Igor Polikarpov

List of Publications by Year
in descending order

299	10,270	47409	58552
papers	citations	49 h-index	86 g-index

305	305	305	14522
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Bovine Î²-lactoglobulin at 1.8 Ã... resolution â€"Â still an enigmatic lipocalin. Structure, 1997, 5, 481-495.	1.6	674
2	Average protein density is a molecular-weight-dependent function. Protein Science, 2009, 13, 2825-2828.	3.1	552
3	Determination of the molecular weight of proteins in solution from a single small-angle X-ray scattering measurement on a relative scale. Journal of Applied Crystallography, 2010, 43, 101-109.	1.9	389
4	Chemical and morphological characterization of sugarcane bagasse submitted to a delignification process for enhanced enzymatic digestibility. Biotechnology for Biofuels, 2011, 4, 54.	6.2	382
5	Crystal structure of the extracellular region of human tissue factor. Nature, 1994, 370, 662-666.	13.7	230
6	Medium Chain Fatty Acids Are Selective Peroxisome Proliferator Activated Receptor (PPAR) Î³ Activators and Pan-PPAR Partial Agonists. PLoS ONE, 2012, 7, e36297.	1.1	165
7	Enzymatic hydrolysis of pretreated sugar cane bagasse using Penicillium funiculosum and Trichoderma harzianum cellulases. Process Biochemistry, 2011, 46, 1196-1201.	1.8	148
8	Substrate binding is required for assembly of the active conformation of the catalytic site in Ntn amidotransferases: evidence from the 1.8 Ã¥ crystal structure of the glutaminase domain of glucosamine 6-phosphate synthase. Structure, 1996, 4, 801-810.	1.6	146
9	Crystal Structure of Exo-inulinase from Aspergillus awamori: The Enzyme Fold and Structural Determinants of Substrate Recognition. Journal of Molecular Biology, 2004, 344, 471-480.	2.0	141
10	Multi-scale structural and chemical analysis of sugarcane bagasse in the process of sequential acidâ€"base pretreatment and ethanol production by Scheffersomyces shehatae and Saccharomyces cerevisiae. Biotechnology for Biofuels, 2014, 7, 63.	6.2	134
11	Î²-Lactoglobulin. International Dairy Journal, 1998, 8, 65-72.	1.5	129
12	The High Resolution Crystal Structure of Yeast Hexokinase PII with the Correct Primary Sequence Provides New Insights into Its Mechanism of Action. Journal of Biological Chemistry, 2000, 275, 20814-20821.	1.6	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. Protein Science, 2019, 28, 454-463.	3.1	122
14	Crystal Structure of Recombinant Human Interleukin-22. Structure, 2002, 10, 1051-1062.	1.6	119
15	Efficient sugar production from sugarcane bagasse by microwave assisted acid and alkali pretreatment. Biomass and Bioenergy, 2016, 93, 269-278.	2.9	115
16	Structural diversity of carbohydrate esterases. Biotechnology Research and Innovation, 2017, 1, 35-51.	0.3	114
17	The two types of 3-dehydroquinase have distinct structures but catalyze the same overall reaction. Nature Structural Biology, 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 â€" part 1. Biotechnology for Biofuels, 2013, 6, 75.	6.2	108

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19	Structural Rearrangements in the Thyroid Hormone Receptor Hinge Domain and Their Putative Role in the Receptor Function. Journal of Molecular Biology, 2006, 360, 586-598.	2.0	106
20	Molecular Mechanism of Peroxisome Proliferator-Activated Receptor Î± Activation by WY14643: a New Mode of Ligand Recognition and Receptor Stabilization. Journal of Molecular Biology, 2013, 425, 2878-2893.	2.0	101
21	Involvement of the C terminus in intramolecular nitrogen channeling in glucosamine 6-phosphate synthase: evidence from a 1.6 Ã¥ crystal structure of the isomerase domain. Structure, 1998, 6, 1047-1055.	1.6	99
22	Evaluating the composition and processing potential of novel sources of Brazilian biomass for sustainable biorenewables production. Biotechnology for Biofuels, 2014, 7, 10.	6.2	87
23	Structural Basis for Low Catalytic Activity in Lys49 Phospholipases A2A Hypothesis:â€‰ The Crystal Structure of Piratoxin II Complexed to Fatty Acid,. Biochemistry, 2001, 40, 28-36.	1.2	84
24	Mode of Peroxisome Proliferator-Activated Receptor Î³ Activation by Luteolin. Molecular Pharmacology, 2012, 81, 788-799.	1.0	84
25	Structural and compositional changes in sugarcane bagasse subjected to hydrothermal and organosolv pretreatments and their impacts on enzymatic hydrolysis. Industrial Crops and Products, 2018, 113, 64-74.	2.5	84
26	Crystal Structures of Î²-Galactosidase from Penicillium sp. and its Complex with Galactose. Journal of Molecular Biology, 2004, 343, 1281-1292.	2.0	83
27	Dissecting structureâ€“functionâ€“stability relationships of a thermostable GH5-CBM3 cellulase from Bacillus subtilis 168. Biochemical Journal, 2012, 441, 95-104.	1.7	81
28	Stability of l-asparaginase: an enzyme used in leukemia treatment. Pharmaceutica Acta Helvetiae, 1999, 74, 1-9.	1.2	79
29	Crystal structure of the ILâ€22/ILâ€22R1 complex and its implications for the ILâ€22 signaling mechanism. FEBS Letters, 2008, 582, 2985-2992.	1.3	76
30	Gaining ligand selectivity in thyroid hormone receptors via entropy. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20717-20722.	3.3	76
31	Carbohydrate binding modules enhance cellulose enzymatic hydrolysis by increasing access of cellulases to the substrate. Carbohydrate Polymers, 2019, 211, 57-68.	5.1	75
32	Molecular Dynamics Simulations of Ligand Dissociation from Thyroid Hormone Receptors:Â Evidence of the Likeliest Escape Pathway and Its Implications for the Design of Novel Ligands. Journal of Medicinal Chemistry, 2006, 49, 23-26.	2.9	73
33	Nuclear receptor full-length architectures: confronting myth and illusion with high resolution. Trends in Biochemical Sciences, 2015, 40, 16-24.	3.7	73
34	Quantitative 13C MultiCP solid-state NMR as a tool for evaluation of cellulose crystallinity index measured directly inside sugarcane biomass. Biotechnology for Biofuels, 2015, 8, 110.	6.2	72
35	Structural features of lignin obtained at different alkaline oxidation conditions from sugarcane bagasse. Industrial Crops and Products, 2012, 35, 61-69.	2.5	71
36	The MX2 macromolecular crystallography beamline: a wiggler X-ray source at the LNLS. Journal of Synchrotron Radiation, 2009, 16, 69-75.	1.0	70

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37	Crystal Structure of Î±-Galactosidase from Trichoderma reesei and Its Complex with Galactose: Implications for Catalytic Mechanism. Journal of Molecular Biology, 2004, 339, 413-422.	2.0	69
38	Molecular Dynamics Simulations Reveal Multiple Pathways of Ligand Dissociation from Thyroid Hormone Receptors. Biophysical Journal, 2005, 89, 2011-2023.	0.2	66
39	Purification, characterization, gene cloning and preliminary X-ray data of the exo-inulinase from Aspergillus awamori. Biochemical Journal, 2002, 362, 131-135.	1.7	65
40	Mechanisms of Peroxisome Proliferator Activated Receptor Î³ Regulation by Non-steroidal Anti-inflammatory Drugs. Nuclear Receptor Signaling, 2015, 13, nrs.13004.	1.0	63
41	Set-up and Experimental Parameters of the Protein Crystallography Beamline at the Brazilian National Synchrotron Laboratory. Journal of Synchrotron Radiation, 1998, 5, 72-76.	1.0	62
42	Mapping the lignin distribution in pretreated sugarcane bagasse by confocal and fluorescence lifetime imaging microscopy. Biotechnology for Biofuels, 2013, 6, 43.	6.2	61
43	Aspergillus niger Î²-Glucosidase Has a Cellulase-like Tadpole Molecular Shape. Journal of Biological Chemistry, 2013, 288, 32991-33005.	1.6	60
44	Sugarcane waste as a valuable source of lipophilic molecules. Industrial Crops and Products, 2015, 76, 95-103.	2.5	59
45	Ajulemic Acid, a Synthetic Nonpsychoactive Cannabinoid Acid, Bound to the Ligand Binding Domain of the Human Peroxisome Proliferator-activated Receptor Î³. Journal of Biological Chemistry, 2007, 282, 18625-18633.	1.6	58
46	Nutrient availability shapes the microbial community structure in sugarcane bagasse compost-derived consortia. Scientific Reports, 2016, 6, 38781.	1.6	56
47	Divergence in macromolecular assembly: X-ray crystallographic structure analysis of lumazine synthase from Brucella abortus11Edited by R. Huber. Journal of Molecular Biology, 2000, 297, 1031-1036.	2.0	55
48	Ligand Dissociation from Estrogen Receptor Is Mediated by Receptor Dimerization: Evidence from Molecular Dynamics Simulations. Molecular Endocrinology, 2008, 22, 1565-1578.	3.7	54
49	A review on bioprocessing of paddy straw to ethanol using simultaneous saccharification and fermentation. Process Biochemistry, 2019, 85, 125-134.	1.8	53
50	Crystal structure of neurotoxin Ts1 from Tityus serrulatus provides insights into the specificity and toxicity of scorpion toxins 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 290, 175-184.	2.0	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. Journal of Physical Chemistry B, 2008, 112, 10741-10751.	1.2	51
52	Crystal structure of a soluble decoy receptor ILâ€22BP bound to interleukinâ€22. FEBS Letters, 2009, 583, 1072-1077.	1.3	50
53	Energetic Contributions and Topographical Organization of Ligand Binding Residues of Tissue Factor. Biochemistry, 1995, 34, 6310-6315.	1.2	49
54	The protein crystallography beamline at LNLS, the Brazilian National Synchrotron Light Source. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 1998, 405, 159-164.	0.7	49

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55	Crystal structure of the Kunitz (STI)-type inhibitor from Delonix regia seeds. Biochemical and Biophysical Research Communications, 2003, 312, 1303-1308.	1.0	49
56	An overview on progress, advances, and future outlook for biohydrogen production technology. International Journal of Hydrogen Energy, 2022, 47, 37264-37281.	3.8	48
57	Interleukin-22 Forms Dimers that are Recognized by Two Interleukin-22R1 Receptor Chains. Biophysical Journal, 2008, 94, 1754-1765.	0.2	46
58	Closed Conformation of the Active Site Loop of Rabbit Muscle Triosephosphate Isomerase in the Absence of Substrate: Evidence of Conformational Heterogeneity. Journal of Molecular Biology, 2003, 334, 1023-1041.	2.0	45
59	Structure and function of interleukin-22 and other members of the interleukin-10 family. Cellular and Molecular Life Sciences, 2010, 67, 2909-2935.	2.4	45
60	High-throughput cloning, expression and purification of glycoside hydrolases using Ligation-Independent Cloning (LIC). Protein Expression and Purification, 2014, 99, 35-42.	0.6	44
61	Defining functional diversity for lignocellulose degradation in a microbial community using multi-omics studies. Biotechnology for Biofuels, 2018, 11, 166.	6.2	44
62	Role of Halogen Bonds in Thyroid Hormone Receptor Selectivity: Pharmacophore-Based 3D-QSSR Studies. Journal of Chemical Information and Modeling, 2009, 49, 2606-2616.	2.5	43
63	Structural Insights into Human Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta) Selective Ligand Binding. PLoS ONE, 2012, 7, e33643.	1.1	43
64	Joint <scp>X</scp>â€ray crystallographic and molecular dynamics study of cellobiohydrolase I from <scp>T</scp>richodermaÂharzianum: deciphering the structural features of cellobiohydrolase catalytic activity. FEBS Journal, 2013, 280, 56-69.	2.2	43
65	Structural and chemical basis for enhanced affinity and potency for a large series of estrogen receptor ligands: 2D and 3D QSAR studies. Journal of Molecular Graphics and Modelling, 2007, 26, 434-442.	1.3	42
66	Structural basis of GC-1 selectivity for thyroid hormone receptor isoforms. BMC Structural Biology, 2008, 8, 8.	2.3	42
67	Novel Zn2+-binding Sites in Human Transthyretin. Journal of Biological Chemistry, 2010, 285, 31731-31741.	1.6	42
68	Crystal structure and statistical coupling analysis of highly glycosylated peroxidase from royal palm tree (Roystonea regia). Journal of Structural Biology, 2010, 169, 226-242.	1.3	41
69	Mapping the Intramolecular Vibrational Energy Flow in Proteins Reveals Functionally Important Residues. Journal of Physical Chemistry Letters, 2011, 2, 2073-2078.	2.1	41
70	Analysis of Agonist and Antagonist Effects on Thyroid Hormone Receptor Conformation by Hydrogen/Deuterium Exchange. Molecular Endocrinology, 2011, 25, 15-31.	3.7	41
71	Flavonoid interactions with human transthyretin: Combined structural and thermodynamic analysis. Journal of Structural Biology, 2012, 180, 143-153.	1.3	41
72	Transcriptome Profile of Trichoderma harzianum IOC-3844 Induced by Sugarcane Bagasse. PLoS ONE, 2014, 9, e88689.	1.1	41

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73	Structure-Based Approach for the Study of Estrogen Receptor Binding Affinity and Subtype Selectivity. Journal of Chemical Information and Modeling, 2008, 48, 2243-2253.	2.5	40
74	Amino acid sequence of piratoxin-II, a myotoxic Lys49 phospholipase A2 homologue from Bothrops pirajai venom. Biochimie, 2000, 82, 245-250.	1.3	39
75	Purification, characterization, gene cloning and preliminary X-ray data of the exo-inulinase from Aspergillus awamori. Biochemical Journal, 2002, 362, 131.	1.7	39
76	Structural comparison ofEscherichia coliL-asparaginase in two monoclinic space groups. Acta Crystallographica Section D: Biological Crystallography, 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. Journal of Structural Biology, 2010, 170, 522-531.	1.3	39
78	Potential of oleaginous yeast Trichosporon sp . , for conversion of sugarcane bagasse hydrolysate into biodiesel. Bioresource Technology, 2017, 242, 161-168.	4.8	39
79	Structural insights into Î²-glucosidase transglycosylation based on biochemical, structural and computational analysis of two GH1 enzymes from Trichoderma harzianum. New Biotechnology, 2018, 40, 218-227.	2.4	39
80	Structural Characterization of B and non-B Subtypes of HIV-Protease: Insights into the Natural Susceptibility to Drug Resistance Development. Journal of Molecular Biology, 2007, 369, 1029-1040.	2.0	38
81	Structural and biochemical characterization of a GH3 Î²-glucosidase from the probiotic bacteria Bifidobacterium adolescentis. Biochimie, 2018, 148, 107-115.	1.3	38
82	Protein crystal structure solution by fast incorporation of negatively and positively charged anomalous scatterers. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 996-1002.	2.5	37
83	Herbaspirillum seropedicae signal transduction protein PII is structurally similar to the enteric GlnK. FEBS Journal, 2002, 269, 3296-3303.	0.2	36
84	Dissection of a Human Septin:Â Definition and Characterization of Distinct Domains within Human SEPT4. Biochemistry, 2006, 45, 13918-13931.	1.2	36
85	Functional characterization of a lytic polysaccharide monooxygenase from the thermophilic fungus Myceliophthora thermophila. PLoS ONE, 2018, 13, e0202148.	1.1	36
86	Structural analysis ofTityus serrulatusTs1 neurotoxin at atomic resolution: insights into interactions with Na+channels. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 405-415.	2.5	35
87	Cellulose nanofibers production using a set of recombinant enzymes. Carbohydrate Polymers, 2021, 256, 117510.	5.1	35
88	Different binding and recognition modes of GL479, a dual agonist of Peroxisome Proliferator-Activated Receptor Î±/Î³. Journal of Structural Biology, 2015, 191, 332-340.	1.3	34
89	Identification of a New Hormone-Binding Site on the Surface of Thyroid Hormone Receptor. Molecular Endocrinology, 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. FEBS Journal, 2001, 268, 477-484.	0.2	33

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91	Cloning, heterologous expression and biochemical characterization of a non-specific endoglucanase family 12 from Aspergillus terreus NIH2624. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 395-403.	1.1	32
92	X-ray Structure and Molecular Dynamics Simulations of Endoglucanase 3 from Trichoderma harzianum: Structural Organization and Substrate Recognition by Endoglucanases That Lack Cellulose Binding Module. PLoS ONE, 2013, 8, e59069.	1.1	32
93	3D QSAR comparative molecular field analysis on nonsteroidal farnesoid X receptor activators. Journal of Molecular Graphics and Modelling, 2007, 25, 921-927.	1.3	31
94	Crystal structure of yeast hexokinase PI in complex with glucose: A classical â€œinduced fitâ€•example revised. Proteins: Structure, Function and Bioinformatics, 2008, 72, 731-740.	1.5	31
95	An alternative conformation of ERÎ² bound to estradiol reveals H12 in a stable antagonist position. Scientific Reports, 2017, 7, 3509.	1.6	31
96	Pressure denaturation of Î²-lactoglobulin. FEBS Journal, 2000, 267, 2235-2241.	0.2	30
97	Three-Dimensional Structure of the Fab from a Human IgM Cold Agglutinin. Journal of Immunology, 2000, 165, 6422-6428.	0.4	30
98	Revealing the insoluble metasecretome of lignocellulose-degrading microbial communities. Scientific Reports, 2017, 7, 2356.	1.6	30
99	Targeted metatranscriptomics of compost-derived consortia reveals a GH11 exerting an unusual exo-1,4-Î²-xylanase activity. Biotechnology for Biofuels, 2017, 10, 254.	6.2	30
100	Crystal structures of bovine Î²-lactoglobulin in the orthorhombic space group C2221. FEBS Journal, 2001, 268, 477-484.	0.2	29
101	Hemocyanin facilitates lignocellulose digestion by wood-boring marine crustaceans. Nature Communications, 2018, 9, 5125.	5.8	29
102	Recent advances in the enzymatic production and applications of xylooligosaccharides. World Journal of Microbiology and Biotechnology, 2021, 37, 169.	1.7	29
103	The X-ray structure of a recombinant major urinary protein at 1.75â€…Ã… resolution. A comparative study of X-ray and NMR-derived structures. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1863-1869.	2.5	28
104	On the subtle tuneability of cellulose hydrogels: implications for binding of biomolecules demonstrated for CBM 1. Journal of Materials Chemistry B, 2017, 5, 3879-3887.	2.9	28
105	1 H NMR investigation of water accessibility in cellulose of pretreated sugarcane bagasse. Biotechnology for Biofuels, 2014, 7, 127.	6.2	28
106	Family 1 carbohydrate binding-modules enhance saccharification rates. AMB Express, 2014, 4, 36.	1.4	27
107	Thermal adaptation strategies of the extremophile bacterium Thermus filiformis based on multi-omics analysis. Extremophiles, 2017, 21, 775-788.	0.9	27
108	Nanoscale conformational ordering in polyanilines investigated by SAXS and AFM. Journal of Colloid and Interface Science, 2007, 316, 376-387.	5.0	26

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109	Thermodynamic characterization of the palm tree Roystonea regia peroxidase stability. Biochimie, 2008, 90, 1737-1749.	1.3	26
110	Molecular Basis of the Thermostability and Thermophilicity of Laminarinases: X-ray Structure of the Hyperthermostable Laminarinase from Rhodothermus marinus and Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2011, 115, 7940-7949.	1.2	26
111	Structure-based identification of novel PPAR gamma ligands. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 5795-5802.	1.0	26
112	Biochemical and structural insights into a thermostable cellobiohydrolase from MyceliophthoraÂthermophila. FEBS Journal, 2018, 285, 559-579.	2.2	26
113	Xyloglucan processing machinery in Xanthomonas pathogens and its role in the transcriptional activation of virulence factors. Nature Communications, 2021, 12, 4049.	5.8	26
114	Three-dimensional structure of an unusual Kunitz (STI) type trypsin inhibitor from Copaifera langsdorffii. Biochimie, 2004, 86, 167-172.	1.3	25
115	Identification of a novel ligand binding motif in the transthyretin channel. Bioorganic and Medicinal Chemistry, 2010, 18, 100-110.	1.4	25
116	Effect of pH and temperature on the global compactness, structure, and activity of cellobiohydrolase Cel7A from Trichoderma harzianum. European Biophysics Journal, 2012, 41, 89-98.	1.2	25
117	Recombinant Trichoderma harzianum endoglucanase I (Cel7B) is a highly acidic and promiscuous carbohydrate-active enzyme. Applied Microbiology and Biotechnology, 2015, 99, 9591-9604.	1.7	25
118	Molecular characterization of a family 5 glycoside hydrolase suggests an induced-fit enzymatic mechanism. Scientific Reports, 2016, 6, 23473.	1.6	25
119	Purification, and Biochemical and Biophysical Characterization of Cellobiohydrolase I from Trichoderma harzianum IOC 3844. Journal of Microbiology and Biotechnology, 2011, 21, 808-817.	0.9	25
120	The structure of the D49 phospholipase A2piratoxin III fromBothrops pirajaireveals unprecedented structural displacement of the calcium-binding loop: possible relationship to cooperative substrate binding. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 255-262.	2.5	24
121	Nuclear magnetic resonance investigation of water accessibility in cellulose of pretreated sugarcane bagasse. Biotechnology for Biofuels, 2014, 7, 127.	6.2	24
122	Design of an enzyme cocktail consisting of different fungal platforms for efficient hydrolysis of sugarcane bagasse: Optimization and synergism studies. Biotechnology Progress, 2016, 32, 1222-1229.	1.3	24
123	Characterization of a New Glyoxal Oxidase from the Thermophilic Fungus Myceliophthora thermophila M77: Hydrogen Peroxide Production Retained in 5-Hydroxymethylfurfural Oxidation. Catalysts, 2018, 8, 476.	1.6	24
124	Environments of the four tryptophans in the extracellular domain of human tissue factor: comparison of results from absorption and fluorescence difference spectra of tryptophan replacement mutants with the crystal structure of the wild-type protein. Biophysical Journal, 1995, 69, 20-29.	0.2	23
125	Enhanced hydrolysis of hydrothermally and autohydrolytically treated sugarcane bagasse and understanding the structural changes leading to improved saccharification. Biomass and Bioenergy, 2020, 139, 105639.	2.9	23
126	Low-Resolution Molecular Models Reveal the Oligomeric State of the PPAR and the Conformational Organization of Its Domains in Solution. PLoS ONE, 2012, 7, e31852.	1.1	23

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127	The Characterization of the Endoglucanase Cel12A from Gloeophyllum trabeum Reveals an Enzyme Highly Active on Î²-Glucan. PLoS ONE, 2014, 9, e108393.	1.1	22
128	Insights into the structure and function of fungal Î²â€mannosidases from glycoside hydrolase familyÂ2 based on multiple crystal structures of the TrichodermaÂharzianum enzyme. FEBS Journal, 2014, 281, 4165-4178.	2.2	22
129	Crystal structure of Î²1â†'6â€galactosidase from Bifidobacterium bifidum S17: trimeric architecture, molecular determinants of the enzymatic activity and its inhibition by Î±â€galactose. FEBS Journal, 2016, 283, 4097-4112.	2.2	22
130	Multifaceted characterization of sugarcane bagasse under different steam explosion severity conditions leading to distinct enzymatic hydrolysis yields. Industrial Crops and Products, 2019, 139, 111542.	2.5	22
131	Functional characterization and comparative analysis of two heterologous endoglucanases from diverging subfamilies of glycosyl hydrolase family 45. Enzyme and Microbial Technology, 2019, 120, 23-35.	1.6	22
132	Catalytic mechanism of inulinase from Arthrobacter sp. S37. Biochemical and Biophysical Research Communications, 2008, 371, 600-605.	1.0	21
133	Structural and thermodynamic analysis of thrombin:suramin interaction in solution and crystal phases. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 873-881.	1.1	21
134	Crystal structures of Leptospira interrogans FAD-containing ferredoxin-NADP+ reductase and its complex with NADP+. BMC Structural Biology, 2007, 7, 69.	2.3	20
135	Crystal structure analysis of peroxidase from the palm tree Chamaerops excelsa. Biochimie, 2015, 111, 58-69.	1.3	20
136	RXR Agonist Modulates TR: Corepressor Dissociation Upon 9-cis Retinoic Acid Treatment. Molecular Endocrinology, 2015, 29, 258-273.	3.7	20
137	Liquid ammonia pretreatment optimization for improved release of fermentable sugars from sugarcane bagasse. Journal of Cleaner Production, 2021, 281, 123922.	4.6	20
138	Structural Insights into the Î²-Mannosidase fromT. reeseiObtained by Synchrotron Small-Angle X-ray Solution Scattering Enhanced by X-ray Crystallographyâ€. Biochemistry, 2002, 41, 9370-9375.	1.2	19
139	2D QSAR studies on thyroid hormone receptor ligands. Bioorganic and Medicinal Chemistry, 2007, 15, 4609-4617.	1.4	19
140	Side by Side Comparison of Chemical Compounds Generated by Aqueous Pretreatments of Maize Stover, Miscanthus and Sugarcane Bagasse. Bioenergy Research, 2014, 7, 1466-1480.	2.2	19
141	Transformation of xylan into value-added biocommodities using Thermobacillus composti GH10 xylanase. Carbohydrate Polymers, 2020, 247, 116714.	5.1	19
142	Phasing on Rapidly Soaked Ions. Methods in Enzymology, 2003, 374, 120-137.	0.4	18
143	A Novel Carbohydrate-binding Module from Sugar Cane Soil Metagenome Featuring Unique Structural and Carbohydrate Affinity Properties. Journal of Biological Chemistry, 2016, 291, 23734-23743.	1.6	18
144	A simple enzymatic assay for the quantification of C1-specific cellulose oxidation by lytic polysaccharide monooxygenases. Biotechnology Letters, 2020, 42, 93-102.	1.1	18

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145	Essential Metabolic Routes as a Way to ESKAPE From Antibiotic Resistance. Frontiers in Public Health, 2020, 8, 26.	1.3	18
146	Low Resolution Structures of the Retinoid X Receptor DNA-binding and Ligand-binding Domains Revealed by Synchrotron X-ray Solution Scattering. Journal of Biological Chemistry, 2003, 278, 16030-16038.	1.6	17
147	Inhibition of Human Transthyretin Aggregation by Non-Steroidal Anti-Inflammatory Compounds: A Structural and Thermodynamic Analysis. International Journal of Molecular Sciences, 2013, 14, 5284-5311.	1.8	17
148	Low-Resolution Structure and Fluorescence Anisotropy Analysis of Protein Tyrosine Phosphatase Î· Catalytic Domain. Biophysical Journal, 2007, 92, 4424-4432.	0.2	16
149	Ligand induced interaction of thyroid hormone receptor beta with its coregulators. Journal of Steroid Biochemistry and Molecular Biology, 2008, 112, 205-212.	1.2	16
150	Exploring oyster mushroom (Pleurotus ostreatus) substrate preparation by varying phase I composting time: changes in bacterial communities and physicochemical composition of biomass impacting mushroom yields. Journal of Applied Microbiology, 2019, 126, 931-944.	1.4	16
151	The Ultimate Wavelength for Protein Crystallography?. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 734-737.	2.5	15
152	X-ray Bragg Diffraction in a Strong Acoustic Field. Journal of Applied Crystallography, 1998, 31, 60-66.	1.9	15
153	Comparison of different crystal forms of 3-dehydroquinase fromSalmonella typhiand its implication for the enzyme activity. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 798-804.	2.5	15
154	Helix 12 Dynamics and Thyroid Hormone Receptor Activity: Experimental and Molecular Dynamics Studies of Ile280 Mutants. Journal of Molecular Biology, 2011, 412, 882-893.	2.0	15
155	Pre-treatment of sugarcane bagasse with a combination of sodium hydroxide and lime for improving the ruminal degradability: optimization of process parameters using response surface methodology. Journal of Applied Animal Research, 2016, 44, 287-296.	0.4	15
156	Cellulose ionics: switching ionic diode responses by surface charge in reconstituted cellulose films. Analyst, The, 2017, 142, 3707-3714.	1.7	15
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