

# Ricardo Aparicio

## List of Publications by Year in descending order

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Version: 2024-02-01

23  
papers

573  
citations

840776

11  
h-index

677142

22  
g-index

25  
all docs

25  
docs citations

25  
times ranked

1035  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Rearrangements in the Thyroid Hormone Receptor Hinge Domain and Their Putative Role in the Receptor Function. <i>Journal of Molecular Biology</i> , 2006, 360, 586-598.	4.2	106
2	Gaining ligand selectivity in thyroid hormone receptors via entropy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20717-20722.	7.1	76
3	Epicolactone – Natural Product Isolated from the Sugarcane Endophytic Fungus <i>Epicoccum nigrum</i> . <i>European Journal of Organic Chemistry</i> , 2012, 2012, 5225-5230.	2.4	57
4	Closed Conformation of the Active Site Loop of Rabbit Muscle Triosephosphate Isomerase in the Absence of Substrate: Evidence of Conformational Heterogeneity. <i>Journal of Molecular Biology</i> , 2003, 334, 1023-1041.	4.2	45
5	Structural basis of GC-1 selectivity for thyroid hormone receptor isoforms. <i>BMC Structural Biology</i> , 2008, 8, 8.	2.3	42
6	Bowman – Birk proteinase inhibitor from <i>Clitoria fairchildiana</i> seeds: Isolation, biochemical properties and insecticidal potential. <i>Phytochemistry</i> , 2015, 118, 224-235.	2.9	42
7	Effects of morin on snake venom phospholipase A2 (PLA2). <i>Toxicon</i> , 2005, 46, 751-758.	1.6	41
8	Improving Protein Template Recognition by Using Small-Angle X-Ray Scattering Profiles. <i>Biophysical Journal</i> , 2011, 101, 2770-2781.	0.5	33
9	Insights into the structure and function of fungal $\beta$ -mannosidases from glycoside hydrolase family 2 based on multiple crystal structures of the <i>Trichoderma reesei</i> enzyme. <i>FEBS Journal</i> , 2014, 281, 4165-4178.	4.7	22
10	Structural Insights into the $\beta$ -Mannosidase from <i>T. reesei</i> Obtained by Synchrotron Small-Angle X-ray Solution Scattering Enhanced by X-ray Crystallography. <i>Biochemistry</i> , 2002, 41, 9370-9375.	2.5	19
11	Crystal structures of the apo form and a complex of human LMW-PTP with a phosphonic acid provide new evidence of a secondary site potentially related to the anchorage of natural substrates. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 4462-4471.	3.0	14
12	Crystal structure of the human Tip41 orthologue, TIPRL, reveals a novel fold and a binding site for the PP2Ac C-terminus. <i>Scientific Reports</i> , 2016, 6, 30813.	3.3	14
13	Oligomerization, Membrane Association, and in Vivo Phosphorylation of Sugarcane UDP-glucose Pyrophosphorylase. <i>Journal of Biological Chemistry</i> , 2014, 289, 33364-33377.	3.4	11
14	An asymmetric substrate-controlled Morita – Baylis – Hillman reaction as approach for the synthesis of pyrrolizidinones and pyrrolizidines. <i>Tetrahedron</i> , 2014, 70, 3319-3326.	1.9	11
15	Is RK-682 a promiscuous enzyme inhibitor? Synthesis and in vitro evaluation of protein tyrosine phosphatase inhibition of racemic RK-682 and analogues. <i>European Journal of Medicinal Chemistry</i> , 2015, 97, 42-54.	5.5	10
16	Crystal structure of a small heat-shock protein from <i>Xylella fastidiosa</i> reveals a distinct high-order structure. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 222-227.	0.8	7
17	A comparative structural analysis reveals distinctive features of co-factor binding and substrate specificity in plant aldo-keto reductases. <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 696-701.	2.1	6
18	C7orf59/LAMTOR4 phosphorylation and structural flexibility modulate Ragulator assembly. <i>FEBS Open Bio</i> , 2019, 9, 1589-1602.	2.3	6

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19	Modulation of the Pharmacological Activities of Secretory Phospholipase A2 from <i>Crotalus durissus cascavella</i> Induced by Naringin. <i>Molecules</i> , 2011, 16, 738-761.	3.8	5
20	Preliminary X-ray diffraction studies of rabbit muscle triose phosphate isomerase (TIM). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1492-1494.	2.5	3
21	Crystal structure of methyl 2-(2H-1,3-benzodioxol-5-yl)-7,9-dibromo-8-oxo-1-oxaspiro[4.5]deca-2,6,9-triene-3-carboxylate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2014, 70, o1275-o1276.	0.2	1
22	Conformational variability of the stationary phase survival protein E from <i>Xylella fastidiosa</i> revealed by X-ray crystallography, small-angle X-ray scattering studies, and normal mode analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1931-1943.	2.6	0
23	Crystal structure of 3-methoxycarbonyl-2-(4-methoxyphenyl)-8-oxo-1-azaspiro[4.5]deca-1,6,9-trien-1-ium-1-olate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2014, 70, o1200-o1201.	0.2	0