

Maria J Marcaida

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,537
citations

361413
20
h-index

454955
30
g-index

34
all docs

34
docs citations

34
times ranked

2182
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of Escherichia coli RNase E catalytic domain and implications for RNA turnover. Nature, 2005, 437, 1187-1191.	27.8	259
2	Cryo-EM structure of aerolysin variants reveals a novel protein fold and the pore-formation process. Nature Communications, 2016, 7, 12062.	12.8	144
3	Oxypurinol Directly and Immediately Activates the Drug-Specific T Cells via the Preferential Use of HLA-B*58:01. Journal of Immunology, 2014, 192, 2984-2993.	0.8	136
4	The RNA degradosome: life in the fast lane of adaptive molecular evolution. Trends in Biochemical Sciences, 2006, 31, 359-365.	7.5	104
5	The Crystal Structure of the Escherichia coli RNase E Apoprotein and a Mechanism for RNA Degradation. Structure, 2008, 16, 1238-1244.	3.3	74
6	Single-molecule sensing of peptides and nucleic acids by engineered aerolysin nanopores. Nature Communications, 2019, 10, 4918.	12.8	74
7	Homing endonucleases: from basics to therapeutic applications. Cellular and Molecular Life Sciences, 2010, 67, 727-748.	5.4	73
8	Molecular Basis of Histone H3K4me3 Recognition by ING4. Journal of Biological Chemistry, 2008, 283, 15956-15964.	3.4	71
9	Mapping the sensing spots of aerolysin for single oligonucleotides analysis. Nature Communications, 2018, 9, 2823.	12.8	60
10	Discovery of a Selective Aurora A Kinase Inhibitor by Virtual Screening. Journal of Medicinal Chemistry, 2016, 59, 7188-7211.	6.4	57
11	Aerolysin nanopores decode digital information stored in tailored macromolecular analytes. Science Advances, 2020, 6, .	10.3	57
12	Modulation of Heme Redox Potential in the Cytochrome <i>c</i> ₆ Family. Journal of the American Chemical Society, 2007, 129, 9468-9475.	13.7	45
13	Structural, physicochemical and dynamic features conserved within the aerolysin pore-forming toxin family. Scientific Reports, 2017, 7, 13932.	3.3	38
14	Bridged bicyclic peptides as potential drug scaffolds: synthesis, structure, protein binding and stability. Chemical Science, 2015, 6, 5473-5490.	7.4	37
15	Structure of Cytochrome c6A, a Novel Dithio-cytochrome of Arabidopsis thaliana, and its Reactivity with Plastocyanin: Implications for Function. Journal of Molecular Biology, 2006, 360, 968-977.	4.2	36
16	Crystal structure of I-Dmol in complex with its target DNA provides new insights into meganuclease engineering. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16888-16893.	7.1	36
17	Palmitoylated acyl protein thioesterase APT2 deforms membranes to extract substrate acyl chains. Nature Chemical Biology, 2021, 17, 438-447.	8.0	31
18	Visualizing phosphodiester-bond hydrolysis by an endonuclease. Nature Structural and Molecular Biology, 2015, 22, 65-72.	8.2	30

#	ARTICLE	IF	CITATIONS
19	Solution Structure of Human Growth Arrest and DNA Damage 45 [±] (Gadd45 [±]) and Its Interactions with Proliferating Cell Nuclear Antigen (PCNA) and Aurora A Kinase. <i>Journal of Biological Chemistry</i> , 2010, 285, 22196-22201.	3.4	25
20	The Polyglutamine Expansion at the N-Terminal of Huntingtin Protein Modulates the Dynamic Configuration and Phosphorylation of the C-Terminal HEAT Domain. <i>Structure</i> , 2020, 28, 1035-1050.e8.	3.3	24
21	Btk SH2-kinase interface is critical for allosteric kinase activation and its targeting inhibits B-cell neoplasms. <i>Nature Communications</i> , 2020, 11, 2319.	12.8	23
22	Structural insights on cholesterol endosynthesis: Binding of squalene and 2,3-oxidosqualene to supernatant protein factor. <i>Journal of Structural Biology</i> , 2015, 190, 261-270.	2.8	21
23	KAP1 is an antiparallel dimer with a functional asymmetry. <i>Life Science Alliance</i> , 2019, 2, e201900349.	2.8	16
24	The Human RNA Helicase DDX21 Presents a Dimerization Interface Necessary for Helicase Activity. <i>IScience</i> , 2020, 23, 101811.	4.1	15
25	X-ray structure of a lectin-bound DNA duplex containing an unnatural phenanthrenyl pair. <i>Chemical Communications</i> , 2016, 52, 4749-4752.	4.1	12
26	Complementing structural information of modular proteins with small angle neutron scattering and contrast variation. <i>European Biophysics Journal</i> , 2008, 37, 603-611.	2.2	9
27	Key Players in I-Dmol Endonuclease Catalysis Revealed from Structure and Dynamics. <i>ACS Chemical Biology</i> , 2016, 11, 1401-1407.	3.4	9
28	Prolyl endopeptidase-like is a (thio)esterase involved in mitochondrial respiratory chain function. <i>IScience</i> , 2021, 24, 103460.	4.1	8
29	Engineering a Nickase on the Homing Endonuclease I-Dmol Scaffold. <i>Journal of Biological Chemistry</i> , 2015, 290, 18534-18544.	3.4	7
30	Structure and dynamics of mesophilic variants from the homing endonuclease I-Dmol. <i>Journal of Computer-Aided Molecular Design</i> , 2017, 31, 1063-1072.	2.9	2