

# Sandra Macedo-Ribeiro

## List of Publications by Year in descending order

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84  
papers

4,175  
citations

147566  
31  
h-index

149479  
56  
g-index

89  
all docs

89  
docs citations

89  
times ranked

6458  
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.	6.5	117
2	A Robust Assay to Monitor Ataxin-3 Amyloid Fibril Assembly. <i>Cells</i> , 2022, 11, 1969.	1.8	3
3	The Repeating, Modular Architecture of the HtrA Proteases. <i>Biomolecules</i> , 2022, 12, 793.	1.8	1
4	interferENZY: A Web-Based Tool for Enzymatic Assay Validation and Standardized Kinetic Analysis. <i>Journal of Molecular Biology</i> , 2021, 433, 166613.	2.0	4
5	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.	1.4	2
6	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
7	CLASP2 binding to curved microtubule tips promotes flux and stabilizes kinetochore attachments. <i>Journal of Cell Biology</i> , 2020, 219, jcb.201905080.	2.3	20
8	Accurate prediction of protein beta-aggregation with generalized statistical potentials. <i>Bioinformatics</i> , 2020, 36, 2076-2081.	1.8	20
9	MIRRAGGE “ Minimum Information Required for Reproducible AGGregation Experiments. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 582488.	1.4	19
10	Protein crystals as a key for deciphering macromolecular crowding effects on biological reactions. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 16143-16149.	1.3	7
11	Pushing myelination: developmental regulation of myosin expression drives oligodendrocyte morphological differentiation. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	8
12	A genuine mycobacterial thermophile: <i>Mycobacterium hassiacum</i> growth, survival and GpgS stability at near-pasteurization temperatures. <i>Microbiology (United Kingdom)</i> , 2020, 166, 474-483.	0.7	6
13	Chemical Kinetic Strategies for High-Throughput Screening of Protein Aggregation Modulators. <i>Chemistry - an Asian Journal</i> , 2019, 14, 500-508.	1.7	13
14	Molecular Fingerprints for a Novel Enzyme Family in <i>Actinobacteria</i> with Glucosamine Kinase Activity. <i>MBio</i> , 2019, 10, .	1.8	2
15	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.	1.1	6
16	Biosynthesis of mycobacterial methylmannose polysaccharides requires a unique 1- <i>O</i> -methyltransferase specific for 3- <i>O</i> -methylated mannosides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 835-844.	3.3	7
17	Anti-TTR Nanobodies Allow the Identification of TTR Neuritogenic Epitope Associated with TTR-Megalín Neurotrophic Activities. <i>ACS Chemical Neuroscience</i> , 2019, 10, 704-715.	1.7	5
18	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.	1.0	16

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19	Polyglutamine-Independent Features in Ataxin-3 Aggregation and Pathogenesis of Machado-Joseph Disease. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1049, 275-288.	0.8	15
20	Polyglutamine expansion diseases: More than simple repeats. <i>Journal of Structural Biology</i> , 2018, 201, 139-154.	1.3	29
21	Probing the Occurrence of Soluble Oligomers through Amyloid Aggregation Scaling Laws. <i>Biomolecules</i> , 2018, 8, 108.	1.8	10
22	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	6.5	242
23	Distribution of Amyloid-Like and Oligomeric Species from Protein Aggregation Kinetics. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 14042-14045.	7.2	15
24	Distribution of Amyloid-Like and Oligomeric Species from Protein Aggregation Kinetics. <i>Angewandte Chemie</i> , 2017, 129, 14230-14233.	1.6	1
25	Molecular motion regulates the activity of the Mitochondrial Serine Protease HtrA2. <i>Cell Death and Disease</i> , 2017, 8, e3119-e3119.	2.7	21
26	Severe neonatal jaundice due to a <i>de novo</i> glucose-6-phosphate dehydrogenase deficient mutation. <i>International Journal of Laboratory Hematology</i> , 2016, 38, e27-9.	0.7	3
27	Disclosing the essentiality of ribose-5-phosphate isomerase B in Trypanosomatids. <i>Scientific Reports</i> , 2016, 6, 26937.	1.6	27
28	Biophysical characterization of laforin-carbohydrate interaction. <i>Biochemical Journal</i> , 2016, 473, 335-345.	1.7	10
29	Ataxin-3 phosphorylation decreases neuronal defects in spinocerebellar ataxia type 3 models. <i>Journal of Cell Biology</i> , 2016, 212, 465-480.	2.3	35
30	Leishmania infantum Asparagine Synthetase A Is Dispensable for Parasites Survival and Infectivity. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004365.	1.3	11
31	Octanoylation of early intermediates of mycobacterial methylglucose lipopolysaccharides. <i>Scientific Reports</i> , 2015, 5, 13610.	1.6	12
32	Ribose 5-Phosphate Isomerase B Knockdown Compromises Trypanosoma brucei Bloodstream Form Infectivity. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e3430.	1.3	19
33	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.	1.8	32
34	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.	1.1	45
35	Structural Basis for Host Membrane Remodeling Induced by Protein 2B of Hepatitis A Virus. <i>Journal of Virology</i> , 2015, 89, 3648-3658.	1.5	16
36	Structure of mycobacterial maltokinase, the missing link in the essential GlgE-pathway. <i>Scientific Reports</i> , 2015, 5, 8026.	1.6	675

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37	Examination of Ataxin-3 (atx-3) Aggregation by Structural Mass Spectrometry Techniques: A Rationale for Expedited Aggregation upon Polyglutamine (polyQ) Expansion*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1241-1253.	2.5	33
38	Molecular and computational analyses of genes involved in mannose 6-phosphate independent trafficking. <i>Clinical Genetics</i> , 2015, 88, 190-194.	1.0	4
39	Ser or Leu: structural snapshots of mistranslation in <i>Candida albicans</i> . <i>Frontiers in Molecular Biosciences</i> , 2014, 1, 27.	1.6	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.	3.3	37
41	A tale of a tail: Structural insights into the conformational properties of the polyglutamine protein ataxin-3. <i>International Journal of Mass Spectrometry</i> , 2013, 345-347, 63-70.	0.7	15
42	BIOCHEMICAL AND BIOPHYSICAL CHARACTERIZATION OF RECOMBINANT YEAST PROTEASOME MATURATION FACTOR UMP1. <i>Computational and Structural Biotechnology Journal</i> , 2013, 7, e201304006.	1.9	20
43	Knockdown of Asparagine Synthetase A Renders <i>Trypanosoma brucei</i> Auxotrophic to Asparagine. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2578.	1.3	15
44	The Apoptogenic Toxin AIP56 Is a Metalloprotease A-B Toxin that Cleaves NF- $\kappa$ B P65. <i>PLoS Pathogens</i> , 2013, 9, e1003128.	2.1	41
45	Trinucleotide Repeats: A Structural Perspective. <i>Frontiers in Neurology</i> , 2013, 4, 76.	1.1	49
46	The <i>Drosophila melanogaster</i> methuselah Gene: A Novel Gene with Ancient Functions. <i>PLoS ONE</i> , 2013, 8, e63747.	1.1	23
47	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.	1.0	17
48	Cdk1 and Plk1 mediate a CLASP2 phospho-switch that stabilizes kinetochore-microtubule attachments. <i>Journal of Cell Biology</i> , 2012, 199, 285-301.	2.3	80
49	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.	3.3	49
50	Lysosomal multienzymatic complex-related diseases: a genetic study among Portuguese patients. <i>Clinical Genetics</i> , 2012, 81, 379-393.	1.0	14
51	Polyglutamine diseases: The special case of ataxin-3 and Machado-Joseph disease. <i>Progress in Neurobiology</i> , 2011, 95, 26-48.	2.8	114
52	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.	1.2	18
53	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
54	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

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55	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.	3.3	43
56	Ataxin-3 Plays a Role in Mouse Myogenic Differentiation through Regulation of Integrin Subunit Levels. <i>PLoS ONE</i> , 2010, 5, e11728.	1.1	25
57	Leech-Derived Thrombin Inhibitors: From Structures to Mechanisms to Clinical Applications. <i>Journal of Medicinal Chemistry</i> , 2010, 53, 3847-3861.	2.9	51
58	Tick-derived Kunitz-type inhibitors as antihemostatic factors. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 579-595.	1.2	86
59	Nucleocytoplasmic Shuttling Activity of Ataxin-3. <i>PLoS ONE</i> , 2009, 4, e5834.	1.1	40
60	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
61	Identification of the mycobacterial glucosyl-3-phosphoglycerate synthase. <i>FEMS Microbiology Letters</i> , 2008, 280, 195-202.	0.7	33
62	Molecular and structural analyses of maple syrup urine disease and identification of a founder mutation in a Portuguese Gypsy community. <i>Molecular Genetics and Metabolism</i> , 2008, 94, 148-156.	0.5	27
63	Crystal Structure of a Trapped Phosphate Intermediate in Vanadium Apochloroperoxidase Catalyzing a Dephosphorylation Reaction. <i>Biochemistry</i> , 2008, 47, 929-934.	1.2	26
64	Mycobacterium tuberculosis Glucosyl-3-Phosphoglycerate Synthase: Structure of a Key Enzyme in Methylglucose Lipopolysaccharide Biosynthesis. <i>PLoS ONE</i> , 2008, 3, e3748.	1.1	21
65	Isolation, Cloning and Structural Characterisation of Boophilin, a Multifunctional Kunitz-Type Proteinase Inhibitor from the Cattle Tick. <i>PLoS ONE</i> , 2008, 3, e1624.	1.1	103
66	Crystal structure of a novel cysteinless plant Kunitz-type protease inhibitor. <i>Biochemical and Biophysical Research Communications</i> , 2007, 360, 735-740.	1.0	37
67	NEDD8: A new ataxin-3 interactor. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2007, 1773, 1619-1627.	1.9	55
68	Human transthyretin in complex with iododiflunisal: structural features associated with a potent amyloid inhibitor. <i>Biochemical Journal</i> , 2005, 388, 615-621.	1.7	53
69	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
70	Towards a Structural Understanding of the Fibrillization Pathway in Machado-Joseph's Disease: Trapping Early Oligomers of Non-expanded Ataxin-3. <i>Journal of Molecular Biology</i> , 2005, 353, 642-654.	2.0	68
71	The factor V C1 domain is involved in membrane binding: identification of functionally important amino acid residues within the C1 domain of factor V using alanine scanning mutagenesis. <i>Thrombosis and Haemostasis</i> , 2004, 91, 16-27.	1.8	43
72	Structural basis for stereo-specific catalysis in NAD <sup>+</sup> -dependent (R)-2-hydroxyglutarate dehydrogenase from <i>Acidaminococcus fermentans</i> . <i>FEBS Journal</i> , 2004, 272, 269-281.	2.2	23

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73	Trypanosoma cruzi macrophage infectivity potentiator has a rotamase core and a highly exposed $\alpha$ -helix. EMBO Reports, 2002, 3, 88-94.	2.0	42
74	Fine Mapping of Inhibitory Anti-factor V Antibodies Using Factor V C2 Domain Mutants. Thrombosis and Haemostasis, 2001, 85, 1048-1054.	1.8	29
75	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.	1.1	34
76	Structure of human biliverdin IXbeta reductase, an early fetal bilirubin IXbeta producing enzyme. Nature Structural Biology, 2001, 8, 215-220.	9.7	99
77	Identification of Functionally Important Amino Acid Residues within the C2-Domain of Human Factor V Using Alanine-Scanning Mutagenesis. Biochemistry, 2000, 39, 1951-1958.	1.2	74
78	Heterologous Expression of the Vanadium-containing Chloroperoxidase from Curvularia inaequalis in Saccharomyces cerevisiae and Site-directed Mutagenesis of the Active Site Residues His496, Lys353, Arg360, and Arg490. Journal of Biological Chemistry, 1999, 274, 23820-23827.	1.6	110
79	Crystal structures of the membrane-binding C2 domain of human coagulation factor V. Nature, 1999, 402, 434-439.	13.7	258
80	X-ray crystal structures of active site mutants of the vanadium-containing chloroperoxidase from the fungus Curvularia inaequalis. Journal of Biological Inorganic Chemistry, 1999, 4, 209-219.	1.1	117
81	Human $\beta$ -tryptase is a ring-like tetramer with active sites facing a central pore. Nature, 1998, 392, 306-311.	13.7	300
82	Small structural changes account for the high thermostability of 1[4Fe-4S] ferredoxin from the hyperthermophilic bacterium Thermotoga maritima. Structure, 1996, 4, 1291-1301.	1.6	118
83	Structure of the Val122Ile Variant Transthyretin – a Cardiomyopathic Mutant. Acta Crystallographica Section D: Biological Crystallography, 1996, 52, 966-972.	2.5	31
84	CARs-DB: A Database of Cryptic Amyloidogenic Regions in Intrinsically Disordered Proteins. Frontiers in Molecular Biosciences, 0, 9, .	1.6	4