

Igor Polikarpov

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298 papers	8,322 citations	46 h-index	79 g-index
305 ext. papers	9,309 ext. citations	4.7 avg, IF	5.87 L-index

#	Paper	IF	Citations
298	Bovine beta-lactoglobulin at 1.8 Å resolution--still an enigmatic lipocalin. <i>Structure</i> , 1997 , 5, 481-95	5.2	629
297	Average protein density is a molecular-weight-dependent function. <i>Protein Science</i> , 2004 , 13, 2825-8	6.3	463
296	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	3.8	340
295	Chemical and morphological characterization of sugarcane bagasse submitted to a delignification process for enhanced enzymatic digestibility. <i>Biotechnology for Biofuels</i> , 2011 , 4, 54	7.8	304
294	Crystal structure of the extracellular region of human tissue factor. <i>Nature</i> , 1994 , 370, 662-6	50.4	205
293	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, 471-80	6.5	133
292	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	4.8	131
291	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, 801-10	5.2	126
290	Medium chain fatty acids are selective peroxisome proliferator activated receptor (PPAR) α activators and pan-PPAR partial agonists. <i>PLoS ONE</i> , 2012 , 7, e36297	3.7	121
289	Lactoglobulin. <i>International Dairy Journal</i> , 1998 , 8, 65-72	3.5	121
288	Crystal structure of recombinant human interleukin-22. <i>Structure</i> , 2002 , 10, 1051-62	5.2	107
287	The two types of 3-dehydroquinase have distinct structures but catalyze the same overall reaction. <i>Nature Structural Biology</i> , 1999 , 6, 521-5		104
286	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	7.8	103
285	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, 586-98	6.5	97
284	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, 20814-21	5.4	95
283	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, 1047-55	5.2	89
282	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	7.8	87

281	Efficient sugar production from sugarcane bagasse by microwave assisted acid and alkali pretreatment. <i>Biomass and Bioenergy</i> , 2016 , 93, 269-278	5.3	87
280	Crystal structures of beta-galactosidase from <i>Penicillium</i> sp. and its complex with galactose. <i>Journal of Molecular Biology</i> , 2004 , 343, 1281-92	6.5	77
279	Mode of peroxisome proliferator-activated receptor α activation by luteolin. <i>Molecular Pharmacology</i> , 2012 , 81, 788-99	4.3	73
278	Structural basis for low catalytic activity in Lys49 phospholipases A2--a hypothesis: the crystal structure of piratoxin II complexed to fatty acid. <i>Biochemistry</i> , 2001 , 40, 28-36	3.2	73
277	Molecular mechanism of peroxisome proliferator-activated receptor α activation by WY14643: a new mode of ligand recognition and receptor stabilization. <i>Journal of Molecular Biology</i> , 2013 , 425, 2878-93	6.5	71
276	Crystal structure of the IL-22/IL-22R1 complex and its implications for the IL-22 signaling mechanism. <i>FEBS Letters</i> , 2008 , 582, 2985-92	3.8	69
275	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, 23-6	8.3	68
274	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, 20717-22	11.5	66
273	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	66
272	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	6.3	66
271	Evaluating the composition and processing potential of novel sources of Brazilian biomass for sustainable biorenewables production. <i>Biotechnology for Biofuels</i> , 2014 , 7, 10	7.8	65
270	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	3.8	65
269	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	5.9	63
268	Crystal structure of alpha-galactosidase from <i>Trichoderma reesei</i> and its complex with galactose: implications for catalytic mechanism. <i>Journal of Molecular Biology</i> , 2004 , 339, 413-22	6.5	62
267	Stability of L-asparaginase: an enzyme used in leukemia treatment. <i>Pharmaceutica Acta Helveticae</i> , 1999 , 74, 1-9		62
266	Quantitative ^{13}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	7.8	61
265	Molecular dynamics simulations reveal multiple pathways of ligand dissociation from thyroid hormone receptors. <i>Biophysical Journal</i> , 2005 , 89, 2011-23	2.9	61
264	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	3.8	61

263	Structural diversity of carbohydrate esterases. <i>Biotechnology Research and Innovation</i> , 2017 , 1, 35-51	10.1	59
262	Set-up and experimental parameters of the protein crystallography beamline at the Brazilian National Synchrotron Laboratory. <i>Journal of Synchrotron Radiation</i> , 1998 , 5, 72-6	2.4	58
261	Structural features of lignin obtained at different alkaline oxidation conditions from sugarcane bagasse. <i>Industrial Crops and Products</i> , 2012 , 35, 61-69	5.9	53
260	Nuclear receptor full-length architectures: confronting myth and illusion with high resolution. <i>Trends in Biochemical Sciences</i> , 2015 , 40, 16-24	10.3	52
259	Divergence in macromolecular assembly: X-ray crystallographic structure analysis of lumazine synthase from <i>Brucella abortus</i> . <i>Journal of Molecular Biology</i> , 2000 , 297, 1031-6	6.5	51
258	<i>Aspergillus niger</i> β -glucosidase has a cellulase-like tadpole molecular shape: insights into glycoside hydrolase family 3 (GH3) β -glucosidase structure and function. <i>Journal of Biological Chemistry</i> , 2013 , 288, 32991-3005	5.4	49
257	Ligand dissociation from estrogen receptor is mediated by receptor dimerization: evidence from molecular dynamics simulations. <i>Molecular Endocrinology</i> , 2008 , 22, 1565-78		49
256	Ajulemic acid, a synthetic nonpsychoactive cannabinoid acid, bound to the ligand binding domain of the human peroxisome proliferator-activated receptor gamma. <i>Journal of Biological Chemistry</i> , 2007 , 282, 18625-18633	5.4	49
255	Crystal structure of neurotoxin Ts1 from <i>Tityus serrulatus</i> provides insights into the specificity and toxicity of scorpion toxins. <i>Journal of Molecular Biology</i> , 1999 , 290, 175-84	6.5	49
254	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, 10741-51	3.4	48
253	Mechanisms of peroxisome proliferator activated receptor γ regulation by non-steroidal anti-inflammatory drugs. <i>Nuclear Receptor Signaling</i> , 2015 , 13, e004	1	47
252	Mapping the lignin distribution in pretreated sugarcane bagasse by confocal and fluorescence lifetime imaging microscopy. <i>Biotechnology for Biofuels</i> , 2013 , 6, 43	7.8	46
251	Sugarcane waste as a valuable source of lipophilic molecules. <i>Industrial Crops and Products</i> , 2015 , 76, 95-103	5.9	45
250	Crystal structure of the Kunitz (STI)-type inhibitor from <i>Delonix regia</i> seeds. <i>Biochemical and Biophysical Research Communications</i> , 2003 , 312, 1303-8	3.4	44
249	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, 1023-41	6.5	43
248	Role of halogen bonds in thyroid hormone receptor selectivity: pharmacophore-based 3D-QSSR studies. <i>Journal of Chemical Information and Modeling</i> , 2009 , 49, 2606-16	6.1	41
247	Energetic contributions and topographical organization of ligand binding residues of tissue factor. <i>Biochemistry</i> , 1995 , 34, 6310-5	3.2	41
246	Nutrient availability shapes the microbial community structure in sugarcane bagasse compost-derived consortia. <i>Scientific Reports</i> , 2016 , 6, 38781	4.9	41

245	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, 226-42	3.4	40
244	Interleukin-22 forms dimers that are recognized by two interleukin-22R1 receptor chains. <i>Biophysical Journal</i> , 2008 , 94, 1754-65	2.9	40
243	Analysis of agonist and antagonist effects on thyroid hormone receptor conformation by hydrogen/deuterium exchange. <i>Molecular Endocrinology</i> , 2011 , 25, 15-31		39
242	Crystal structure of a soluble decoy receptor IL-22BP bound to interleukin-22. <i>FEBS Letters</i> , 2009 , 583, 1072-7	3.8	38
241	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, 434-42 ^{2.8}		38
240	Carbohydrate binding modules enhance cellulose enzymatic hydrolysis by increasing access of cellulases to the substrate. <i>Carbohydrate Polymers</i> , 2019 , 211, 57-68	10.3	37
239	Structure-based approach for the study of estrogen receptor binding affinity and subtype selectivity. <i>Journal of Chemical Information and Modeling</i> , 2008 , 48, 2243-53	6.1	37
238	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	5.7	36
237	Structural basis of GC-1 selectivity for thyroid hormone receptor isoforms. <i>BMC Structural Biology</i> , 2008 , 8, 8	2.7	36
236	Amino acid sequence of piratoxin-II, a myotoxic lys49 phospholipase A(2) homologue from <i>Bothrops pirajai</i> venom. <i>Biochimie</i> , 2000 , 82, 245-50	4.6	36
235	Flavonoid interactions with human transthyretin: combined structural and thermodynamic analysis. <i>Journal of Structural Biology</i> , 2012 , 180, 143-53	3.4	35
234	Structural insights into human peroxisome proliferator activated receptor delta (PPAR-delta) selective ligand binding. <i>PLoS ONE</i> , 2012 , 7, e33643	3.7	35
233	Novel Zn ²⁺ -binding sites in human transthyretin: implications for amyloidogenesis and retinol-binding protein recognition. <i>Journal of Biological Chemistry</i> , 2010 , 285, 31731-41	5.4	35
232	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, 522-31	3.4	35
231	Structure and function of interleukin-22 and other members of the interleukin-10 family. <i>Cellular and Molecular Life Sciences</i> , 2010 , 67, 2909-35	10.3	35
230	High-throughput cloning, expression and purification of glycoside hydrolases using Ligation-Independent Cloning (LIC). <i>Protein Expression and Purification</i> , 2014 , 99, 35-42	2	34
229	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, 1029-40	6.5	34
228	Herbaspirillum seropedicae signal transduction protein PII is structurally similar to the enteric GlnK. <i>FEBS Journal</i> , 2002 , 269, 3296-303		33

227	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		33
226	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		33
225	Dissection of a human septin: definition and characterization of distinct domains within human SEPT4. <i>Biochemistry</i> , 2006 , 45, 13918-31	3.2	32
224	Purification, characterization, gene cloning and preliminary X-ray data of the exo-inulinase from <i>Aspergillus awamori</i> . <i>Biochemical Journal</i> , 2002 , 362, 131-5	3.8	32
223	A review on bioprocessing of paddy straw to ethanol using simultaneous saccharification and fermentation. <i>Process Biochemistry</i> , 2019 , 85, 125-134	4.8	31
222	Identification of a new hormone-binding site on the surface of thyroid hormone receptor. <i>Molecular Endocrinology</i> , 2014 , 28, 534-45		31
221	Mapping the Intramolecular Vibrational Energy Flow in Proteins Reveals Functionally Important Residues. <i>Journal of Physical Chemistry Letters</i> , 2011 , 2, 2073-2078	6.4	31
220	Potential of oleaginous yeast <i>Trichosporon</i> sp., for conversion of sugarcane bagasse hydrolysate into biodiesel. <i>Bioresource Technology</i> , 2017 , 242, 161-168	11	30
219	Different binding and recognition modes of GL479, a dual agonist of Peroxisome Proliferator-Activated Receptor α . <i>Journal of Structural Biology</i> , 2015 , 191, 332-40	3.4	30
218	Structural analysis of Tityus serrulatus Ts1 neurotoxin at atomic resolution: insights into interactions with Na ⁺ channels. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 405-15		30
217	Structural comparison of Escherichia coli L-asparaginase in two monoclinic space groups. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 416-22		30
216	Defining functional diversity for lignocellulose degradation in a microbial community using multi-omics studies. <i>Biotechnology for Biofuels</i> , 2018 , 11, 166	7.8	29
215	Functional characterization of a lytic polysaccharide monooxygenase from the thermophilic fungus <i>Myceliophthora thermophila</i> . <i>PLoS ONE</i> , 2018 , 13, e0202148	3.7	29
214	Pressure denaturation of beta-lactoglobulin. Different stabilities of isoforms A and B, and an investigation of the Tanford transition. <i>FEBS Journal</i> , 2000 , 267, 2235-41		29
213	3D QSAR comparative molecular field analysis on nonsteroidal farnesoid X receptor activators. <i>Journal of Molecular Graphics and Modelling</i> , 2007 , 25, 921-7	2.8	28
212	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	4	27
211	Structural insights into β -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	6.4	27
210	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, 731-40	4.2	27

209	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, 1863-9		27
208	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	3.7	27
207	Three-dimensional structure of the Fab from a human IgM cold agglutinin. <i>Journal of Immunology</i> , 2000 , 165, 6422-8	5.3	26
206	Family 1 carbohydrate binding-modules enhance saccharification rates. <i>AMB Express</i> , 2014 , 4, 36	4.1	24
205	Identification of a novel ligand binding motif in the transthyretin channel. <i>Bioorganic and Medicinal Chemistry</i> , 2010 , 18, 100-10	3.4	24
204	Thermodynamic characterization of the palm tree <i>Roystonea regia</i> peroxidase stability. <i>Biochimie</i> , 2008 , 90, 1737-49	4.6	24
203	Transcriptome profile of <i>Trichoderma harzianum</i> IOC-3844 induced by sugarcane bagasse. <i>PLoS ONE</i> , 2014 , 9, e88689	3.7	24
202	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, 9591-604	5.7	23
201	Targeted metatranscriptomics of compost-derived consortia reveals a GH11 exerting an unusual exo-1,4-xyylanase activity. <i>Biotechnology for Biofuels</i> , 2017 , 10, 254	7.8	23
200	Revealing the insoluble metasecretome of lignocellulose-degrading microbial communities. <i>Scientific Reports</i> , 2017 , 7, 2356	4.9	23
199	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, 7940-9	3.4	23
198	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	1.2	23
197	Three-dimensional structure of an unusual Kunitz (STI) type trypsin inhibitor from <i>Copaifera langsdorffii</i> . <i>Biochimie</i> , 2004 , 86, 167-72	4.6	23
196	¹ H NMR investigation of water accessibility in cellulose of pretreated sugarcane bagasse. <i>Biotechnology for Biofuels</i> , 2014 , 7, 127	7.8	23
195	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	7.3	22
194	An alternative conformation of ER bound to estradiol reveals H12 in a stable antagonist position. <i>Scientific Reports</i> , 2017 , 7, 3509	4.9	22
193	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. <i>Biophysical Journal</i> , 1995 , 69, 20-9	2.9	22
192	Nuclear magnetic resonance investigation of water accessibility in cellulose of pretreated sugarcane bagasse. <i>Biotechnology for Biofuels</i> , 2014 , 7, 127	7.8	21

191	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	1.9	20
190	The structure of the D49 phospholipase A2 piratoxin III from <i>Bothrops pirajai</i> reveals unprecedented structural displacement of the calcium-binding loop: possible relationship to cooperative substrate binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 255-62		20
189	Low-resolution molecular models reveal the oligomeric state of the PPAR and the conformational organization of its domains in solution. <i>PLoS ONE</i> , 2012 , 7, e31852	3.7	20
188	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, 808-17	3.3	20
187	Design of an enzyme cocktail consisting of different fungal platforms for efficient hydrolysis of sugarcane bagasse: Optimization and synergism studies. <i>Biotechnology Progress</i> , 2016 , 32, 1222-1229	2.8	20
186	Structure-based identification of novel PPAR gamma ligands. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2013 , 23, 5795-802	2.9	19
185	The characterization of the endoglucanase Cel12A from <i>Gloeophyllum trabeum</i> reveals an enzyme highly active on Eglucan. <i>PLoS ONE</i> , 2014 , 9, e108393	3.7	19
184	Nanoscale conformational ordering in polyanilines investigated by SAXS and AFM. <i>Journal of Colloid and Interface Science</i> , 2007 , 316, 376-87	9.3	19
183	Structural and thermodynamic analysis of thrombin:suramin interaction in solution and crystal phases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009 , 1794, 873-81	4	18
182	Catalytic mechanism of inulinase from <i>Arthrobacter</i> sp. S37. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 371, 600-5	3.4	18
181	2D QSAR studies on thyroid hormone receptor ligands. <i>Bioorganic and Medicinal Chemistry</i> , 2007 , 15, 4609-17	3.4	18
180	Crystal structures of bovine beta-lactoglobulin in the orthorhombic space group C222(1). Structural differences between genetic variants A and B and features of the Tanford transition. <i>FEBS Journal</i> , 2001 , 268, 477-83		18
179	Molecular characterization of a family 5 glycoside hydrolase suggests an induced-fit enzymatic mechanism. <i>Scientific Reports</i> , 2016 , 6, 23473	4.9	17
178	Insights into the structure and function of fungal β -mannosidases from glycoside hydrolase family 2 based on multiple crystal structures of the <i>Trichoderma harzianum</i> enzyme. <i>FEBS Journal</i> , 2014 , 281, 4165-78	5.7	17
177	RXR agonist modulates TR: corepressor dissociation upon 9-cis retinoic acid treatment. <i>Molecular Endocrinology</i> , 2015 , 29, 258-73		17
176	Inhibition of human transthyretin aggregation by non-steroidal anti-inflammatory compounds: a structural and thermodynamic analysis. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 5284-311	6.3	17
175	Crystal structures of <i>Leptospira interrogans</i> FAD-containing ferredoxin-NADP ⁺ reductase and its complex with NADP ⁺ . <i>BMC Structural Biology</i> , 2007 , 7, 69	2.7	17
174	Crystal structure of β -galactosidase from <i>Bifidobacterium bifidum</i> S17: trimeric architecture, molecular determinants of the enzymatic activity and its inhibition by β -galactose. <i>FEBS Journal</i> , 2016 , 283, 4097-4112	5.7	17

173	Biochemical and structural insights into a thermostable cellobiohydrolase from <i>Myceliophthora thermophila</i> . <i>FEBS Journal</i> , 2018 , 285, 559-579	5.7	17
172	Thermal adaptation strategies of the extremophile bacterium <i>Thermus filiformis</i> based on multi-omics analysis. <i>Extremophiles</i> , 2017 , 21, 775-788	3	16
171	Multifaceted characterization of sugarcane bagasse under different steam explosion severity conditions leading to distinct enzymatic hydrolysis yields. <i>Industrial Crops and Products</i> , 2019 , 139, 111542	5.9	16
170	Hemocyanin facilitates lignocellulose digestion by wood-boring marine crustaceans. <i>Nature Communications</i> , 2018 , 9, 5125	17.4	16
169	A simple enzymatic assay for the quantification of C1-specific cellulose oxidation by lytic polysaccharide monooxygenases. <i>Biotechnology Letters</i> , 2020 , 42, 93-102	3	15
168	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	3.8	15
167	Structural and biochemical characterization of a GH3 Eglucosidase from the probiotic bacteria <i>Bifidobacterium adolescentis</i> . <i>Biochimie</i> , 2018 , 148, 107-115	4.6	14
166	Side by Side Comparison of Chemical Compounds Generated by Aqueous Pretreatments of Maize Stover, Miscanthus and Sugarcane Bagasse. <i>Bioenergy Research</i> , 2014 , 7, 1466-1480	3.1	14
165	Crystal structure analysis of peroxidase from the palm tree <i>Chamaerops excelsa</i> . <i>Biochimie</i> , 2015 , 111, 58-69	4.6	14
164	Helix 12 dynamics and thyroid hormone receptor activity: experimental and molecular dynamics studies of Ile280 mutants. <i>Journal of Molecular Biology</i> , 2011 , 412, 882-93	6.5	14
163	The ultimate wavelength for protein crystallography?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997 , 53, 734-7		14
162	X-ray Bragg Diffraction in a Strong Acoustic Field. <i>Journal of Applied Crystallography</i> , 1998 , 31, 60-66	3.8	14
161	Ligand induced interaction of thyroid hormone receptor beta with its coregulators. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2008 , 112, 205-12	5.1	14
160	Phasing on rapidly soaked ions. <i>Methods in Enzymology</i> , 2003 , 374, 120-37	1.7	14
159	Structural insights into the beta-mannosidase from <i>T. reesei</i> obtained by synchrotron small-angle X-ray solution scattering enhanced by X-ray crystallography. <i>Biochemistry</i> , 2002 , 41, 9370-5	3.2	14
158	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. <i>Journal of Applied Animal Research</i> , 2016 , 44, 287-296	1.7	13
157	A Novel Carbohydrate-binding Module from Sugar Cane Soil Metagenome Featuring Unique Structural and Carbohydrate Affinity Properties. <i>Journal of Biological Chemistry</i> , 2016 , 291, 23734-23743	5.4	13
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