Pedro José Barbosa Pereira

List of Publications by Year in descending order

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90 papers 3,636 citations

147801 31 h-index 52 g-index

95 all docs 95 docs citations

95 times ranked

5835 citing authors

#	Article	IF	CITATIONS
1	Structure of mycobacterial maltokinase, the missing link in the essential GlgE-pathway. Scientific Reports, 2015, 5, 8026.	3.3	675
2	Human \hat{I}^2 -tryptase is a ring-like tetramer with active sites facing a central pore. Nature, 1998, 392, 306-311.	27.8	300
3	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	14.5	141
4	Trifluoroethanethiol: An Additive for Efficient One-Pot Peptide Ligationâ^Desulfurization Chemistry. Journal of the American Chemical Society, 2014, 136, 8161-8164.	13.7	124
5	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	14.5	117
6	Data publication with the structural biology data grid supports live analysis. Nature Communications, 2016, 7, 10882.	12.8	113
7	Isolation, Cloning and Structural Characterisation of Boophilin, a Multifunctional Kunitz-Type Proteinase Inhibitor from the Cattle Tick. PLoS ONE, 2008, 3, e1624.	2.5	103
8	Structure of human biliverdin IXbeta reductase, an early fetal bilirubin IXbeta producing enzyme. Nature Structural Biology, 2001, 8, 215-220.	9.7	99
9	Caspase-1 and IL-1Î ² Processing in a Teleost Fish. PLoS ONE, 2012, 7, e50450.	2.5	90
10	Tick-derived Kunitz-type inhibitors as antihemostatic factors. Insect Biochemistry and Molecular Biology, 2009, 39, 579-595.	2.7	86
11	Tyrosine sulfation modulates activity of tick-derived thrombin inhibitors. Nature Chemistry, 2017, 9, 909-917.	13.6	85
12	Specific inhibition of insect \hat{l} ±-amylases: yellow meal worm \hat{l} ±-amylase in complex with the Amaranth \hat{l} ±-amylase inhibitor at 2.0 \hat{A} resolution. Structure, 1999, 7, 1079-1088.	3.3	84
13	The structure of the human beta II-tryptase tetramer: Fo(u)r better or worse. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 10984-10991.	7.1	81
14	Crystal structure of the human alpha-thrombin-haemadin complex: an exosite II-binding inhibitor. EMBO Journal, 2000, 19, 5650-5660.	7.8	67
15	Human Procarboxypeptidase B: Three-dimensional Structure and Implications for Thrombin-activatable Fibrinolysis Inhibitor (TAFI). Journal of Molecular Biology, 2002, 321, 537-547.	4.2	66
16	Activation of Human Prothrombin by Arginine-specific Cysteine Proteinases (Gingipains R) from Porphyromonas gingivalis *. Journal of Biological Chemistry, 2001, 276, 18984-18991.	3.4	64
17	Accelerated Protein Synthesis via One-Pot Ligation-Deselenization Chemistry. CheM, 2017, 2, 703-715.	11.7	64
18	Molecular cloning and expression analysis of sea bass (Dicentrarchus labrax L.) tumor necrosis factor- \hat{l} ± (TNF- \hat{l} ±). Fish and Shellfish Immunology, 2007, 23, 701-710.	3.6	56

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19	The 2.2 å crystal structure of human chymase in complex with succinyl-ala-ala-pro-phe-chloromethylketone: structural explanation for its dipeptidyl carboxypeptidase specificity. Journal of Molecular Biology, 1999, 286, 163-173.	4.2	53
20	Leech-Derived Thrombin Inhibitors: From Structures to Mechanisms to Clinical Applications. Journal of Medicinal Chemistry, 2010, 53, 3847-3861.	6.4	51
21	Unique thrombin inhibition mechanism by anophelin, an anticoagulant from the malaria vector. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3649-58.	7.1	49
22	The Crystal Structure of Transthyretin in Complex with Diethylstilbestrol. Journal of Biological Chemistry, 2004, 279, 53483-53490.	3.4	45
23	What a difference a cluster makes: The multifaceted roles of IscR in gene regulation and DNA recognition. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1101-1112.	2.3	45
24	Unveiling the structural basis for translational ambiguity tolerance in a human fungal pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14091-14096.	7.1	43
25	Trypanosoma cruzi macrophage infectivity potentiator has a rotamase core and a highly exposed αâ€helix. EMBO Reports, 2002, 3, 88-94.	4.5	42
26	Characterization of Binding Epitopes of CA125 Monoclonal Antibodies. Journal of Proteome Research, 2014, 13, 3349-3359.	3.7	42
27	The Apoptogenic Toxin AIP56 Is a Metalloprotease A-B Toxin that Cleaves NF-ήb P65. PLoS Pathogens, 2013, 9, e1003128.	4.7	41
28	Expression and functional characterization of boophilin, a thrombin inhibitor from Rhipicephalus (Boophilus) microplus midgut. Veterinary Parasitology, 2012, 187, 521-528.	1.8	37
29	The unique regulation of iron-sulfur cluster biogenesis in a Gram-positive bacterium. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2251-60.	7.1	37
30	Mosquito-Derived Anophelin Sulfoproteins Are Potent Antithrombotics. ACS Central Science, 2018, 4, 468-476.	11.3	37
31	New insights into the thermostability of bacterial ferredoxins: high-resolution crystal structure of the seven-iron ferredoxin from Thermus thermophilus. Journal of Biological Inorganic Chemistry, 2001, 6, 663-674.	2.6	34
32	The Crystal and Solution Structures of Glyceraldehyde-3-phosphate Dehydrogenase Reveal Different Quaternary Structures. Journal of Biological Chemistry, 2006, 281, 33433-33440.	3 . 4	34
33	Rapid assembly and profiling of an anticoagulant sulfoprotein library. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13873-13878.	7.1	33
34	SUMOylation of the brain-predominant Ataxin-3 isoform modulates its interaction with p97. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2015, 1852, 1950-1959.	3.8	32
35	The structures of cytosolic and plastid-located glutamine synthetases from <i>Medicago truncatula</i> reveal a common and dynamic architecture. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 981-993.	2.5	25
36	The X-ray Crystal Structures of Two Constitutively Active Mutants of the Escherichia coli PhoB Receiver Domain Give Insights into Activation. Journal of Molecular Biology, 2007, 366, 626-641.	4.2	23

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37	Rational Design and Characterization of D-Phe-Pro-D-Arg-Derived Direct Thrombin Inhibitors. PLoS ONE, 2012, 7, e34354.	2.5	23
38	Mycobacterium tuberculosis Glucosyl-3-Phosphoglycerate Synthase: Structure of a Key Enzyme in Methylglucose Lipopolysaccharide Biosynthesis. PLoS ONE, 2008, 3, e3748.	2.5	21
39	Molecular motion regulates the activity of the Mitochondrial Serine Protease HtrA2. Cell Death and Disease, 2017, 8, e3119-e3119.	6.3	21
40	Aprotinin binding to amyloid fibrils. FEBS Journal, 2000, 267, 2307-2311.	0.2	20
41	Bioengineered surfaces to improve the blood compatibility of biomaterials through direct thrombin inactivation. Acta Biomaterialia, 2012, 8, 4101-4110.	8.3	20
42	Functional analyses yield detailed insight into the mechanism of thrombin inhibition by the antihemostatic salivary protein cE5 from Anopheles gambiae. Journal of Biological Chemistry, 2017, 292, 12632-12642.	3.4	20
43	MIRRAGGE – Minimum Information Required for Reproducible AGGregation Experiments. Frontiers in Molecular Neuroscience, 2020, 13, 582488.	2.9	19
44	The Tick-Derived Anticoagulant Madanin Is Processed by Thrombin and Factor Xa. PLoS ONE, 2013, 8, e71866.	2.5	19
45	Crystallization and preliminary crystallographic characterization of glutamine synthetase from <i>Medicago truncatula</i> . Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 1309-1312.	0.7	18
46	Functional and structural characterization of a novel mannosylâ€3â€phosphoglycerate synthase from ⟨i⟩Rubrobacter xylanophilus⟨/i⟩ reveals its dual substrate specificity. Molecular Microbiology, 2011, 79, 76-93.	2.5	18
47	Genome Sequence of Mycobacterium hassiacum DSM 44199, a Rare Source of Heat-Stable Mycobacterial Proteins. Journal of Bacteriology, 2012, 194, 7010-7011.	2.2	17
48	Structural Basis for Host Membrane Remodeling Induced by Protein 2B of Hepatitis A Virus. Journal of Virology, 2015, 89, 3648-3658.	3.4	16
49	The structural characterization of a glucosylglycerate hydrolase provides insights into the molecular mechanism of mycobacterial recovery from nitrogen starvation. IUCrJ, 2019, 6, 572-585.	2.2	16
50	Molecular cloning and characterization of sea bass (Dicentrarchus labrax, L.) MHC class I heavy chain and \hat{l}^2 2-microglobulin. Developmental and Comparative Immunology, 2013, 39, 234-254.	2.3	15
51	Functional and structural characterization of synthetic cardosin B-derived rennet. Applied Microbiology and Biotechnology, 2017, 101, 6951-6968.	3.6	15
52	Sulfotyrosine-Mediated Recognition of Human Thrombin by a Tsetse Fly Anticoagulant Mimics Physiological Substrates. Cell Chemical Biology, 2021, 28, 26-33.e8.	5.2	15
53	The binding of 2,4-dinitrophenol to wild-type and amyloidogenic transthyretin. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 512-519.	2.5	14
54	Potent Cyclic Peptide Inhibitors of FXIIa Discovered by mRNA Display with Genetic Code Reprogramming. Journal of Medicinal Chemistry, 2021, 64, 7853-7876.	6.4	14

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55	Sea bass (Dicentrarchus labrax) invariant chain and class II major histocompatibility complex: Sequencing and structural analysis using 3D homology modelling. Molecular Immunology, 2007, 44, 3758-3776.	2.2	13
56	X-ray crystallographic studies of two transthyretin variants: further insights into amyloidogenesis. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 333-339.	2.5	12
57	Octanoylation of early intermediates of mycobacterial methylglucose lipopolysaccharides. Scientific Reports, 2015, 5, 13610.	3.3	12
58	Transporters associated with antigen processing (TAP) in sea bass (Dicentrarchus labrax, L.): Molecular cloning and characterization of TAP1 and TAP2. Developmental and Comparative Immunology, 2011, 35, 1173-1181.	2.3	10
59	Host-defense peptides AC12, DK16 and RC11 with immunomodulatory activity isolated from Hypsiboas raniceps skin secretion. Peptides, 2019, 113, 11-21.	2.4	10
60	Crystallization and preliminary crystallographic analysis of mannosyl-3-phosphoglycerate synthase fromRubrobacter xylanophilus. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 760-763.	0.7	9
61	Potent Trivalent Inhibitors of Thrombin through Hybridization of Salivary Sulfopeptides from Hematophagous Arthropods. Angewandte Chemie - International Edition, 2021, 60, 5348-5356.	13.8	9
62	Molecular cloning and characterization of sea bass (Dicentrarchus labrax, L.) calreticulin. Fish and Shellfish Immunology, 2013, 34, 1611-1618.	3.6	8
63	Ser or Leu: structural snapshots of mistranslation in Candida albicans. Frontiers in Molecular Biosciences, 2014, 1, 27.	3.5	8
64	Selective albumin-binding surfaces modified with a thrombin-inhibiting peptide. Acta Biomaterialia, 2014, 10, 1227-1237.	8.3	8
65	Two thioredoxin-superfamily members from sea bass (Dicentrarchus labrax, L.): Characterization of PDI (PDIA1) and ERp57 (PDIA3). Fish and Shellfish Immunology, 2013, 35, 1163-1175.	3.6	7
66	In silico and crystallographic studies identify key structural features of biliverdin $ X ^2$ reductase inhibitors having nanomolar potency. Journal of Biological Chemistry, 2018, 293, 5431-5446.	3.4	7
67	Biosynthesis of mycobacterial methylmannose polysaccharides requires a unique 1 - $\langle i \rangle O \langle i \rangle$ -methyltransferase specific for 3 - $\langle i \rangle O \langle i \rangle$ -methylated mannosides. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 835-844.	7.1	7
68	Protein crystals as a key for deciphering macromolecular crowding effects on biological reactions. Physical Chemistry Chemical Physics, 2020, 22, 16143-16149.	2.8	7
69	A simple linearization method unveils hidden enzymatic assay interferences. Biophysical Chemistry, 2019, 252, 106193.	2.8	6
70	Genetic code ambiguity modulates the activity of a C. albicans MAP kinase linked to cell wall remodeling. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 654-661.	2.3	6
71	Chemical synthesis of a haemathrin sulfoprotein library reveals enhanced thrombin inhibition following tyrosine sulfation. RSC Chemical Biology, 2020, 1, 379-384.	4.1	6
72	Biochemical characterization of biliverdins $IX\hat{I}^2/\hat{I}$ generated by a selective heme oxygenase. Biochemical Journal, 2020, 477, 601-614.	3.7	6

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73	Purification, crystallization and preliminary X-ray diffraction analysis of the seryl-tRNA synthetase fromCandida albicans. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 153-156.	0.7	5
74	Crystallization and preliminary crystallographic characterization of three peptidic inhibitors in complex with \hat{l}_{\pm} -thrombin. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 54-58.	0.7	4
75	High-resolution structure of a Kazal-type serine protease inhibitor from the dengue vector <i>Aedes aegypti</i> . Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 469-475.	0.8	4
76	interferENZY: A Web-Based Tool for Enzymatic Assay Validation and Standardized Kinetic Analysis. Journal of Molecular Biology, 2021, 433, 166613.	4.2	4
77	The 2.2 A crystal structure of human chymase in complex with Succinyl-Ala-Ala-Pro-Phe-Chloromethylketone: structural explanation for its dipeptidyl carboxypeptidase specificity. Journal of Molecular Biology, 1999, 287, 817.	4.2	3
78	Cloning, purification and preliminary crystallographic studies of the 2AB protein from hepatitis A virus. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1224-1227.	0.7	3
79	Molecular cloning and characterization of sea bass (Dicentrarchus labrax, L.) Tapasin. Fish and Shellfish Immunology, 2012, 32, 110-120.	3.6	3
80	Crystallization and preliminary crystallographic characterization of the N-terminal Kunitz domain of boophilin. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 436-439.	0.7	3
81	Synthesis and evaluation of peptidic thrombin inhibitors bearing acid-stable sulfotyrosine analogues. Chemical Communications, 2021, 57, 10923-10926.	4.1	3
82	A Secreted NlpC/P60 Endopeptidase from Photobacterium damselae subsp. <i>piscicida</i> Cleaves the Peptidoglycan of Potentially Competing Bacteria. MSphere, 2021, 6, .	2.9	3
83	Structure and Function of Human Chymase. , 2000, , 275-292e.		3
84	Molecular Fingerprints for a Novel Enzyme Family in <i>Actinobacteria</i> with Glucosamine Kinase Activity. MBio, 2019, 10, .	4.1	2
85	Major Improvements in Robustness and Efficiency during the Screening of Novel Enzyme Effectors by the 3-Point Kinetics Assay. SLAS Discovery, 2021, 26, 373-382.	2.7	2
86	Tyrosine- $\langle i \rangle$ O $\langle i \rangle$ -sulfation is a widespread affinity enhancer among thrombin interactors. Biochemical Society Transactions, 2022, 50, 387-401.	3.4	2
87	In-house UV radiation-damage-induced phasing of selenomethionine-labeled protein structures. Journal of Structural Biology, 2013, 181, 89-94.	2.8	1
88	Production, crystallization and structure determination of a mycobacterial glucosylglycerate hydrolase. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 536-540.	0.8	1
89	Rücktitelbild: Potent Trivalent Inhibitors of Thrombin through Hybridization of Salivary Sulfopeptides from Hematophagous Arthropods (Angew. Chem. 10/2021). Angewandte Chemie, 2021, 133, 5632-5632.	2.0	0
90	Potent Trivalent Inhibitors of Thrombin through Hybridization of Salivary Sulfopeptides from Hematophagous Arthropods. Angewandte Chemie, 2021, 133, 5408-5416.	2.0	0