

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	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
2	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
3	Three-Dimensional Structure of 2-Amino-3-ketobutyrate CoA Ligase from <i>Escherichia coli</i> Complexed with a PLP ^α -Substrate Intermediate: Inferred Reaction Mechanism. <i>Biochemistry</i> , 2001, 40, 5151-5160.	2.5	89
4	A Draft of the Human Septin Interactome. <i>PLoS ONE</i> , 2010, 5, e13799.	2.5	78
5	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
6	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
7	Crystal Structure of the Bowman-Birk Inhibitor from <i>Vigna unguiculata</i> Seeds in Complex with ¹²⁵ I ² -Trypsin at 1.55 Å... Resolution and Its Structural Properties in Association with Proteinases. <i>Biophysical Journal</i> , 2007, 92, 1638-1650.	0.5	44
8	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
9	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
10	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
11	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
12	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
13	The multigene families of actinoporins (part I): Isoforms and genetic structure. <i>Toxicon</i> , 2015, 103, 176-187.	1.6	30
14	Gcn1 and Actin Binding to Yih1. <i>Journal of Biological Chemistry</i> , 2011, 286, 10341-10355.	3.4	28
15	The crystal structure of a lysozyme c from housefly <i>Musca domestica</i> , the first structure of a digestive lysozyme. <i>Journal of Structural Biology</i> , 2007, 160, 83-92.	2.8	26
16	A Redox 2-Cys Mechanism Regulates the Catalytic Activity of Divergent Cyclophilins. <i>Plant Physiology</i> , 2013, 162, 1311-1323.	4.8	26
17	Crystallographic structure and substrate-binding interactions of the molybdate-binding protein of the phytopathogen <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 393-399.	2.3	25
18	Substrate-Assisted Catalysis in Sialic Acid Aldolase. <i>Journal of Organic Chemistry</i> , 1999, 64, 945-949.	3.2	24

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19	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. <i>Photochemistry and Photobiology</i> , 2007, 84, 071018085748004-???	2.5	24
20	The Trypanosoma cruzi Virulence Factor Oligopeptidase B (OPBTc) Assembles into an Active and Stable Dimer. <i>PLoS ONE</i> , 2012, 7, e30431.	2.5	24
21	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
22	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
23	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
24	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
25	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
26	Clavanin bacterial sepsis control using a novel methacrylate nanocarrier. <i>International Journal of Nanomedicine</i> , 2014, 9, 5055.	6.7	18
27	Crystal structure of VapC21 from <i>Mycobacterium tuberculosis</i> at 1.31 Å resolution. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 1370-1375.	2.1	17
28	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
29	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
30	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
31	The acidic domain of hnRNPQ (NSAP1) has structural similarity to Barstar and binds to Apobec1. <i>Biochemical and Biophysical Research Communications</i> , 2006, 350, 288-297.	2.1	13
32	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
33	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
34	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
35	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
36	Homology modeling and molecular dynamics provide structural insights into tospovirus nucleoprotein. <i>BMC Bioinformatics</i> , 2016, 17, 489.	2.6	11

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37	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
38	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
39	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
40	Functional and structural characterization of a novel GH3 β -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
41	Crystallization and preliminary X-ray diffraction analysis of NADPH-dependent thioredoxin reductase I from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 387-390.	0.7	8
42	Biophysical characterization of the recombinant merozoite surface protein-3 of <i>Plasmodium vivax</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2008, 1780, 983-988.	2.4	8
43	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
44	Crystallization, data collection and phasing of infestin 4, a factor XIIa inhibitor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2051-2053.	2.5	7
45	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
46	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
47	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
48	Crystallization, data collection and phasing of the molybdate-binding protein of the phytopathogen <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 289-291.	0.7	6
49	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> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2010, 155, 387-395.	1.6	6
50	The small nuclear ribonucleoprotein U1A interacts with NS5 from yellow fever virus. <i>Archives of Virology</i> , 2011, 156, 931-938.	2.1	6
51	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
52	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
53	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
54	Crystallization, data collection and processing of the chymotrypsin-BTCL-trypsin ternary complex. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 1087-1090.	0.7	5

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55	Expression, purification, crystallization and preliminary X-ray analysis of YaeQ (XAC2396) from <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 493-495.	0.7	4
56	Structure of <i>Xanthomonas axonopodis</i> pv. <i>citri</i> YaeQ reveals a new compact protein fold built around a variation of the PD(E)XK nuclease motif. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 644-651.	2.6	4
57	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
58	Expression, crystallization and preliminary crystallographic analysis of SufE (XAC2355) from <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 268-270.	0.7	3
59	Crystallization and preliminary crystallographic studies of <i>Schizolobium parahybae</i> chymotrypsin inhibitor (SPCI) at 1.8 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 929-931.	0.7	3
60	Purification, crystallization and preliminary crystallographic studies of SPCI-chymotrypsin complex at 2.8 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 914-917.	0.7	3
61	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
62	The structural molecular biology network of the State of São Paulo, Brazil. <i>Anais Da Academia Brasileira De Ciencias</i> , 2006, 78, 241-253.	0.8	3
63	Crystallization, data collection and phasing of black-eyed pea trypsin/chymotrypsin inhibitor in complex with bovine β -trypsin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1828-1830.	2.5	2
64	Cloning, Overexpression, Purification and Preliminary Characterization of Human Septin 8. <i>Protein Journal</i> , 2010, 29, 328-335.	1.6	2
65	Crystal structure of thioredoxin 1 from <i>Cryptococcus neoformans</i> at 1.8 Å resolution shows unexpected plasticity of the loop preceding the catalytic site. <i>Biochemistry and Biophysics Reports</i> , 2020, 21, 100724.	1.3	2
66	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
67	Crystallization, data collection and data processing of maltose-binding protein (MalE) from the phytopathogen <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 105-107.	0.7	1
68	The structure of the extended E2 DNA-binding domain of the bovine papillomavirus 1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 106-112.	2.6	1
69	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
70	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
71	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
72	Crystallization and preliminary X-ray diffraction analysis of Q4DV70 from <i>Trypanosoma cruzi</i> , a hypothetical protein with a putative thioredoxin domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 641-644.	0.7	0

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73	Expression, purification and structural analysis of the <i>Pyrococcus abyssi</i> RNA binding protein PAB1135. BMC Research Notes, 2010, 3, 97.	1.4	0
74	An insight into dengue virus proteins as potential drug/vaccine targets. Future Virology, 2019, 14, 671-691.	1.8	0