

# Mariapina D'onofrio

## List of Publications by Year in descending order

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54  
papers

1,285  
citations

331538

21  
h-index

395590

33  
g-index

55  
all docs

55  
docs citations

55  
times ranked

1610  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ubiquitination of Alzheimer's-related tau protein affects liquid-liquid phase separation in a site- and cofactor-dependent manner. <i>International Journal of Biological Macromolecules</i> , 2022, 201, 173-181.	3.6	16
2	Structural Basis for Chaperone-Independent Ubiquitination of Tau Protein by Its E3 Ligase CHIP. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	9
3	Alterations in calmodulin-cardiac ryanodine receptor molecular recognition in congenital arrhythmias. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 127.	2.4	5
4	Camouflaged Fluorescent Silica Nanoparticles Target Aggregates and Condensates of the Amyloidogenic Protein Tau. <i>Bioconjugate Chemistry</i> , 2022, 33, 1261-1268.	1.8	4
5	Alpha-Synuclein-Nanoparticle Interactions: Understanding, Controlling and Exploiting Conformational Plasticity. <i>Molecules</i> , 2020, 25, 5625.	1.7	15
6	Semisynthetic and Enzyme-Mediated Conjugate Preparations Illuminate the Ubiquitination-Dependent Aggregation of Tau Protein. <i>Angewandte Chemie</i> , 2020, 132, 6669-6673.	1.6	2
7	Unsaturated Fatty Acid-Induced Conformational Transitions and Aggregation of the Repeat Domain of Tau. <i>Molecules</i> , 2020, 25, 2716.	1.7	15
8	Semisynthetic Modification of Tau Protein with Di-Ubiquitin Chains for Aggregation Studies. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4400.	1.8	20
9	Solution NMR insights into dynamic supramolecular assemblies of disordered amyloidogenic proteins. <i>Archives of Biochemistry and Biophysics</i> , 2020, 683, 108304.	1.4	8
10	Semisynthetic and Enzyme-Mediated Conjugate Preparations Illuminate the Ubiquitination-Dependent Aggregation of Tau Protein. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 6607-6611.	7.2	24
11	Cation and peptide binding properties of CML7, a calmodulin-like protein from <i>Arabidopsis thaliana</i> . <i>Journal of Inorganic Biochemistry</i> , 2019, 199, 110796.	1.5	16
12	Specific Interaction Sites Determine Differential Adsorption of Protein Structural Isomers on Nanoparticle Surfaces. <i>Chemistry - A European Journal</i> , 2018, 24, 5911-5919.	1.7	14
13	Alzheimer's disease-associated ubiquitin mutant Ubb+1: Properties of the carboxy-terminal domain and its influence on biomolecular interactions. <i>International Journal of Biological Macromolecules</i> , 2018, 108, 24-31.	3.6	10
14	Binding of calcium and target peptide to calmodulin-like protein CML19, the centrin 2 of <i>Arabidopsis thaliana</i> . <i>International Journal of Biological Macromolecules</i> , 2018, 108, 1289-1299.	3.6	30
15	Preferential Binding of Mg <sup>2+</sup> Over Ca <sup>2+</sup> to CIB2 Triggers an Allosteric Switch Impaired in Usher Syndrome Type 1J. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 274.	1.4	26
16	Unsaturated Long-Chain Fatty Acids Are Preferred Ferritin Ligands That Enhance Iron Biom mineralization. <i>Chemistry - A European Journal</i> , 2017, 23, 9879-9887.	1.7	10
17	Identification of primary and secondary UBA footprints on the surface of ubiquitin in cell-mimicking crowded solution. <i>FEBS Letters</i> , 2017, 591, 979-990.	1.3	9
18	The long variant of human ileal bile acid-binding protein associated with colorectal cancer exhibits sub-cellular localization and lipid binding behaviour distinct from those of the common isoform. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2315-2324.	1.1	6

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19	Arabidopsis calmodulin-like protein CML36 is a calcium (Ca <sup>2+</sup> ) sensor that interacts with the plasma membrane Ca <sup>2+</sup> -ATPase isoform ACA8 and stimulates its activity. <i>Journal of Biological Chemistry</i> , 2017, 292, 15049-15061.	1.6	52
20	Molecular differences between human liver fatty acid binding protein and its T94A variant in their unbound and lipid-bound states. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1152-1159.	1.1	5
21	Metal binding affinity and structural properties of calmodulin-like protein 14 from <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , 2016, 25, 1461-1471.	3.1	35
22	Effects of macromolecular crowding on a small lipid binding protein probed at the single-amino acid level. <i>Archives of Biochemistry and Biophysics</i> , 2016, 606, 99-110.	1.4	12
23	Paramagnetic Nanoparticles Leave Their Mark on Nuclear Spins of Transiently Adsorbed Proteins. <i>Journal of the American Chemical Society</i> , 2016, 138, 72-75.	6.6	32
24	The study of transient protein-nanoparticle interactions by solution NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 102-114.	1.1	55
25	Transient Interactions of a Cytosolic Protein with Macromolecular and Vesicular Cosolutes: Unspecific and Specific Effects. <i>ChemBioChem</i> , 2015, 16, 2633-2645.	1.3	10
26	Polyhydroxylated [60]fullerene binds specifically to functional recognition sites on a monomeric and a dimeric ubiquitin. <i>Nanoscale</i> , 2015, 7, 7197-7205.	2.8	35
27	Bile salt recognition by human liver fatty acid binding protein. <i>FEBS Journal</i> , 2015, 282, 1271-1288.	2.2	11
28	The unique ligand binding features of subfamily-II iLBPs with respect to bile salts and related drugs. <i>Prostaglandins Leukotrienes and Essential Fatty Acids</i> , 2015, 95, 1-10.	1.0	8
29	Noncanonical sortase-mediated assembly of pilus type 2b in group B <i>Streptococcus</i> . <i>FASEB Journal</i> , 2015, 29, 4629-4640.	0.2	10
30	The role of dynamics in modulating ligand exchange in intracellular lipid binding proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1268-1278.	1.1	27
31	<sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C chemical shift assignments of the C-Ala domain of the alanyl-tRNA synthetase of the psychrophilic bacterium <i>Bizionia argentinensis</i> sp. nov.. <i>Biomolecular NMR Assignments</i> , 2014, 8, 415-418.	0.4	0
32	Dynamics of a Globular Protein Adsorbed to Liposomal Nanoparticles. <i>Journal of the American Chemical Society</i> , 2014, 136, 13158-13161.	6.6	29
33	A proton nuclear magnetic resonance-based metabolomic approach in IgA nephropathy urinary profiles. <i>Metabolomics</i> , 2013, 9, 740-751.	1.4	11
34	Evidence from NMR interaction studies challenges the hypothesis of direct lipid transfer from FABP to malaria sporozoite protein UIS3. <i>Protein Science</i> , 2013, 22, 133-138.	3.1	6
35	Ligand Binding Promiscuity of Human Liver Fatty Acid Binding Protein: Structural and Dynamic Insights from an Interaction Study with Glycocholate and Oleate. <i>ChemBioChem</i> , 2013, 14, 1807-1819.	1.3	29
36	Hyper conserved elements in vertebrate mRNA 3'-UTRs reveal a translational network of RNA-binding proteins controlled by HuR. <i>Nucleic Acids Research</i> , 2013, 41, 3201-3216.	6.5	38

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37	NMR investigation of the equilibrium partitioning of a water-soluble bile salt protein carrier to phospholipid vesicles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1776-1791.	1.5	32
38	Group B <i>Streptococcus</i> pilus sortase regulation: a single mutation in the lid region induces pilin protein polymerization in vitro. <i>FASEB Journal</i> , 2013, 27, 3144-3154.	0.2	10
39	New insights into the role of the glutamic acid of the E-box motif in group B <i>Streptococcus</i> pilus 2a assembly. <i>FASEB Journal</i> , 2012, 26, 2008-2018.	0.2	11
40	Recombinant proteins incorporating short non-native extensions may display increased aggregation propensity as detected by high resolution NMR spectroscopy. <i>Biochemical and Biophysical Research Communications</i> , 2012, 427, 677-681.	1.0	3
41	High Relaxivity Supramolecular Adducts Between Human Liver Fatty Acid-Binding Protein and Amphiphilic Gd <sup>III</sup> Complexes: Structural Basis for the Design of Intracellular Targeting MRI Probes. <i>Chemistry - A European Journal</i> , 2012, 18, 9919-9928.	1.7	25
42	Structure analysis and site-directed mutagenesis of defined key residues and motives for pilus-related sortase C1 in group B <i>Streptococcus</i> . <i>FASEB Journal</i> , 2011, 25, 1874-1886.	0.2	29
43	Structural Requirements for Cooperativity in Ileal Bile Acid-binding Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 39307-39317.	1.6	16
44	Site-Specific Investigation of the Steady-State Kinetics and Dynamics of the Multistep Binding of Bile Acid Molecules to a Lipid Carrier Protein. <i>Chemistry - A European Journal</i> , 2010, 16, 11300-11310.	1.7	19
45	Towards the elucidation of molecular determinants of cooperativity in the liver bile acid binding protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 718-731.	1.5	19
46	NMR Studies Reveal the Role of Biomembranes in Modulating Ligand Binding and Release by Intracellular Bile Acid Binding Proteins. <i>Journal of Molecular Biology</i> , 2009, 394, 852-863.	2.0	21
47	NMR unfolding studies on a liver bile acid binding protein reveal a global two-state unfolding and localized singular behaviors. <i>Archives of Biochemistry and Biophysics</i> , 2009, 481, 21-29.	1.4	21
48	Structure and dynamics of copper-free SOD: The protein before binding copper. <i>Protein Science</i> , 2009, 11, 2479-2492.	3.1	70
49	Mapping the Interactions between Lys48 and Lys63-Linked Di-ubiquitins and a Ubiquitin-Interacting Motif of S5a. <i>Journal of Molecular Biology</i> , 2007, 368, 753-766.	2.0	31
50	Ubistatins Inhibit Proteasome-Dependent Degradation by Binding the Ubiquitin Chain. <i>Science</i> , 2004, 306, 117-120.	6.0	183
51	Solution Structure and Backbone Dynamics of the Cu(I) and Apo Forms of the Second Metal-Binding Domain of the Menkes Protein ATP7A. <i>Biochemistry</i> , 2004, 43, 3396-3403.	1.2	63
52	Solution structure of the N-terminal domain of a potential copper-translocating P-type ATPase from <i>Bacillus subtilis</i> in the apo and Cu(I) loaded states. <i>Journal of Molecular Biology</i> , 2002, 317, 415-429.	2.0	67
53	Isolation and Characterization of Two Peroxidases from <i>Cucumis sativus</i> . <i>Archives of Biochemistry and Biophysics</i> , 2001, 388, 100-112.	1.4	21
54	Structural Basis for Chaperone-Independent Ubiquitination of Tau Protein by its E3 Ligase CHIP. <i>Angewandte Chemie</i> , 0, , .	1.6	0