICLE                                                                                                                                                                                                                                              | IF   | CITATIONS |
|-----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 91  | 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.           | 2.3  | 32        |
| 92  | X-ray Structure and Molecular Dynamics Simulations of Endoglucanase 3 from <i>Trichoderma harzianum</i> : Structural Organization and Substrate Recognition by Endoglucanases That Lack Cellulose Binding Module. <i>PLoS ONE</i> , 2013, 8, e59069. | 2.5  | 32        |
| 93  | 3D QSAR comparative molecular field analysis on nonsteroidal farnesoid X receptor activators. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 25, 921-927.                                                                                | 2.4  | 31        |
| 94  | Crystal structure of yeast hexokinase PI in complex with glucose: A classical "induced fit" example revised. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 731-740.                                                            | 2.6  | 31        |
| 95  | An alternative conformation of ER $\beta$ bound to estradiol reveals H12 in a stable antagonist position. <i>Scientific Reports</i> , 2017, 7, 3509.                                                                                                 | 3.3  | 31        |
| 96  | Pressure denaturation of $\beta$ -lactoglobulin. <i>FEBS Journal</i> , 2000, 267, 2235-2241.                                                                                                                                                         | 0.2  | 30        |
| 97  | Three-Dimensional Structure of the Fab from a Human IgM Cold Agglutinin. <i>Journal of Immunology</i> , 2000, 165, 6422-6428.                                                                                                                        | 0.8  | 30        |
| 98  | Revealing the insoluble metasecretome of lignocellulose-degrading microbial communities. <i>Scientific Reports</i> , 2017, 7, 2356.                                                                                                                  | 3.3  | 30        |
| 99  | Targeted metatranscriptomics of compost-derived consortia reveals a GH11 exerting an unusual exo-1,4- $\beta$ -xylanase activity. <i>Biotechnology for Biofuels</i> , 2017, 10, 254.                                                                 | 6.2  | 30        |
| 100 | Crystal structures of bovine $\beta$ -lactoglobulin in the orthorhombic space group C2221. <i>FEBS Journal</i> , 2001, 268, 477-484.                                                                                                                 | 0.2  | 29        |
| 101 | Hemocyanin facilitates lignocellulose digestion by wood-boring marine crustaceans. <i>Nature Communications</i> , 2018, 9, 5125.                                                                                                                     | 12.8 | 29        |
| 102 | Recent advances in the enzymatic production and applications of xylooligosaccharides. <i>World Journal of Microbiology and Biotechnology</i> , 2021, 37, 169.                                                                                        | 3.6  | 29        |
| 103 | The X-ray structure of a recombinant major urinary protein at 1.75 Å resolution. A comparative study of X-ray and NMR-derived structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1863-1869.                 | 2.5  | 28        |
| 104 | On the subtle tuneability of cellulose hydrogels: implications for binding of biomolecules demonstrated for CBM 1. <i>Journal of Materials Chemistry B</i> , 2017, 5, 3879-3887.                                                                     | 5.8  | 28        |
| 105 | <sup>1</sup> H NMR investigation of water accessibility in cellulose of pretreated sugarcane bagasse. <i>Biotechnology for Biofuels</i> , 2014, 7, 127.                                                                                              | 6.2  | 28        |
| 106 | Family 1 carbohydrate binding-modules enhance saccharification rates. <i>AMB Express</i> , 2014, 4, 36.                                                                                                                                              | 3.0  | 27        |
| 107 | Thermal adaptation strategies of the extremophile bacterium <i>Thermus filiformis</i> based on multi-omics analysis. <i>Extremophiles</i> , 2017, 21, 775-788.                                                                                       | 2.3  | 27        |
| 108 | Nanoscale conformational ordering in polyanilines investigated by SAXS and AFM. <i>Journal of Colloid and Interface Science</i> , 2007, 316, 376-387.                                                                                                | 9.4  | 26        |



| #   | ARTICLE                                                                                                                                                                                                                                                                                                         | IF   | CITATIONS |
|-----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 109 | Thermodynamic characterization of the palm tree <i>Roystonea regia</i> peroxidase stability. <i>Biochimie</i> , 2008, 90, 1737-1749.                                                                                                                                                                            | 2.6  | 26        |
| 110 | Molecular Basis of the Thermostability and Thermophilicity of Laminarinases: X-ray Structure of the Hyperthermostable Laminarinase from <i>Rhodothermus marinus</i> and Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2011, 115, 7940-7949.                                          | 2.6  | 26        |
| 111 | Structure-based identification of novel PPAR gamma ligands. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013, 23, 5795-5802.                                                                                                                                                                            | 2.2  | 26        |
| 112 | Biochemical and structural insights into a thermostable cellobiohydrolase from <i>Myceliophthora thermophila</i> . <i>FEBS Journal</i> , 2018, 285, 559-579.                                                                                                                                                    | 4.7  | 26        |
| 113 | Xyloglucan processing machinery in <i>Xanthomonas</i> pathogens and its role in the transcriptional activation of virulence factors. <i>Nature Communications</i> , 2021, 12, 4049.                                                                                                                             | 12.8 | 26        |
| 114 | Three-dimensional structure of an unusual Kunitz (STI) type trypsin inhibitor from <i>Copaifera langsdorffii</i> . <i>Biochimie</i> , 2004, 86, 167-172.                                                                                                                                                        | 2.6  | 25        |
| 115 | Identification of a novel ligand binding motif in the transthyretin channel. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 100-110.                                                                                                                                                                     | 3.0  | 25        |
| 116 | Effect of pH and temperature on the global compactness, structure, and activity of cellobiohydrolase Cel7A from <i>Trichoderma harzianum</i> . <i>European Biophysics Journal</i> , 2012, 41, 89-98.                                                                                                            | 2.2  | 25        |
| 117 | Recombinant <i>Trichoderma harzianum</i> endoglucanase I (Cel7B) is a highly acidic and promiscuous carbohydrate-active enzyme. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 9591-9604.                                                                                                            | 3.6  | 25        |
| 118 | Molecular characterization of a family 5 glycoside hydrolase suggests an induced-fit enzymatic mechanism. <i>Scientific Reports</i> , 2016, 6, 23473.                                                                                                                                                           | 3.3  | 25        |
| 119 | Purification, and Biochemical and Biophysical Characterization of Cellobiohydrolase I from <i>Trichoderma harzianum</i> IOC 3844. <i>Journal of Microbiology and Biotechnology</i> , 2011, 21, 808-817.                                                                                                         | 2.1  | 25        |
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