

# 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	Gut microbiome of the largest living rodent harbors unprecedented enzymatic systems to degrade plant polysaccharides. <i>Nature Communications</i> , 2022, 13, 629.	5.8	26
2	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
3	Influence of the C-terminal domain on the bioluminescence activity and color determination in green and red emitting beetle luciferases and luciferase-like enzyme. <i>Photochemical and Photobiological Sciences</i> , 2021, 20, 113-122.	1.6	1
4	Structure of the class XI myosin globular tail reveals evolutionary hallmarks for cargo recognition in plants. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 522-533.	1.1	0
5	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.	5.8	26
6	Two distinct catalytic pathways for GH43 xylanolytic enzymes unveiled by X-ray and QM/MM simulations. <i>Nature Communications</i> , 2021, 12, 367.	5.8	27
7	Voices of chemical biology. <i>Nature Chemical Biology</i> , 2021, 17, 1-4.	3.9	7
8	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
9	Luciferase isozymes from the Brazilian <i>Aspizoma 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
10	A rationally identified marine GH1 $\beta$ -glucosidase has distinguishing functional features for simultaneous saccharification and fermentation. <i>Biofuels, Bioproducts and Biorefining</i> , 2020, 14, 1163-1179.	1.9	5
11	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
12	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
13	Substrate and Product-Assisted Catalysis: Molecular Aspects behind Structural Switches along Organic Hydroperoxide Resistance Protein Catalytic Cycle. <i>ACS Catalysis</i> , 2020, 10, 6587-6602.	5.5	4
14	A single P115Q mutation modulates specificity in the <i>Corynebacterium pseudotuberculosis</i> arginine repressor. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129597.	1.1	0
15	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
16	Crystal structure of a novel xylose isomerase from <i>Streptomyces</i> sp. F-1 revealed the presence of unique features that differ from conventional classes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129549.	1.1	6
17	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
18	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

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19	Rational engineering of the <i>Trichoderma reesei</i> RUT-C30 strain into an industrially relevant platform for cellulase production. <i>Biotechnology for Biofuels</i> , 2020, 13, 93.	6.2	68
20	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
21	An actinobacteria lytic polysaccharide monoxygenase acts on both cellulose and xylan to boost biomass saccharification. <i>Biotechnology for Biofuels</i> , 2019, 12, 117.	6.2	31
22	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
23	In-solution behavior and protective potential of asparagine synthetase A from <i>Trypanosoma cruzi</i> . <i>Molecular and Biochemical Parasitology</i> , 2019, 230, 1-7.	0.5	1
24	Myosin Va interacts with the exosomal protein spermine synthase. <i>Bioscience Reports</i> , 2019, 39, .	1.1	3
25	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
26	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
27	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
28	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
29	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
30	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
31	Structural basis of exo- $\beta$ -mannanase activity in the GH2 family. <i>Journal of Biological Chemistry</i> , 2018, 293, 13636-13649.	1.6	16
32	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
33	Adenosine Kinase couples sensing of cellular potassium depletion to purine metabolism. <i>Scientific Reports</i> , 2018, 8, 11988.	1.6	8
34	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
35	The molecular motor Myosin Va interacts with the cilia-centrosomal protein RPGRI1L. <i>Scientific Reports</i> , 2017, 7, 43692.	1.6	33
36	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

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37	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
38	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
39	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
40	Bacterial and Arachnid Sphingomyelinases D: Comparison of Biophysical and Pathological Activities. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 2053-2063.	1.2	6
41	Structure and function of a novel GH8 endoglucanase from the bacterial cellulose synthase complex of <i>Raoultella ornithinolytica</i> . <i>PLoS ONE</i> , 2017, 12, e0176550.	1.1	24
42	Effects of the linker region on the structure and function of modular GH5 cellulases. <i>Scientific Reports</i> , 2016, 6, 28504.	1.6	40
43	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
44	The dark and bright sides of an enzyme: a three dimensional structure of the N-terminal domain of <i>Zophobas morio</i> luciferase-like enzyme, inferences on the biological function and origin of oxygenase/luciferase activity. <i>Photochemical and Photobiological Sciences</i> , 2016, 15, 654-665.	1.6	4
45	Crystal structure of $\beta$ -D-galactosidase from <i>Bifidobacterium bifidum</i> S17: trimeric architecture, molecular determinants of the enzymatic activity and its inhibition by $\beta$ -D-galactose. <i>FEBS Journal</i> , 2016, 283, 4097-4112.	2.2	22
46	Oligomerization as a strategy for cold adaptation: Structure and dynamics of the GH1 $\beta$ -glucosidase from <i>Exiguobacterium antarcticum</i> B7. <i>Scientific Reports</i> , 2016, 6, 23776.	1.6	57
47	A comparative structural analysis reveals distinctive features of co-factor binding and substrate specificity in plant aldo-keto reductases. <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 696-701.	1.0	6
48	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
49	Tyrosine binding and promiscuity in the arginine repressor from the pathogenic bacterium <i>Corynebacterium pseudotuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 475, 350-355.	1.0	4
50	Xylan-specific carbohydrate-binding module belonging to family 6 enhances the catalytic performance of a GH11 endo-xylanase. <i>New Biotechnology</i> , 2016, 33, 467-472.	2.4	26
51	A novel cold-adapted and glucose-tolerant GH1 $\beta$ -glucosidase from <i>Exiguobacterium antarcticum</i> B7. <i>International Journal of Biological Macromolecules</i> , 2016, 82, 375-380.	3.6	55
52	Biophysical Characterization of Alanine Aminotransferase from <i>Trypanosoma cruzi</i> . <i>Protein and Peptide Letters</i> , 2016, 23, 1118-1122.	0.4	2
53	Adaptive evolution in the toxicity of a spider's venom enzymes. <i>BMC Evolutionary Biology</i> , 2015, 15, 290.	3.2	16
54	Kinase Inhibitor Profile for Human Nek1, Nek6, and Nek7 and Analysis of the Structural Basis for Inhibitor Specificity. <i>Molecules</i> , 2015, 20, 1176-1191.	1.7	24

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55	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
56	Structure and Mechanism of Dimer $\leftrightarrow$ Monomer Transition of a Plant Poly(A)-Binding Protein upon RNA Interaction: Insights into Its Poly(A) Tail Assembly. <i>Journal of Molecular Biology</i> , 2015, 427, 2491-2506.	2.0	5
57	Enhanced xyloglucan-specific endo- $\beta$ -1,4-glucanase efficiency in an engineered CBM44-XegA chimera. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5095-5107.	1.7	25
58	Structural Basis for Xyloglucan Specificity and $\beta$ -D-Xylp(1 $\rightarrow$ 6)-Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 Td (6)- $\beta$ -D-xylofuranose 1930-1942.	1.2	23
59	The role of the C-terminus and Kpn loop in the quaternary structure stability of nucleoside diphosphate kinase from <i>Leishmania</i> parasites. <i>Journal of Structural Biology</i> , 2015, 192, 336-341.	1.3	6
60	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
61	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
62	Molecular cloning, overexpression, purification and crystallographic analysis of a GH43 $\beta$ -xylosidase from <i>Bacillus licheniformis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 962-965.	0.4	1
63	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
64	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
65	Cloning of a Novel Feruloyl Esterase from Rumen Microbial Metagenome for Substantial Yield of Mono- and Diferulic Acids from Natural Substrates. <i>Protein and Peptide Letters</i> , 2015, 22, 681-688.	0.4	3
66	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
67	Effects of High Pressure Homogenization on the Activity, Stability, Kinetics and Three-Dimensional Conformation of a Glucose Oxidase Produced by <i>Aspergillus niger</i> . <i>PLoS ONE</i> , 2014, 9, e103410.	1.1	27
68	In Vitro, In Vivo and In Silico Analysis of the Anticancer and Estrogen-like Activity of Guava Leaf Extracts. <i>Current Medicinal Chemistry</i> , 2014, 21, 2322-2330.	1.2	25
69	Molecular Mechanisms Associated with Xylan Degradation by <i>Xanthomonas</i> Plant Pathogens. <i>Journal of Biological Chemistry</i> , 2014, 289, 32186-32200.	1.6	57
70	Crystallization and preliminary X-ray diffraction studies of an $\alpha$ -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
71	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
72	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

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73	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
74	Recent advances in the understanding of brown spider venoms: From the biology of spiders to the molecular mechanisms of toxins. <i>Toxicon</i> , 2014, 83, 91-120.	0.8	116
75	Mechanistic Strategies for Catalysis Adopted by Evolutionary Distinct Family 43 Arabinanases. <i>Journal of Biological Chemistry</i> , 2014, 289, 7362-7373.	1.6	21
76	Structural basis for glucose tolerance in GH1 $\beta$ -glucosidases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1631-1639.	2.5	115
77	Analysis of peptidase activities of a cathepsin B-like (TcoCBc1) from <i>Trypanosoma congolense</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1260-1267.	1.1	1
78	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
79	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
80	Structural Insights into Functional Overlapping and Differentiation among Myosin V Motors. <i>Journal of Biological Chemistry</i> , 2013, 288, 34131-34145.	1.6	29
81	Crystal structure of Jararacussinâ€š: The highly negatively charged catalytic interface contributes to macromolecular selectivity in snake venom thrombinâ€šlike enzymes. <i>Protein Science</i> , 2013, 22, 128-132.	3.1	19
82	Assembling a xylanaseâ€šlichenase chimera through all-atom molecular dynamics simulations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1492-1500.	1.1	32
83	Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of the mitochondrial trypanothione peroxidase from <i>Leishmania braziliensis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 408-411.	0.7	5
84	A Redox 2-Cys Mechanism Regulates the Catalytic Activity of Divergent Cyclophilins $\beta$ . <i>Plant Physiology</i> , 2013, 162, 1311-1323.	2.3	26
85	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
86	Crystallization and preliminary X-ray diffraction analysis of a new xyloglucanase from <i>Xanthomonas campestris</i> pv. <i>campestris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 676-678.	0.7	0
87	Biophysical and Structural Characterization of the Recombinant Human eIF3L. <i>Protein and Peptide Letters</i> , 2013, 21, 56-62.	0.4	4
88	Protein C Activators from Snake Venom. , 2013, , 3045-3048.		0
89	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
90	Structure and Function of a Novel Cellulase 5 from Sugarcane Soil Metagenome. <i>PLoS ONE</i> , 2013, 8, e83635.	1.1	59

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91	The <i>Penicillium echinulatum</i> Secretome on Sugar Cane Bagasse. <i>PLoS ONE</i> , 2012, 7, e50571.	1.1	70
92	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.	1.7	81
93	The accessory domain changes the accessibility and molecular topography of the catalytic interface in monomeric GH39 $\beta$ -xylosidases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1339-1345.	2.5	25
94	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
95	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
96	Molecular insights into substrate specificity and thermal stability of a bacterial GH5-CBM27 endo-1,4- $\beta$ -D-mannanase. <i>Journal of Structural Biology</i> , 2012, 177, 469-476.	1.3	42
97	Functional characterization and oligomerization of a recombinant xyloglucan-specific endo- $\beta$ -1,4-glucanase (GH12) from <i>Aspergillus niveus</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 461-467.	1.1	45
98	Structural insights into selectivity and cofactor binding in snake venom l-amino acid oxidases. <i>Biochemical and Biophysical Research Communications</i> , 2012, 421, 124-128.	1.0	25
99	Correlation between catalysis and tertiary structure arrangement in an archaeal halophilic subtilase. <i>Biochimie</i> , 2012, 94, 798-805.	1.3	11
100	Two structurally discrete GH7-cellobiohydrolases compete for the same cellulosic substrate fiber. <i>Biotechnology for Biofuels</i> , 2012, 5, 21.	6.2	22
101	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
102	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
103	Batroxase, a new metalloproteinase from <i>B. atrox</i> snake venom with strong fibrinolytic activity. <i>Toxicon</i> , 2012, 60, 70-82.	0.8	85
104	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
105	The structure of a native <i>Vipera ammodytes 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
106	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
107	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
108	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

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109	The Water Effect on the Kinetics of the Bovine Liver Catalase. <i>Protein and Peptide Letters</i> , 2011, 18, 879-885.	0.4	7
110	Enzymatic toxins from snake venom: structural characterization and mechanism of catalysis. <i>FEBS Journal</i> , 2011, 278, 4544-4576.	2.2	233
111	Functional and biophysical characterization of a hyperthermostable GH51 Î±-l-arabinofuranosidase from <i>Thermotoga petrophila</i> . <i>Biotechnology Letters</i> , 2011, 33, 131-137.	1.1	19
112	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
113	Biochemical and structural characterization of a Î²-1,3-Î±-1,4-glucanase from <i>Bacillus subtilis</i> 168. <i>Process Biochemistry</i> , 2011, 46, 1202-1206.	1.8	55
114	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
115	Molecular cloning, overexpression, purification, crystallization and preliminary X-ray diffraction analysis of a purine nucleoside phosphorylase from <i>Bacillus subtilis</i> strain 168. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 618-622.	0.7	3
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	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
118	Structure of a novel thermostable GH51 Î±-l-arabinofuranosidase from <i>Thermotoga petrophila</i> RKU-1. <i>Protein Science</i> , 2011, 20, 1632-1637.	3.1	22
119	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
120	Plant Pathogenic Bacteria Utilize Biofilm Growth-associated Repressor (BigR), a Novel Winged-helix Redox Switch, to Control Hydrogen Sulfide Detoxification under Hypoxia. <i>Journal of Biological Chemistry</i> , 2011, 286, 26148-26157.	1.6	73
121	Engineering Bifunctional Laccase-Xylanase Chimeras for Improved Catalytic Performance. <i>Journal of Biological Chemistry</i> , 2011, 286, 43026-43038.	1.6	52
122	Cloning, expression, purification, crystallization and preliminary X-ray diffraction studies of the catalytic domain of a hyperthermostable endo-1,4-Î²-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
123	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
124	Structural studies of BmooMPÎ±-1, a non-hemorrhagic metalloproteinase from <i>Bothrops moojeni</i> venom. <i>Toxicon</i> , 2010, 55, 361-368.	0.8	37
125	Substrate cleavage pattern, biophysical characterization and low-resolution structure of a novel hyperthermostable arabinanase from <i>Thermotoga petrophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2010, 399, 505-511.	1.0	23
126	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



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127	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
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136	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
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