

Rafael Molina

List of Publications by Year in descending order

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papers

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citations

471509

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477307

29
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docs citations

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times ranked

1448
citing authors

#	ARTICLE	IF	CITATIONS
1	The Crystal Structure of Feruloyl Esterase A from <i>Aspergillus niger</i> Suggests Evolutive Functional Convergence in Feruloyl Esterase Family. <i>Journal of Molecular Biology</i> , 2004, 338, 495-506.	4.2	110
2	Structure of Csx1-cOA4 complex reveals the basis of RNA decay in Type III-B CRISPR-Cas. <i>Nature Communications</i> , 2019, 10, 4302.	12.8	72
3	Structure of p15PAF-PCNA complex and implications for clamp sliding during DNA replication and repair. <i>Nature Communications</i> , 2015, 6, 6439.	12.8	65
4	Conformational Dynamics in Penicillin-Binding Protein 2a of Methicillin-Resistant <i>Staphylococcus aureus</i> , Allosteric Communication Network and Enablement of Catalysis. <i>Journal of the American Chemical Society</i> , 2017, 139, 2102-2110.	13.7	65
5	Probing the determinants of substrate specificity of a feruloyl esterase, AnFaeA, from <i>Aspergillus niger</i> . <i>FEBS Journal</i> , 2005, 272, 4362-4371.	4.7	59
6	Crystal structure of CbpF, a bifunctional choline-binding protein and autolysis regulator from <i>Streptococcus pneumoniae</i> . <i>EMBO Reports</i> , 2009, 10, 246-251.	4.5	56
7	Carbohydrate recognition and lysis by bacterial peptidoglycan hydrolases. <i>Current Opinion in Structural Biology</i> , 2017, 44, 87-100.	5.7	45
8	Structural basis of CRISPR-Cas Type III prokaryotic defence systems. <i>Current Opinion in Structural Biology</i> , 2020, 65, 119-129.	5.7	42
9	A one-pot, simple methodology for cassette randomisation and recombination for focused directed evolution. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 567-576.	2.1	34
10	Visualizing phosphodiester-bond hydrolysis by an endonuclease. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 65-72.	8.2	30
11	Enhancement of the Stability of a Prolipase from <i>Rhizopus oryzae</i> toward Aldehydes by Saturation Mutagenesis. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7291-7299.	3.1	28
12	Structure of the AvrBs3-DNA complex provides new insights into the initial thymine-recognition mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1707-1716.	2.5	28
13	Tuning of the FMN binding and oxido-reduction properties by neighboring side chains in <i>Anabaena flavodoxin</i> . <i>Archives of Biochemistry and Biophysics</i> , 2007, 467, 206-217.	3.0	24
14	Non-specific protein-DNA interactions control I-Crel target binding and cleavage. <i>Nucleic Acids Research</i> , 2012, 40, 6936-6945.	14.5	24
15	BuD, a helix-loop-helix DNA-binding domain for genome modification. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2042-2052.	2.5	24
16	Renew or die: The molecular mechanisms of peptidoglycan recycling and antibiotic resistance in Gram-negative pathogens. <i>Drug Resistance Updates</i> , 2016, 28, 91-104.	14.4	24
17	5- ² -Cytosine-Phosphoguanine (CpG) Methylation Impacts the Activity of Natural and Engineered Meganucleases. <i>Journal of Biological Chemistry</i> , 2012, 287, 30139-30150.	3.4	23
18	Orthologous and Paralogous AmpD Peptidoglycan Amidases from Gram-Negative Bacteria. <i>Microbial Drug Resistance</i> , 2016, 22, 470-476.	2.0	23

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19	Expression, purification, crystallization and preliminary X-ray diffraction analysis of the novel modular DNA-binding protein BurrH in its apo form and in complex with its target DNA. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 87-91.	0.8	17
20	Molecular scissors for <i>in situ</i> cellular repair. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2012, 47, 207-221.	5.2	16
21	Expression, purification, crystallization and preliminary X-ray diffraction analysis of the dihydroorotase domain of human CAD. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1341-1345.	0.7	12
22	Understanding the indirect DNA read-out specificity of I-Crel Meganuclease. <i>Scientific Reports</i> , 2018, 8, 10286.	3.3	12
23	Three-dimensional structures of Lipoproteins from <i>Streptococcus pneumoniae</i> and <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2018, 308, 692-704.	3.6	11
24	Structural basis of cyclic oligoadenylate degradation by ancillary Type III CRISPR-Cas ring nucleases. <i>Nucleic Acids Research</i> , 2021, 49, 12577-12590.	14.5	10
25	Key Players in I-Dmol Endonuclease Catalysis Revealed from Structure and Dynamics. <i>ACS Chemical Biology</i> , 2016, 11, 1401-1407.	3.4	9
26	X-ray Structure of Catenated Lytic Transglycosylase SltB1. <i>Biochemistry</i> , 2017, 56, 6317-6320.	2.5	9
27	Crystallization and preliminary X-ray diffraction studies of choline-binding protein F from <i>Streptococcus pneumoniae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 742-745.	0.7	8
28	Characterization of gadolinium complexes for SAD phasing in macromolecular crystallography: application to CbpF. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 823-831.	2.5	8
29	Crystallization and preliminary crystallographic analysis of the catalytic module of endolysin from Cp-7, a phage infecting <i>Streptococcus pneumoniae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 670-673.	0.7	7
30	A complement to the modern crystallographer's toolbox: caged gadolinium complexes with versatile binding modes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1506-1516.	2.5	7
31	Engineering a Nickase on the Homing Endonuclease I-Dmol Scaffold. <i>Journal of Biological Chemistry</i> , 2015, 290, 18534-18544.	3.4	7
32	Structure of the I-SceI nuclease complexed with its dsDNA target and three catalytic metal ions. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 473-479.	0.8	6
33	Crystal structure of CbpF, a bifunctional choline-binding protein and autolysis regulator from <i>Streptococcus pneumoniae</i> . <i>EMBO Reports</i> , 2009, 10, 413-413.	4.5	2
34	Crystallization and preliminary X-ray diffraction analysis of the homing endonuclease I-Cvul from <i>Chlorella vulgaris</i> in complex with its target DNA. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 256-259.	0.8	2
35	Crystal Structure of the Homing Endonuclease I-Cvul Provides a New Template for Genome Modification. <i>Journal of Biological Chemistry</i> , 2015, 290, 28727-28736.	3.4	2
36	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

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37	Crystal Structure and Pathophysiological Role of the Pneumococcal Nucleoside-binding Protein PnrA. <i>Journal of Molecular Biology</i> , 2021, 433, 166723.	4.2	2
38	Integrative structural biology of the penicillin-binding protein-1 from <i>Staphylococcus aureus</i> , an essential component of the divisome machinery. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5392-5405.	4.1	2
39	Effect of DNA on the conformational dynamics of the endonucleases <i>l</i> â€šmol as provided by molecular dynamics simulations. <i>Biopolymers</i> , 2016, 105, 898-904.	2.4	1