

# Mario Tyago Murakami

## List of Publications by Year in descending order

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158  
papers

4,129  
citations

101543

36  
h-index

175258

52  
g-index

161  
all docs

161  
docs citations

161  
times ranked

4862  
citing authors

#	ARTICLE	IF	CITATIONS
1	Enzymatic toxins from snake venom: structural characterization and mechanism of catalysis. FEBS Journal, 2011, 278, 4544-4576.	4.7	233
2	Recent advances in the understanding of brown spider venoms: From the biology of spiders to the molecular mechanisms of toxins. Toxicon, 2014, 83, 91-120.	1.6	116
3	Structural basis for glucose tolerance in GH1 $\beta$ -glucosidases. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1631-1639.	2.5	115
4	Inhibition of Myotoxic Activity of <i>Bothrops asper</i> Myotoxin II by the Anti-trypanosomal Drug Suramin. Journal of Molecular Biology, 2005, 350, 416-426.	4.2	106
5	Structural Basis for Metal Ion Coordination and the Catalytic Mechanism of Sphingomyelinases D. Journal of Biological Chemistry, 2005, 280, 13658-13664.	3.4	90
6	Batroxase, a new metalloproteinase from <i>B. atrox</i> snake venom with strong fibrinolytic activity. Toxicon, 2012, 60, 70-82.	1.6	85
7	Dissecting structure-function-stability relationships of a thermostable GH5-CBM3 cellulase from <i>Bacillus subtilis</i> 168. Biochemical Journal, 2012, 441, 95-104.	3.7	81
8	Plant Pathogenic Bacteria Utilize Biofilm Growth-associated Repressor (BigR), a Novel Winged-helix Redox Switch, to Control Hydrogen Sulfide Detoxification under Hypoxia. Journal of Biological Chemistry, 2011, 286, 26148-26157.	3.4	73
9	The <i>Penicillium echinulatum</i> Secretome on Sugar Cane Bagasse. PLoS ONE, 2012, 7, e50571.	2.5	70
10	Rational engineering of the <i>Trichoderma reesei</i> RUT-C30 strain into an industrially relevant platform for cellulase production. Biotechnology for Biofuels, 2020, 13, 93.	6.2	68
11	Structural insights into the catalytic mechanism of sphingomyelinases D and evolutionary relationship to glycerophosphodiester phosphodiesterases. Biochemical and Biophysical Research Communications, 2006, 342, 323-329.	2.1	63
12	Structure and Function of a Novel Cellulase 5 from Sugarcane Soil Metagenome. PLoS ONE, 2013, 8, e83635.	2.5	59
13	Interfacial surface charge and free accessibility to the PLA2-active site-like region are essential requirements for the activity of Lys49 PLA2 homologues. Toxicon, 2007, 49, 378-387.	1.6	58
14	Molecular Mechanisms Associated with Xylan Degradation by <i>Xanthomonas</i> Plant Pathogens. Journal of Biological Chemistry, 2014, 289, 32186-32200.	3.4	57
15	Oligomerization as a strategy for cold adaptation: Structure and dynamics of the GH1 $\beta$ -glucosidase from <i>Exiguobacterium antarcticum</i> B7. Scientific Reports, 2016, 6, 23776.	3.3	57
16	Crystal structure of the platelet activator convulxin, a disulfide-linked $\beta$ -4 $\beta$ 24 cyclic tetramer from the venom of <i>Crotalus durissus terrificus</i> . Biochemical and Biophysical Research Communications, 2003, 310, 478-482.	2.1	55
17	Biochemical and structural characterization of a $\beta$ -1,3 $\alpha$ -1,4-glucanase from <i>Bacillus subtilis</i> 168. Process Biochemistry, 2011, 46, 1202-1206.	3.7	55
18	A novel cold-adapted and glucose-tolerant GH1 $\beta$ -glucosidase from <i>Exiguobacterium antarcticum</i> B7. International Journal of Biological Macromolecules, 2016, 82, 375-380.	7.5	55

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19	Structural basis for branching enzyme activity of glycoside hydrolase family 57: Structure and stability studies of a novel branching enzyme from the hyperthermophilic archaeon <i>Thermococcus kodakaraensis</i> KOD1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 547-557.	2.6	54
20	Engineering Bifunctional Laccase-Xylanase Chimeras for Improved Catalytic Performance. <i>Journal of Biological Chemistry</i> , 2011, 286, 43026-43038.	3.4	52
21	Structure of a novel class II phospholipase D: Catalytic cleft is modified by a disulphide bridge. <i>Biochemical and Biophysical Research Communications</i> , 2011, 409, 622-627.	2.1	49
22	Correlation of temperature induced conformation change with optimum catalytic activity in the recombinant G/11 xylanase A from <i>Bacillus subtilis</i> strain 168 (1A1). <i>FEBS Letters</i> , 2005, 579, 6505-6510.	2.8	46
23	Isolation, characterization and biological activity of acidic phospholipase A2 isoforms from <i>Bothrops jararacussu</i> snake venom. <i>Biochimie</i> , 2003, 85, 983-991.	2.6	45
24	Functional characterization and oligomerization of a recombinant xyloglucan-specific endo- $\beta$ -1,4-glucanase (GH12) from <i>Aspergillus niger</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 461-467.	2.3	45
25	Crystal structure and biochemical characterization of the recombinant ThBgl, a GH1 $\beta$ -glucosidase overexpressed in <i>Trichoderma harzianum</i> under biomass degradation conditions. <i>Biotechnology for Biofuels</i> , 2016, 9, 71.	6.2	45
26	Thrombomodulin-independent Activation of Protein C and Specificity of Hemostatically Active Snake Venom Serine Proteinases. <i>Journal of Biological Chemistry</i> , 2005, 280, 39309-39315.	3.4	43
27	Mode of operation and low-resolution structure of a multi-domain and hyperthermophilic endo- $\beta$ -1,3-glucanase from <i>Thermotoga petrophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2011, 406, 590-594.	2.1	43
28	How pH Modulates the Dimer-Decamer Interconversion of 2-Cys Peroxiredoxins from the Prx1 Subfamily. <i>Journal of Biological Chemistry</i> , 2015, 290, 8582-8590.	3.4	43
29	Crystal structure of mature 2S albumin from <i>Moringa oleifera</i> seeds. <i>Biochemical and Biophysical Research Communications</i> , 2015, 468, 365-371.	2.1	43
30	Molecular insights into substrate specificity and thermal stability of a bacterial GH5-CBM27 endo- $\beta$ -1,4-d-mannanase. <i>Journal of Structural Biology</i> , 2012, 177, 469-476.	2.8	42
31	Effects of the linker region on the structure and function of modular GH5 cellulases. <i>Scientific Reports</i> , 2016, 6, 28504.	3.3	40
32	The repeat domain of the type III effector protein PthA shows a TPR-like structure and undergoes conformational changes upon DNA interaction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3386-3395.	2.6	39
33	A structure based model for liposome disruption and the role of catalytic activity in myotoxic phospholipase A2s. <i>Toxicon</i> , 2003, 42, 903-913.	1.6	38
34	SMase II, a new sphingomyelinase D from <i>Loxosceles laeta</i> venom gland: Molecular cloning, expression, function and structural analysis. <i>Toxicon</i> , 2009, 53, 743-753.	1.6	38
35	Molecular characterization of an acidic phospholipase A2 from <i>Bothrops pirajai</i> snake venom: synthetic C-terminal peptide identifies its antiplatelet region. <i>Archives of Toxicology</i> , 2011, 85, 1219-1233.	4.2	38
36	Structural studies of BmooMP1-L, a non-hemorrhagic metalloproteinase from <i>Bothrops moojeni</i> venom. <i>Toxicon</i> , 2010, 55, 361-368.	1.6	37

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37	Structure of the polypeptide crotamine from the Brazilian rattlesnake <i>Crotalus durissus terrificus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1958-1964.	2.5	37
38	Purification, characterization and crystallization of Jararacussin-I, a fibrinogen-clotting enzyme isolated from the venom of <i>Bothrops jararacussu</i> . <i>Toxicon</i> , 2002, 40, 1307-1312.	1.6	36
39	Intermolecular Interactions and Characterization of the Novel Factor Xa Exosite Involved in Macromolecular Recognition and Inhibition: Crystal Structure of Human Gla-domainless Factor Xa Complexed with the Anticoagulant Protein NAPc2 from the Hematophagous Nematode <i>Ancylostoma caninum</i> . <i>Journal of Molecular Biology</i> , 2007, 366, 602-610.	4.2	36
40	Thermal-induced conformational changes in the product release area drive the enzymatic activity of xylanases 10B: Crystal structure, conformational stability and functional characterization of the xylanase 10B from <i>Thermotoga petrophila</i> RKU-1. <i>Biochemical and Biophysical Research Communications</i> , 2010, 403, 214-219.	2.1	36
41	Molecular adaptability of nucleoside diphosphate kinase b from trypanosomatid parasites: stability, oligomerization and structural determinants of nucleotide binding. <i>Molecular BioSystems</i> , 2011, 7, 2189.	2.9	36
42	An engineered GH1 $\beta$ -glucosidase displays enhanced glucose tolerance and increased sugar release from lignocellulosic materials. <i>Scientific Reports</i> , 2019, 9, 4903.	3.3	36
43	Gene cloning, expression and biochemical characterization of a glucose- and xylose-stimulated $\beta$ -glucosidase from <i>Humicola insolens</i> RP86. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2014, 106, 1-10.	1.8	33
44	The molecular motor Myosin Va interacts with the cilia-centrosomal protein RPGRIP1L. <i>Scientific Reports</i> , 2017, 7, 43692.	3.3	33
45	Assembling a xylanase-lichenase chimera through all-atom molecular dynamics simulations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1492-1500.	2.3	32
46	Cloning, heterologous expression and biochemical characterization of a non-specific endoglucanase family 12 from <i>Aspergillus terreus</i> NIH2624. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 395-403.	2.3	32
47	An actinobacteria lytic polysaccharide monooxygenase acts on both cellulose and xylan to boost biomass saccharification. <i>Biotechnology for Biofuels</i> , 2019, 12, 117.	6.2	31
48	Crystal structure of an acidic platelet aggregation inhibitor and hypotensive phospholipase A2 in the monomeric and dimeric states: insights into its oligomeric state. <i>Biochemical and Biophysical Research Communications</i> , 2004, 323, 24-31.	2.1	30
49	Structural Insights into Functional Overlapping and Differentiation among Myosin V Motors. <i>Journal of Biological Chemistry</i> , 2013, 288, 34131-34145.	3.4	29
50	Development of a chimeric hemicellulase to enhance the xylose production and thermotolerance. <i>Enzyme and Microbial Technology</i> , 2015, 69, 31-37.	3.2	29
51	Active site mapping of <i>Loxosceles</i> phospholipases D: Biochemical and biological features. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2016, 1861, 970-979.	2.4	29
52	The mechanism by which a distinguishing arabinofuranosidase can cope with internal di-substitutions in arabinoxylans. <i>Biotechnology for Biofuels</i> , 2018, 11, 223.	6.2	29
53	Development and Biotechnological Application of a Novel Endoxylanase Family GH10 Identified from Sugarcane Soil Metagenome. <i>PLoS ONE</i> , 2013, 8, e70014.	2.5	28
54	The structure of a native <i>Vipera ammodytes</i> amino acid oxidase, the major component of the <i>Vipera ammodytes</i> venom, reveals dynamic active site and quaternary structure stabilization by divalent ions. <i>Molecular BioSystems</i> , 2011, 7, 379-384.	2.9	27



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73	Crystal structure of $\beta$ -galactosidase from <i>Bifidobacterium bifidum</i> S17: trimeric architecture, molecular determinants of the enzymatic activity and its inhibition by $\beta$ -galactose. <i>FEBS Journal</i> , 2016, 283, 4097-4112.	4.7	22
74	Crystal Structure and Regulation of the Citrus Pol III Repressor MAF1 by Auxin and Phosphorylation. <i>Structure</i> , 2017, 25, 1360-1370.e4.	3.3	22
75	Functional characterization and comparative analysis of two heterologous endoglucanases from diverging subfamilies of glycosyl hydrolase family 45. <i>Enzyme and Microbial Technology</i> , 2019, 120, 23-35.	3.2	22
76	Functional and structural analysis of two fibrinogen-activating enzymes isolated from the venoms of <i>Crotalus durissus terrificus</i> and <i>Crotalus durissus collilineatus</i> . <i>Acta Biochimica Et Biophysica Sinica</i> , 2009, 41, 21-29.	2.0	21
77	Molecular cloning and biochemical characterization of a myotoxin inhibitor from <i>Bothrops alternatus</i> snake plasma. <i>Biochimie</i> , 2011, 93, 583-592.	2.6	21
78	Mechanistic Strategies for Catalysis Adopted by Evolutionary Distinct Family 43 Arabinanases. <i>Journal of Biological Chemistry</i> , 2014, 289, 7362-7373.	3.4	21
79	Kinetic and mechanistic characterization of the Sphingomyelinases D from <i>Loxosceles intermedia</i> spider venom. <i>Toxicon</i> , 2006, 47, 380-386.	1.6	19
80	Functional and biophysical characterization of a hyperthermostable GH51 $\beta$ -l-arabinofuranosidase from <i>Thermotoga petrophila</i> . <i>Biotechnology Letters</i> , 2011, 33, 131-137.	2.2	19
81	Crystal structure of Jararacussin: The highly negatively charged catalytic interface contributes to macromolecular selectivity in snake venom thrombin-like enzymes. <i>Protein Science</i> , 2013, 22, 128-132.	7.6	19
82	Structural insights into $\beta$ -1,3-glucan cleavage by a glycoside hydrolase family. <i>Nature Chemical Biology</i> , 2020, 16, 920-929.	8.0	19
83	Structural studies of the <i>Trypanosoma cruzi</i> Old Yellow Enzyme: Insights into enzyme dynamics and specificity. <i>Biophysical Chemistry</i> , 2013, 184, 44-53.	2.8	18
84	Effect of dynamic high pressure on functional and structural properties of bovine serum albumin. <i>Food Research International</i> , 2017, 99, 748-754.	6.2	18
85	N-glycan Utilization by <i>Bifidobacterium</i> Gut Symbionts Involves a Specialist $\beta$ -Mannosidase. <i>Journal of Molecular Biology</i> , 2019, 431, 732-747.	4.2	18
86	Reduction of sulfenic acids by ascorbate in proteins, connecting thiol-dependent to alternative redox pathways. <i>Free Radical Biology and Medicine</i> , 2020, 156, 207-216.	2.9	18
87	Crystallographic portrayal of different conformational states of a Lys49 phospholipase A2 homologue: Insights into structural determinants for myotoxicity and dimeric configuration. <i>International Journal of Biological Macromolecules</i> , 2012, 51, 209-214.	7.5	17
88	P-I class metalloproteinase from <i>Bothrops moojeni</i> venom is a post-proline cleaving peptidase with kininogenase activity: Insights into substrate selectivity and kinetic behavior. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 545-552.	2.3	17
89	Crystal structure of a novel myotoxic Arg49 phospholipase A2 homolog (zhaoermiatoxin) from <i>Zhaoermia mangshanensis</i> snake venom: Insights into Arg49 coordination and the role of Lys122 in the polarization of the C-terminus. <i>Toxicon</i> , 2008, 51, 723-735.	1.6	16
90	Adaptive evolution in the toxicity of a spider's venom enzymes. <i>BMC Evolutionary Biology</i> , 2015, 15, 290.	3.2	16

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91	Structural basis of exo- $\beta$ -mannanase activity in the GH2 family. <i>Journal of Biological Chemistry</i> , 2018, 293, 13636-13649.	3.4	16
92	Targeting <i>Loxosceles</i> spider Sphingomyelinase D with small-molecule inhibitors as a potential therapeutic approach for loxoscelism. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2019, 34, 310-321.	5.2	16
93	Structural Insights into Substrate Binding of Brown Spider Venom Class II Phospholipases D. <i>Current Protein and Peptide Science</i> , 2015, 16, 768-774.	1.4	16
94	Structure-guided design combined with evolutionary diversity led to the discovery of the xylose-releasing exo-xylanase activity in the glycoside hydrolase family 43. <i>Biotechnology and Bioengineering</i> , 2019, 116, 734-744.	3.3	15
95	Purification, Biochemical and Functional Characterization of Miliin, a New Thiol-Dependent Serine Protease Isolated from the Latex of <i>Euphorbia milii</i> . <i>Protein and Peptide Letters</i> , 2008, 15, 724-730.	0.9	14
96	How high pressure pre-treatments affect the function and structure of hen egg-white lysozyme. <i>Innovative Food Science and Emerging Technologies</i> , 2018, 47, 195-203.	5.6	14
97	Biochemical and Structural Investigations of Bothropstoxin-II, a Myotoxic Asp49 Phospholipase A2 from <i>Bothrops jararacussu</i> Venom. <i>Protein and Peptide Letters</i> , 2008, 15, 1002-1008.	0.9	13
98	Crystallization and preliminary X-ray diffraction analysis of a class II phospholipase D from <i>Loxosceles intermedia</i> venom. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 234-236.	0.7	13
99	Expression, purification and spectroscopic analysis of an HdrC: An iron-sulfur cluster-containing protein from <i>Acidithiobacillus ferrooxidans</i> . <i>Process Biochemistry</i> , 2011, 46, 1335-1341.	3.7	13
100	Crystal structure of <i>Staphylococcus aureus</i> exfoliative toxin D-like protein: Structural basis for the high specificity of exfoliative toxins. <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 171-177.	2.1	13
101	A Novel Fungal Lipase With Methanol Tolerance and Preference for Macaw Palm Oil. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 304.	4.1	13
102	Characterization of a Hexameric Exo-Acting GH51 $\beta$ -D-Arabinofuranosidase from the Mesophilic <i>Bacillus subtilis</i> . <i>Molecular Biotechnology</i> , 2013, 55, 260-267.	2.4	12
103	Correlation between catalysis and tertiary structure arrangement in an archaeal halophilic subtilase. <i>Biochimie</i> , 2012, 94, 798-805.	2.6	11
104	A novel $\beta$ -glucosidase isolated from the microbial metagenome of Lake Poraquã (Amazon, Brazil). <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 569-579.	2.3	11
105	Luciferase isozymes from the Brazilian <i>Aspisoma lineatum</i> (Lampyridae) firefly: origin of efficient pH-sensitive lantern luciferases from fat body pH-insensitive ancestors. <i>Photochemical and Photobiological Sciences</i> , 2020, 19, 1750-1764.	2.9	11
106	Exploring the Molecular Basis for Substrate Affinity and Structural Stability in Bacterial GH39 $\beta$ -Xylosidases. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 419.	4.1	11
107	Structure of myotoxin II, a catalytically inactive Lys49 phospholipase A2 homologue from <i>Atropoides nummifer</i> venom. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 423-426.	0.7	10
108	Expression, purification, crystallization and preliminary crystallographic analysis of an endo-1,5- $\beta$ -D-arabinanase from hyperthermophilic <i>Thermotoga petrophila</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 902-905.	0.7	10

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109	Insights into Phosphate Cooperativity and Influence of Substrate Modifications on Binding and Catalysis of Hexameric Purine Nucleoside Phosphorylases. <i>PLoS ONE</i> , 2012, 7, e44282.	2.5	10
110	Pyrrrole-indolinone SU11652 targets the nucleoside diphosphate kinase from <i>Leishmania</i> parasites. <i>Biochemical and Biophysical Research Communications</i> , 2017, 488, 461-465.	2.1	10
111	Calcium and magnesium ions modulate the oligomeric state and function of mitochondrial 2-Cys peroxiredoxins in <i>Leishmania</i> parasites. <i>Journal of Biological Chemistry</i> , 2017, 292, 7023-7039.	3.4	10
112	Crystallization and preliminary X-ray crystallographic analysis of the heterodimeric crotoxin complex and the isolated subunits crotopotin and phospholipase A2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 287-290.	0.7	9
113	Spatially remote motifs cooperatively affect substrate preference of a ruminal GH26-type endo- $\beta$ -1,4-mannanase. <i>Journal of Biological Chemistry</i> , 2020, 295, 5012-5021.	3.4	9
114	Identification of a cold-adapted and metal-stimulated $\beta$ -1,4-glucanase with potential use in the extraction of bioactive compounds from plants. <i>International Journal of Biological Macromolecules</i> , 2021, 166, 190-199.	7.5	9
115	Cloning, expression, purification, crystallization and preliminary X-ray diffraction studies of the catalytic domain of a hyperthermostable endo-1,4- $\beta$ -D-mannanase from <i>Thermotoga petrophila</i> RKU-1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1078-1081.	0.7	8
116	The small heat shock proteins from <i>Acidithiobacillus ferrooxidans</i> : gene expression, phylogenetic analysis, and structural modeling. <i>BMC Microbiology</i> , 2011, 11, 259.	3.3	8
117	Crystallization and preliminary X-ray diffraction analysis of an L-amino-acid oxidase from <i>Bothrops jararacussu</i> venom. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 211-213.	0.7	8
118	Crystallization and preliminary X-ray diffraction studies of an L-amino-acid oxidase from <i>Lachesis muta</i> venom. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1556-1559.	0.8	8
119	Crystallization and preliminary X-ray diffraction analysis of a novel sphingomyelinase D from <i>Loxosceles gaucho</i> venom. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1418-1420.	0.8	8
120	Adenosine Kinase couples sensing of cellular potassium depletion to purine metabolism. <i>Scientific Reports</i> , 2018, 8, 11988.	3.3	8
121	Crystal Structure of Bucain, a Three-Fingered Toxin from the Venom of the Malayan Krait ( <i>Bungarus</i> ) Tj ETQq1 1 0.784314 rgBT /Over 0,9		
122	The Water Effect on the Kinetics of the Bovine Liver Catalase. <i>Protein and Peptide Letters</i> , 2011, 18, 879-885.	0.9	7
123	Crystal structure and biophysical characterization of the nucleoside diphosphate kinase from <i>Leishmania braziliensis</i> . <i>BMC Structural Biology</i> , 2015, 15, 2.	2.3	7
124	New contributions for industrial n-butanol fermentation: An optimized <i>Clostridium</i> strain and the use of xylooligosaccharides as a fermentation additive. <i>Biomass and Bioenergy</i> , 2018, 119, 304-313.	5.7	7
125	Unveiling the interaction between the molecular motor Myosin Vc and the small GTPase Rab3A. <i>Journal of Proteomics</i> , 2020, 212, 103549.	2.4	7
126	Voices of chemical biology. <i>Nature Chemical Biology</i> , 2021, 17, 1-4.	8.0	7

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127	Crystallization and preliminary X-ray diffraction analysis of suramin, a highly charged polysulfonated naphthylurea, complexed with a myotoxic PLA2 from <i>Bothrops asper</i> venom. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1703, 83-85.	2.3	6
128	Purification, crystallization and preliminary X-ray diffraction analysis of a class P-III metalloproteinase (BmMP-III) from the venom of <i>Bothrops moojeni</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1222-1225.	0.7	6
129	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.	2.8	6
130	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.	2.1	6
131	Bacterial and Arachnid Sphingomyelinases D: Comparison of Biophysical and Pathological Activities. <i>Journal of Cellular Biochemistry</i> , 2017, 118, 2053-2063.	2.6	6
132	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.	2.4	6
133	Crystallization and preliminary crystallographic analysis of SMase I, a sphingomyelinase from <i>Loxosceles laetaspider</i> venom. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1112-1114.	2.5	5
134	Crystallization and high-resolution X-ray diffraction data collection of an Asp49 PLA2 from <i>Bothrops jararacussu</i> venom both in the presence and absence of Ca <sup>2+</sup> ions. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1703, 79-81.	2.3	5
135	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
136	Structure and Mechanism of Dimer to 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.	4.2	5
137	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.	3.7	5
138	Crystallization and preliminary X-ray crystallographic studies of the mesophilic xylanase A from <i>Bacillus subtilis</i> 1A1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 219-220.	0.7	4
139	Biophysical and Structural Characterization of the Recombinant Human eIF3L. <i>Protein and Peptide Letters</i> , 2013, 21, 56-62.	0.9	4
140	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.	2.9	4
141	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.	2.1	4
142	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.	11.2	4
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