

Maria J Marcaida

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7498389/publications.pdf>

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	Palmitoylated acyl protein thioesterase APT2 deforms membranes to extract substrate acyl chains. <i>Nature Chemical Biology</i> , 2021, 17, 438-447.	8.0	31
2	Prolyl endopeptidase-like is a (thio)esterase involved in mitochondrial respiratory chain function. <i>IScience</i> , 2021, 24, 103460.	4.1	8
3	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
4	The Human RNA Helicase DDX21 Presents a Dimerization Interface Necessary for Helicase Activity. <i>IScience</i> , 2020, 23, 101811.	4.1	15
5	Aerolysin nanopores decode digital information stored in tailored macromolecular analytes. <i>Science Advances</i> , 2020, 6, .	10.3	57
6	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
7	Single-molecule sensing of peptides and nucleic acids by engineered aerolysin nanopores. <i>Nature Communications</i> , 2019, 10, 4918.	12.8	74
8	KAP1 is an antiparallel dimer with a functional asymmetry. <i>Life Science Alliance</i> , 2019, 2, e201900349.	2.8	16
9	Mapping the sensing spots of aerolysin for single oligonucleotides analysis. <i>Nature Communications</i> , 2018, 9, 2823.	12.8	60
10	Structural, physicochemical and dynamic features conserved within the aerolysin pore-forming toxin family. <i>Scientific Reports</i> , 2017, 7, 13932.	3.3	38
11	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
12	Discovery of a Selective Aurora A Kinase Inhibitor by Virtual Screening. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 7188-7211.	6.4	57
13	Cryo-EM structure of aerolysin variants reveals a novel protein fold and the pore-formation process. <i>Nature Communications</i> , 2016, 7, 12062.	12.8	144
14	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
15	Key Players in I-Dmol Endonuclease Catalysis Revealed from Structure and Dynamics. <i>ACS Chemical Biology</i> , 2016, 11, 1401-1407.	3.4	9
16	Engineering a Nickase on the Homing Endonuclease I-Dmol Scaffold. <i>Journal of Biological Chemistry</i> , 2015, 290, 18534-18544.	3.4	7
17	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
18	Bridged bicyclic peptides as potential drug scaffolds: synthesis, structure, protein binding and stability. <i>Chemical Science</i> , 2015, 6, 5473-5490.	7.4	37

#	ARTICLE	IF	CITATIONS
19	Visualizing phosphodiester-bond hydrolysis by an endonuclease. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 65-72.	8.2	30
20	Oxypurinol Directly and Immediately Activates the Drug-Specific T Cells via the Preferential Use of HLA-B*58:01. <i>Journal of Immunology</i> , 2014, 192, 2984-2993.	0.8	136
21	Homing endonucleases: from basics to therapeutic applications. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 727-748.	5.4	73
22	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
23	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
24	The Crystal Structure of the Escherichia coli RNase E Apoprotein and a Mechanism for RNA Degradation. <i>Structure</i> , 2008, 16, 1238-1244.	3.3	74
25	Crystal structure of I-Dmol in complex with its target DNA provides new insights into meganuclease engineering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16888-16893.	7.1	36
26	Molecular Basis of Histone H3K4me3 Recognition by ING4. <i>Journal of Biological Chemistry</i> , 2008, 283, 15956-15964.	3.4	71
27	Modulation of Heme Redox Potential in the Cytochrome <i>c</i> ₆ Family. <i>Journal of the American Chemical Society</i> , 2007, 129, 9468-9475.	13.7	45
28	Structure of Cytochrome c6A, a Novel Dithio-cytochrome of Arabidopsis thaliana, and its Reactivity with Plastocyanin: Implications for Function. <i>Journal of Molecular Biology</i> , 2006, 360, 968-977.	4.2	36
29	The RNA degradosome: life in the fast lane of adaptive molecular evolution. <i>Trends in Biochemical Sciences</i> , 2006, 31, 359-365.	7.5	104
30	Structure of Escherichia coli RNase E catalytic domain and implications for RNA turnover. <i>Nature</i> , 2005, 437, 1187-1191.	27.8	259