

João Arg Barbosa

List of Publications by Year in descending order

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74
papers

1,656
citations

331670

21
h-index

302126

39
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74
all docs

74
docs citations

74
times ranked

2537
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and biochemical analysis reveals how ferulic acid improves catalytic efficiency of <i>Humicola grisea</i> xylanase. <i>Scientific Reports</i> , 2022, 12, .	3.3	1
2	Dissecting protein domain variability in the core RNA interference machinery of five insect orders. <i>RNA Biology</i> , 2021, 18, 1653-1681.	3.1	16
3	Crystallographic approach to fragment-based hit discovery against <i>Schistosoma mansoni</i> purine nucleoside phosphorylase. <i>Biochemical Journal</i> , 2021, 478, 3655-3670.	3.7	1
4	The structure of the extended E2 DNA-binding domain of the bovine papillomavirus. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 106-112.	2.6	1
5	Functional and structural characterization of a novel GH3 Î²-glucosidase from the gut metagenome of the Brazilian Cerrado termite <i>Syntermes wheeleri</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 165, 822-834.	7.5	9
6	Head-to-Tail Cyclization after Interaction with Trypsin: A Scorpion Venom Peptide that Resembles Plant Cyclotides. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 9500-9511.	6.4	11
7	Crystal structure of thioredoxin 1 from <i>Cryptococcus neoformans</i> at 1.8Å resolution shows unexpected plasticity of the loop preceding the catalytic site. <i>Biochemistry and Biophysics Reports</i> , 2020, 21, 100724.	1.3	2
8	Crystallographic structure of a complex between trypsin and a nonapeptide derived from a Bowman-Birk inhibitor found in <i>Vigna unguiculata</i> seeds. <i>Archives of Biochemistry and Biophysics</i> , 2019, 665, 79-86.	3.0	4
9	An insight into dengue virus proteins as potential drug/vaccine targets. <i>Future Virology</i> , 2019, 14, 671-691.	1.8	0
10	Structural and functional characterisation of xylanase purified from <i>Penicillium chrysogenum</i> produced in response to raw agricultural waste. <i>International Journal of Biological Macromolecules</i> , 2019, 127, 385-395.	7.5	15
11	Self-homodimerization of an actinoporin by disulfide bridging reveals implications for their structure and pore formation. <i>Scientific Reports</i> , 2018, 8, 6614.	3.3	6
12	Structural and functional characterization of a novel lipolytic enzyme from a Brazilian Cerrado soil metagenomic library. <i>Biotechnology Letters</i> , 2018, 40, 1395-1406.	2.2	7
13	The intrinsic antimicrobial activity of citric acid-coated manganese ferrite nanoparticles is enhanced after conjugation with the antifungal peptide Cm-p5. <i>International Journal of Nanomedicine</i> , 2016, Volume 11, 3849-3857.	6.7	24
14	A Bowman-Birk inhibitor induces apoptosis in human breast adenocarcinoma through mitochondrial impairment and oxidative damage following proteasome 20S inhibition. <i>Cell Death Discovery</i> , 2016, 2, 15067.	4.7	31
15	Functional and structural characterization of a novel putative cysteine protease cell wall-modifying multi-domain enzyme selected from a microbial metagenome. <i>Scientific Reports</i> , 2016, 6, 38031.	3.3	9
16	Homology modeling and molecular dynamics provide structural insights into tospovirus nucleoprotein. <i>BMC Bioinformatics</i> , 2016, 17, 489.	2.6	11
17	The multigene families of actinoporins (part II): Strategies for heterologous production in <i>Escherichia coli</i> . <i>Toxicon</i> , 2016, 118, 64-81.	1.6	6
18	Crystal structure of VapC21 from <i>Mycobacterium tuberculosis</i> at 1.31Å resolution. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 1370-1375.	2.1	17

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19	The multigene families of actinoporins (part I): Isoforms and genetic structure. <i>Toxicon</i> , 2015, 103, 176-187.	1.6	30
20	Clavanin bacterial sepsis control using a novel methacrylate nanocarrier. <i>International Journal of Nanomedicine</i> , 2014, 9, 5055.	6.7	18
21	A specific interdomain interaction preserves the structural and binding properties of the ModA protein from the phytopathogen <i>Xanthomonas citri</i> domain interaction and transport in ModA. <i>Archives of Biochemistry and Biophysics</i> , 2013, 539, 20-30.	3.0	3
22	A Route from Darkness to Light: Emergence and Evolution of Luciferase Activity in AMP-CoA-Ligases Inferred from a Mealworm Luciferase-like Enzyme. <i>Biochemistry</i> , 2013, 52, 3963-3973.	2.5	12
23	A Redox 2-Cys Mechanism Regulates the Catalytic Activity of Divergent Cyclophilins. <i>Plant Physiology</i> , 2013, 162, 1311-1323.	4.8	26
24	Structural and Physiological Analyses of the Alkanesulphonate-Binding Protein (SsuA) of the Citrus Pathogen <i>Xanthomonas citri</i> . <i>PLoS ONE</i> , 2013, 8, e80083.	2.5	13
25	Structural characterization of the RNA chaperone Hfq from the nitrogen-fixing bacterium <i>Herbaspirillum seropedicae</i> SmR1. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 359-365.	2.3	8
26	The <i>Trypanosoma cruzi</i> Virulence Factor Oligopeptidase B (OPBTc) Assembles into an Active and Stable Dimer. <i>PLoS ONE</i> , 2012, 7, e30431.	2.5	24
27	The Kazal-type inhibitors infestins 1 and 4 differ in specificity but are similar in three-dimensional structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 695-702.	2.5	24
28	Structural and Functional Characterization of a Multifunctional Alanine-Rich Peptide Analogue from <i>Pleuronectes americanus</i> . <i>PLoS ONE</i> , 2012, 7, e47047.	2.5	35
29	Structural evolution of luciferase activity in <i>Zophobas</i> mealworm AMP/CoA-ligase (protoluciferase) through site-directed mutagenesis of the luciferin binding site. <i>Photochemical and Photobiological Sciences</i> , 2011, 10, 1226-1232.	2.9	7
30	The small nuclear ribonucleoprotein U1A interacts with NS5 from yellow fever virus. <i>Archives of Virology</i> , 2011, 156, 931-938.	2.1	6
31	Calcium effect and pH-dependence on self-association and structural stability of the <i>Apis mellifera</i> major royal jelly protein 1. <i>Apidologie</i> , 2011, 42, 252-269.	2.0	14
32	Gcn1 and Actin Binding to Yih1. <i>Journal of Biological Chemistry</i> , 2011, 286, 10341-10355.	3.4	28
33	The origin of luciferase activity in <i>Zophobas</i> mealworm AMP/CoA-ligase (protoluciferase): luciferin stereoselectivity as a switch for the oxygenase activity. <i>Photochemical and Photobiological Sciences</i> , 2010, 9, 1111-1119.	2.9	9
34	Cloning, Overexpression, Purification and Preliminary Characterization of Human Septin 8. <i>Protein Journal</i> , 2010, 29, 328-335.	1.6	2
35	Expression, purification and structural analysis of the <i>Pyrococcus abyssi</i> RNA binding protein PAB1135. <i>BMC Research Notes</i> , 2010, 3, 97.	1.4	0
36	Laboratory simulation of interplanetary ultraviolet radiation (broad spectrum) and its effects on <i>Deinococcus radiodurans</i> . <i>Planetary and Space Science</i> , 2010, 58, 1180-1187.	1.7	20

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37	A Draft of the Human Septin Interactome. PLoS ONE, 2010, 5, e13799.	2.5	78
38	Role of the triad N46, S106 and T107 and the surface charges in the determination of the acidic pH optimum of digestive lysozymes from <i>Musca domestica</i> . Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2010, 155, 387-395.	1.6	6
39	Crystallization, data collection and data processing of maltose-binding protein (MalE) from the phytopathogen <i>Xanthomonas axonopodis</i> pv. citri. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 105-107.	0.7	1
40	Crystallization and preliminary X-ray diffraction analysis of Q4DV70 from <i>Trypanosoma cruzi</i> , a hypothetical protein with a putative thioredoxin domain. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 641-644.	0.7	0
41	Purification, crystallization and preliminary crystallographic studies of SPCI-chymotrypsin complex at 2.8 Å resolution. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 914-917.	0.7	3
42	Crystallographic structure and substrate-binding interactions of the molybdate-binding protein of the phytopathogen <i>Xanthomonas axonopodis</i> pv. citri. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 393-399.	2.3	25
43	Biophysical characterization of the recombinant merozoite surface protein-3 of <i>Plasmodium vivax</i> . Biochimica Et Biophysica Acta - General Subjects, 2008, 1780, 983-988.	2.4	8
44	The crystal structure of a lysozyme c from housefly <i>Musca domestica</i> , the first structure of a digestive lysozyme. Journal of Structural Biology, 2007, 160, 83-92.	2.8	26
45	Crystal Structure of the Bowman-Birk Inhibitor from <i>Vigna unguiculata</i> Seeds in Complex with β -Trypsin at 1.55 Å Resolution and Its Structural Properties in Association with Proteinases. Biophysical Journal, 2007, 92, 1638-1650.	0.5	44
46	Crystallization and preliminary crystallographic studies of <i>Schizolobium parahyba</i> chymotrypsin inhibitor (SPCI) at 1.8 Å resolution. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 929-931.	0.7	3
47	Crystallization, data collection and processing of the chymotrypsin-BTCl-trypsin ternary complex. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 1087-1090.	0.7	5
48	Structure of <i>Xanthomonas axonopodis</i> pv. citri YaeQ reveals a new compact protein fold built around a variation of the PD(E)XK nuclease motif. Proteins: Structure, Function and Bioinformatics, 2007, 69, 644-651.	2.6	4
49	The Influence of the Loop between Residues 223-235 in Beetle Luciferase Bioluminescence Spectra: A Solvent Gate for the Active Site of pH-Sensitive Luciferases. Photochemistry and Photobiology, 2007, 84, 071018085748004-???	2.5	24
50	The acidic domain of hnRNPO (NSAP1) has structural similarity to Barstar and binds to Apobec1. Biochemical and Biophysical Research Communications, 2006, 350, 288-297.	2.1	13
51	Crystallization, data collection and phasing of the molybdate-binding protein of the phytopathogen <i>Xanthomonas axonopodis</i> pv. citri. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 289-291.	0.7	6
52	Expression, crystallization and preliminary crystallographic analysis of SufE (XAC2355) from <i>Xanthomonas axonopodis</i> pv. citri. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 268-270.	0.7	3
53	The structural molecular biology network of the State of São Paulo, Brazil. Anais Da Academia Brasileira De Ciencias, 2006, 78, 241-253.	0.8	3
54	Crystallization and preliminary X-ray diffraction analysis of NADPH-dependent thioredoxin reductase I from <i>Saccharomyces cerevisiae</i> . Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 387-390.	0.7	8

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55	Expression, purification, crystallization and preliminary X-ray analysis of YaeQ (XAC2396) from <i>Xanthomonas axonopodis</i> pv. citri. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 493-495.	0.7	4
56	pH Dependence Thermal Stability of a Chymotrypsin Inhibitor from <i>Schizolobium parahyba</i> Seeds. <i>Biophysical Journal</i> , 2005, 88, 3509-3517.	0.5	12
57	Crystallization and preliminary X-ray diffraction analysis of an oxidized state of Ohr from <i>Xylella fastidiosa</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 337-339.	2.5	6
58	Crystallization and preliminary X-ray diffraction analysis of HeLp, a heme lipoprotein from the hemolymph of the cattle tick <i>Boophilus microplus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1639-1640.	2.5	1
59	Crystallization, data collection and phasing of infestin 4, a factor Xlla inhibitor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2051-2053.	2.5	7
60	Expression and purification of a small heat shock protein from the plant pathogen <i>Xylella fastidiosa</i> . <i>Protein Expression and Purification</i> , 2004, 33, 297-303.	1.3	12
61	Structural comparison of <i>Escherichia coli</i> L-asparaginase in two monoclinic space groups. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 416-422.	2.5	39
62	Crystallization, data collection and phasing of black-eyed pea trypsin/chymotrypsin inhibitor in complex with bovine I ² -trypsin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1828-1830.	2.5	2
63	Crystal structure of a trimeric form of dephosphocoenzyme A kinase from <i>Escherichia coli</i> . <i>Protein Science</i> , 2003, 12, 327-336.	7.6	31
64	Purification and primary structure determination of Tf4, the first bioactive peptide isolated from the venom of the Brazilian scorpion <i>Tityus fasciolatus</i> . <i>Toxicon</i> , 2003, 41, 737-745.	1.6	18
65	Mechanism of action and NAD ⁺ -binding mode revealed by the crystal structure of L-histidinol dehydrogenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1859-1864.	7.1	52
66	Three-Dimensional Structure of 2-Amino-3-ketobutyrate CoA Ligase from <i>Escherichia coli</i> Complexed with a PLP ⁺ Substrate Intermediate: Inferred Reaction Mechanism. <i>Biochemistry</i> , 2001, 40, 5151-5160.	2.5	89
67	Crystallization and X-Ray Data Analysis of the Extended Dna-Binding Domain of the E2 Bovine Papillomavirus Type 1 Protein. <i>Protein and Peptide Letters</i> , 2001, 8, 323-326.	0.9	1
68	Active site modulation in the N-acetylneuraminase lyase sub-family as revealed by the structure of the inhibitor-complexed <i>Haemophilus influenzae</i> enzyme. <i>Journal of Molecular Biology</i> , 2000, 303, 405-421.	4.2	77
69	Substrate-Assisted Catalysis in Sialic Acid Aldolase. <i>Journal of Organic Chemistry</i> , 1999, 64, 945-949.	3.2	24
70	Expression in <i>Escherichia coli</i> of the Putative N-Acetylneuraminase Lyase Gene (nanA) from <i>Haemophilus influenzae</i> : Overproduction, Purification, and Crystallization. <i>Protein Expression and Purification</i> , 1998, 12, 295-304.	1.3	21
71	Structure and mechanism of a sub-family of enzymes related to N -acetylneuraminase lyase 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 1997, 266, 381-399.	4.2	103
72	Novel features of serine protease active sites and specificity pockets: sequence analysis and modelling studies of glutamate-specific endopeptidases and epidermolytic toxins. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 591-601.	2.1	35

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73	Sequence and structure of VH domain from naturally occurring camel heavy chain immunoglobulins lacking light chains. <i>Protein Engineering, Design and Selection</i> , 1994, 7, 1129-1135.	2.1	407
74	A structural model for the glutamate-specific endopeptidase from <i>Streptomyces griseus</i> that explains substrate specificity. <i>FEBS Letters</i> , 1993, 324, 45-50.	2.8	5