

Pedro JosÃ© Barbosa Pereira

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

3,636
citations

147801

31
h-index

175258

52
g-index

95
all docs

95
docs citations

95
times ranked

5835
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487. | 14.5 | 117 |
| 2 | Tyrosine-O-sulfation is a widespread affinity enhancer among thrombin interactors. <i>Biochemical Society Transactions</i> , 2022, 50, 387-401. | 3.4 | 2 |
| 3 | interferENZY: A Web-Based Tool for Enzymatic Assay Validation and Standardized Kinetic Analysis. <i>Journal of Molecular Biology</i> , 2021, 433, 166613. | 4.2 | 4 |
| 4 | Major Improvements in Robustness and Efficiency during the Screening of Novel Enzyme Effectors by the 3-Point Kinetics Assay. <i>SLAS Discovery</i> , 2021, 26, 373-382. | 2.7 | 2 |
| 5 | Potent Trivalent Inhibitors of Thrombin through Hybridization of Salivary Sulfopeptides from Hematophagous Arthropods. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 5348-5356. | 13.8 | 9 |
| 6 | Sulfotyrosine-Mediated Recognition of Human Thrombin by a Tsetse Fly Anticoagulant Mimics Physiological Substrates. <i>Cell Chemical Biology</i> , 2021, 28, 26-33.e8. | 5.2 | 15 |
| 7 | Synthesis and evaluation of peptidic thrombin inhibitors bearing acid-stable sulfotyrosine analogues. <i>Chemical Communications</i> , 2021, 57, 10923-10926. | 4.1 | 3 |
| 8 | A Secreted NlpC/P60 Endopeptidase from <i>Photobacterium damsela</i> subsp. <i>piscicida</i> Cleaves the Peptidoglycan of Potentially Competing Bacteria. <i>MSphere</i> , 2021, 6, . | 2.9 | 3 |
| 9 | R“cktitelbild: Potent Trivalent Inhibitors of Thrombin through Hybridization of Salivary Sulfopeptides from Hematophagous Arthropods (<i>Angew. Chem.</i> 10/2021). <i>Angewandte Chemie</i> , 2021, 133, 5632-5632. | 2.0 | 0 |
| 10 | Potent Cyclic Peptide Inhibitors of FXIIa Discovered by mRNA Display with Genetic Code Reprogramming. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 7853-7876. | 6.4 | 14 |
| 11 | Potent Trivalent Inhibitors of Thrombin through Hybridization of Salivary Sulfopeptides from Hematophagous Arthropods. <i>Angewandte Chemie</i> , 2021, 133, 5408-5416. | 2.0 | 0 |
| 12 | DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276. | 14.5 | 141 |
| 13 | MIRRAGGE " Minimum Information Required for Reproducible AGGregation Experiments. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 582488. | 2.9 | 19 |
| 14 | Protein crystals as a key for deciphering macromolecular crowding effects on biological reactions. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 16143-16149. | 2.8 | 7 |
| 15 | Chemical synthesis of a haemathrin sulfoprotein library reveals enhanced thrombin inhibition following tyrosine sulfation. <i>RSC Chemical Biology</i> , 2020, 1, 379-384. | 4.1 | 6 |
| 16 | Biochemical characterization of biliverdins IX ^{2/1} generated by a selective heme oxygenase. <i>Biochemical Journal</i> , 2020, 477, 601-614. | 3.7 | 6 |
| 17 | Rapid assembly and profiling of an anticoagulant sulfoprotein library. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13873-13878. | 7.1 | 33 |
| 18 | A simple linearization method unveils hidden enzymatic assay interferences. <i>Biophysical Chemistry</i> , 2019, 252, 106193. | 2.8 | 6 |

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|----|--|------|-----------|
| 19 | Molecular Fingerprints for a Novel Enzyme Family in <i>Actinobacteria</i> with Glucosamine Kinase Activity. <i>MBio</i> , 2019, 10, . | 4.1 | 2 |
| 20 | Genetic code ambiguity modulates the activity of a <i>C. albicans</i> MAP kinase linked to cell wall remodeling. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 654-661. | 2.3 | 6 |
| 21 | Biosynthesis of mycobacterial methylmannose polysaccharides requires a unique 1-O-methyltransferase specific for 3-O-methylated mannosides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 835-844. | 7.1 | 7 |
| 22 | Host-defense peptides AC12, DK16 and RC11 with immunomodulatory activity isolated from <i>Hypsiboas raniceps</i> skin secretion. <i>Peptides</i> , 2019, 113, 11-21. | 2.4 | 10 |
| 23 | The structural characterization of a glucosylglycerate hydrolase provides insights into the molecular mechanism of mycobacterial recovery from nitrogen starvation. <i>IUCr</i> , 2019, 6, 572-585. | 2.2 | 16 |
| 24 | Mosquito-Derived Anophelin Sulfoproteins Are Potent Antithrombotics. <i>ACS Central Science</i> , 2018, 4, 468-476. | 11.3 | 37 |
| 25 | In silico and crystallographic studies identify key structural features of biliverdin IX ^β reductase inhibitors having nanomolar potency. <i>Journal of Biological Chemistry</i> , 2018, 293, 5431-5446. | 3.4 | 7 |
| 26 | Functional analyses yield detailed insight into the mechanism of thrombin inhibition by the antihemostatic salivary protein cE5 from <i>Anopheles gambiae</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 12632-12642. | 3.4 | 20 |
| 27 | Accelerated Protein Synthesis via One-Pot Ligation-Deselenization Chemistry. <i>CheM</i> , 2017, 2, 703-715. | 11.7 | 64 |
| 28 | Tyrosine sulfation modulates activity of tick-derived thrombin inhibitors. <i>Nature Chemistry</i> , 2017, 9, 909-917. | 13.6 | 85 |
| 29 | Production, crystallization and structure determination of a mycobacterial glucosylglycerate hydrolase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 536-540. | 0.8 | 1 |
| 30 | Functional and structural characterization of synthetic cardosin B-derived rennet. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 6951-6968. | 3.6 | 15 |
| 31 | High-resolution structure of a Kazal-type serine protease inhibitor from the dengue vector <i>Aedes aegypti</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 469-475. | 0.8 | 4 |
| 32 | Molecular motion regulates the activity of the Mitochondrial Serine Protease HtrA2. <i>Cell Death and Disease</i> , 2017, 8, e31119-e31119. | 6.3 | 21 |
| 33 | Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , 2016, 7, 10882. | 12.8 | 113 |
| 34 | Octanoylation of early intermediates of mycobacterial methylglucose lipopolysaccharides. <i>Scientific Reports</i> , 2015, 5, 13610. | 3.3 | 12 |
| 35 | SUMOylation of the brain-predominant Ataxin-3 isoform modulates its interaction with p97. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2015, 1852, 1950-1959. | 3.8 | 32 |
| 36 | What a difference a cluster makes: The multifaceted roles of IscR in gene regulation and DNA recognition. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1101-1112. | 2.3 | 45 |

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|----|--|------|-----------|
| 37 | Structural Basis for Host Membrane Remodeling Induced by Protein 2B of Hepatitis A Virus. <i>Journal of Virology</i> , 2015, 89, 3648-3658. | 3.4 | 16 |
| 38 | Structure of mycobacterial maltokinase, the missing link in the essential GlgE-pathway. <i>Scientific Reports</i> , 2015, 5, 8026. | 3.3 | 675 |
| 39 | Ser or Leu: structural snapshots of mistranslation in <i>Candida albicans</i> . <i>Frontiers in Molecular Biosciences</i> , 2014, 1, 27. | 3.5 | 8 |
| 40 | The unique regulation of iron-sulfur cluster biogenesis in a Gram-positive bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2251-60. | 7.1 | 37 |
| 41 | Trifluoroethanethiol: An Additive for Efficient One-Pot Peptide Ligation~Desulfurization Chemistry. <i>Journal of the American Chemical Society</i> , 2014, 136, 8161-8164. | 13.7 | 124 |
| 42 | Selective albumin-binding surfaces modified with a thrombin-inhibiting peptide. <i>Acta Biomaterialia</i> , 2014, 10, 1227-1237. | 8.3 | 8 |
| 43 | Characterization of Binding Epitopes of CA125 Monoclonal Antibodies. <i>Journal of Proteome Research</i> , 2014, 13, 3349-3359. | 3.7 | 42 |
| 44 | The structures of cytosolic and plastid-located glutamine synthetases from <i>Medicago truncatula</i> reveal a common and dynamic architecture. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 981-993. | 2.5 | 25 |
| 45 | Molecular cloning and characterization of sea bass (<i>Dicentrarchus labrax</i> , L.) calreticulin. <i>Fish and Shellfish Immunology</i> , 2013, 34, 1611-1618. | 3.6 | 8 |
| 46 | Two thioredoxin-superfamily members from sea bass (<i>Dicentrarchus labrax</i> , L.): Characterization of PDI (PDIA1) and ERp57 (PDIA3). <i>Fish and Shellfish Immunology</i> , 2013, 35, 1163-1175. | 3.6 | 7 |
| 47 | In-house UV radiation-damage-induced phasing of selenomethionine-labeled protein structures. <i>Journal of Structural Biology</i> , 2013, 181, 89-94. | 2.8 | 1 |
| 48 | Molecular cloning and characterization of sea bass (<i>Dicentrarchus labrax</i> , L.) MHC class I heavy chain and β 2-microglobulin. <i>Developmental and Comparative Immunology</i> , 2013, 39, 234-254. | 2.3 | 15 |
| 49 | The Apoptogenic Toxin AIP56 Is a Metalloprotease A-B Toxin that Cleaves NF- κ B P65. <i>PLoS Pathogens</i> , 2013, 9, e1003128. | 4.7 | 41 |
| 50 | The Tick-Derived Anticoagulant Madanin Is Processed by Thrombin and Factor Xa. <i>PLoS ONE</i> , 2013, 8, e71866. | 2.5 | 19 |
| 51 | Genome Sequence of <i>Mycobacterium hassiacum</i> DSM 44199, a Rare Source of Heat-Stable Mycobacterial Proteins. <i>Journal of Bacteriology</i> , 2012, 194, 7010-7011. | 2.2 | 17 |
| 52 | Unique thrombin inhibition mechanism by anophelin, an anticoagulant from the malaria vector. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3649-58. | 7.1 | 49 |
| 53 | Molecular cloning and characterization of sea bass (<i>Dicentrarchus labrax</i> , L.) Tapasin. <i>Fish and Shellfish Immunology</i> , 2012, 32, 110-120. | 3.6 | 3 |
| 54 | Bioengineered surfaces to improve the blood compatibility of biomaterials through direct thrombin inactivation. <i>Acta Biomaterialia</i> , 2012, 8, 4101-4110. | 8.3 | 20 |

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|----|--|-----|-----------|
| 55 | Expression and functional characterization of boophilin, a thrombin inhibitor from <i>Rhipicephalus (Boophilus) microplus</i> midgut. <i>Veterinary Parasitology</i> , 2012, 187, 521-528. | 1.8 | 37 |
| 56 | Crystallization and preliminary crystallographic characterization of the N-terminal Kunitz domain of boophilin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 436-439. | 0.7 | 3 |
| 57 | Rational Design and Characterization of D-Phe-Pro-D-Arg-Derived Direct Thrombin Inhibitors. <i>PLoS ONE</i> , 2012, 7, e34354. | 2.5 | 23 |
| 58 | Caspase-1 and IL-1 β Processing in a Teleost Fish. <i>PLoS ONE</i> , 2012, 7, e50450. | 2.5 | 90 |
| 59 | Transporters associated with antigen processing (TAP) in sea bass (<i>Dicentrarchus labrax</i> , L.): Molecular cloning and characterization of TAP1 and TAP2. <i>Developmental and Comparative Immunology</i> , 2011, 35, 1173-1181. | 2.3 | 10 |
| 60 | Functional and structural characterization of a novel mannosyl-3-phosphoglycerate synthase from <i>Rubrobacter xylanophilus</i> reveals its dual substrate specificity. <i>Molecular Microbiology</i> , 2011, 79, 76-93. | 2.5 | 18 |
| 61 | Crystallization and preliminary crystallographic characterization of three peptidic inhibitors in complex with β -thrombin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 54-58. | 0.7 | 4 |
| 62 | Purification, crystallization and preliminary X-ray diffraction analysis of the seryl-tRNA synthetase from <i>Candida albicans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 153-156. | 0.7 | 5 |
| 63 | Cloning, purification and preliminary crystallographic studies of the 2AB protein from hepatitis A virus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1224-1227. | 0.7 | 3 |
| 64 | Unveiling the structural basis for translational ambiguity tolerance in a human fungal pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14091-14096. | 7.1 | 43 |
| 65 | Leech-Derived Thrombin Inhibitors: From Structures to Mechanisms to Clinical Applications. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 3847-3861. | 6.4 | 51 |
| 66 | Crystallization and preliminary crystallographic characterization of glutamine synthetase from <i>Medicago truncatula</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 1309-1312. | 0.7 | 18 |
| 67 | Tick-derived Kunitz-type inhibitors as antihemostatic factors. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 579-595. | 2.7 | 86 |
| 68 | Crystallization and preliminary crystallographic analysis of mannosyl-3-phosphoglycerate synthase from <i>Rubrobacter xylanophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 760-763. | 0.7 | 9 |
| 69 | <i>Mycobacterium tuberculosis</i> Glucosyl-3-Phosphoglycerate Synthase: Structure of a Key Enzyme in Methylglucose Lipopolysaccharide Biosynthesis. <i>PLoS ONE</i> , 2008, 3, e3748. | 2.5 | 21 |
| 70 | Isolation, Cloning and Structural Characterisation of Boophilin, a Multifunctional Kunitz-Type Proteinase Inhibitor from the Cattle Tick. <i>PLoS ONE</i> , 2008, 3, e1624. | 2.5 | 103 |
| 71 | Molecular cloning and expression analysis of sea bass (<i>Dicentrarchus labrax</i> L.) tumor necrosis factor- β (TNF- β). <i>Fish and Shellfish Immunology</i> , 2007, 23, 701-710. | 3.6 | 56 |
| 72 | The X-ray Crystal Structures of Two Constitutively Active Mutants of the <i>Escherichia coli</i> PhoB Receiver Domain Give Insights into Activation. <i>Journal of Molecular Biology</i> , 2007, 366, 626-641. | 4.2 | 23 |

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|----|---|------|-----------|
| 73 | Sea bass (<i>Dicentrarchus labrax</i>) invariant chain and class II major histocompatibility complex: Sequencing and structural analysis using 3D homology modelling. <i>Molecular Immunology</i> , 2007, 44, 3758-3776. | 2.2 | 13 |
| 74 | The binding of 2,4-dinitrophenol to wild-type and amyloidogenic transthyretin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 512-519. | 2.5 | 14 |
| 75 | The Crystal and Solution Structures of Glyceraldehyde-3-phosphate Dehydrogenase Reveal Different Quaternary Structures. <i>Journal of Biological Chemistry</i> , 2006, 281, 33433-33440. | 3.4 | 34 |
| 76 | X-ray crystallographic studies of two transthyretin variants: further insights into amyloidogenesis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 333-339. | 2.5 | 12 |
| 77 | The Crystal Structure of Transthyretin in Complex with Diethylstilbestrol. <i>Journal of Biological Chemistry</i> , 2004, 279, 53483-53490. | 3.4 | 45 |
| 78 | Human Procarboxypeptidase B: Three-dimensional Structure and Implications for Thrombin-activatable Fibrinolysis Inhibitor (TAFI). <i>Journal of Molecular Biology</i> , 2002, 321, 537-547. | 4.2 | 66 |
| 79 | <i>Trypanosoma cruzi</i> macrophage infectivity potentiator has a rotamase core and a highly exposed α -helix. <i>EMBO Reports</i> , 2002, 3, 88-94. | 4.5 | 42 |
| 80 | New insights into the thermostability of bacterial ferredoxins: high-resolution crystal structure of the seven-iron ferredoxin from <i>Thermus thermophilus</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2001, 6, 663-674. | 2.6 | 34 |
| 81 | Structure of human biliverdin IXbeta reductase, an early fetal bilirubin IXbeta producing enzyme. <i>Nature Structural Biology</i> , 2001, 8, 215-220. | 9.7 | 99 |
| 82 | Activation of Human Prothrombin by Arginine-specific Cysteine Proteinases (Gingipains R) from <i>Porphyromonas gingivalis</i> *. <i>Journal of Biological Chemistry</i> , 2001, 276, 18984-18991. | 3.4 | 64 |
| 83 | Aprotinin binding to amyloid fibrils. <i>FEBS Journal</i> , 2000, 267, 2307-2311. | 0.2 | 20 |
| 84 | Crystal structure of the human alpha-thrombin-haemadin complex: an exosite II-binding inhibitor. <i>EMBO Journal</i> , 2000, 19, 5650-5660. | 7.8 | 67 |
| 85 | Structure and Function of Human Chymase. , 2000, , 275-292e. | | 3 |
| 86 | The structure of the human beta II-tryptase tetramer: Fo(u)r better or worse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 10984-10991. | 7.1 | 81 |
| 87 | Specific inhibition of insect α -amylases: yellow meal worm α -amylase in complex with the Amaranth α -amylase inhibitor at 2.0 Å... resolution. <i>Structure</i> , 1999, 7, 1079-1088. | 3.3 | 84 |
| 88 | 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. <i>Journal of Molecular Biology</i> , 1999, 286, 163-173. | 4.2 | 53 |
| 89 | 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. <i>Journal of Molecular Biology</i> , 1999, 287, 817. | 4.2 | 3 |
| 90 | Human β -tryptase is a ring-like tetramer with active sites facing a central pore. <i>Nature</i> , 1998, 392, 306-311. | 27.8 | 300 |