

# Guillermo Montoya

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

2,786  
citations

218677

26  
h-index

197818

49  
g-index

65  
all docs

65  
docs citations

65  
times ranked

3346  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and Optimization of Novel Small-Molecule Cas9 Inhibitors by Cell-Based High-Throughput Screening. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 3266-3305.	6.4	5
2	Mechanics of CRISPR-Cas12a and engineered variants on $\lambda$ -DNA. <i>Nucleic Acids Research</i> , 2022, 50, 5208-5225.	14.5	13
3	Chemogenetic profiling reveals PP2A-independent cytotoxicity of proposed PP2A activators iHAP1 and DT061. <i>EMBO Journal</i> , 2022, 41, .	7.8	14
4	A highly conserved pocket on PP2A856 is required for hSgo1 binding and cohesion protection during mitosis. <i>EMBO Reports</i> , 2021, 22, e52295.	4.5	9
5	Structure of the mini-RNA-guided endonuclease CRISPR-Cas12j3. <i>Nature Communications</i> , 2021, 12, 4476.	12.8	23
6	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
7	Editorial overview: Protein-nucleic acid interactions: "Takes two to Tango"™. <i>Current Opinion in Structural Biology</i> , 2020, 65, v-vi.	5.7	0
8	Structures of the Cmr- $\lambda^2$ Complex Reveal the Regulation of the Immunity Mechanism of Type III-B CRISPR-Cas. <i>Molecular Cell</i> , 2020, 79, 741-757.e7.	9.7	43
9	Structural basis of CRISPR-Cas Type III prokaryotic defence systems. <i>Current Opinion in Structural Biology</i> , 2020, 65, 119-129.	5.7	42
10	CRISPR-Cas12a: Functional overview and applications. <i>Biomedical Journal</i> , 2020, 43, 8-17.	3.1	151
11	Molecular Basis of the Mechanisms Controlling MASTL. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 326-343.	3.8	7
12	The TRiC/CCT Chaperonin and Its Role in Uncontrolled Proliferation. <i>Advances in Experimental Medicine and Biology</i> , 2020, 1243, 21-40.	1.6	21
13	DeepFRET, a software for rapid and automated single-molecule FRET data classification using deep learning. <i>ELife</i> , 2020, 9, .	6.0	47
14	Oncogenic Mutations Rewire Signaling Pathways by Switching Protein Recruitment to Phosphotyrosine Sites. <i>Cell</i> , 2019, 179, 543-560.e26.	28.9	65
15	A Consensus Binding Motif for the PP4 Protein Phosphatase. <i>Molecular Cell</i> , 2019, 76, 953-964.e6.	9.7	59
16	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
17	High-Resolution Structure of Cas13b and Biochemical Characterization of RNA Targeting and Cleavage. <i>Cell Reports</i> , 2019, 26, 3741-3751.e5.	6.4	102
18	Molecular architecture of the Jumonji C family histone demethylase KDM5B. <i>Scientific Reports</i> , 2019, 9, 4019.	3.3	16

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19	Conformational Activation Promotes CRISPR-Cas12a Catalysis and Resetting of the Endonuclease Activity. <i>Cell</i> , 2018, 175, 1856-1871.e21.	28.9	167
20	A Type III-B Cmr effector complex catalyzes the synthesis of cyclic oligoadenylate second messengers by cooperative substrate binding. <i>Nucleic Acids Research</i> , 2018, 46, 10319-10330.	14.5	51
21	Molecular basis of Tosl-like Kinase 2 activation. <i>Nature Communications</i> , 2018, 9, 2535.	12.8	24
22	Understanding the indirect DNA read-out specificity of I-Crel Meganuclease. <i>Scientific Reports</i> , 2018, 8, 10286.	3.3	12
23	Structure of the Cpf1 endonuclease R-loop complex after target DNA cleavage. <i>Nature</i> , 2017, 546, 559-563.	27.8	170
24	Class 2 CRISPR-Cas RNA-guided endonucleases: Swiss Army knives of genome editing. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 882-892.	8.2	55
25	Assembly of <i>Francisella novicida</i> Cpf1 endonuclease in complex with guide RNA and target DNA. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 409-415.	0.8	6
26	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
27	A novel TPR-BEN domain interaction mediates PICH-BEND3 association. <i>Nucleic Acids Research</i> , 2017, 45, 11413-11424.	14.5	12
28	Electron Microscopy Structural Insights into CPAP Oligomeric Behavior: A Plausible Assembly Process of a Supramolecular Scaffold of the Centrosome. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 17.	3.5	5
29	Allosteric regulation of Csx1, a type IIIB-associated CARF domain ribonuclease by RNAs carrying a tetraadenylate tail. <i>Nucleic Acids Research</i> , 2017, 45, 10740-10750.	14.5	43
30	The genome editing revolution: A CRISPR-Cas TALE off-target story. <i>BioEssays</i> , 2016, 38, S4-S13.	2.5	51
31	The genome editing revolution: A CRISPR-Cas TALE off-target story. <i>Inside the Cell</i> , 2016, 1, 7-16.	0.4	0
32	A Conserved Motif Provides Binding Specificity to the PP2A-B56 Phosphatase. <i>Molecular Cell</i> , 2016, 63, 686-695.	9.7	235
33	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
34	Molecular architecture of the recombinant human MCM2-7 helicase in complex with nucleotides and DNA. <i>Cell Cycle</i> , 2016, 15, 2431-2440.	2.6	8
35	Key Players in I-Dmol Endonuclease Catalysis Revealed from Structure and Dynamics. <i>ACS Chemical Biology</i> , 2016, 11, 1401-1407.	3.4	9
36	TRAIIP is a PCNA-binding ubiquitin ligase that protects genome stability after replication stress. <i>Journal of Cell Biology</i> , 2016, 212, 63-75.	5.2	65

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37	A PTIP-PA1 subcomplex promotes transcription for IgH class switching independently from the associated MLL3/MLL4 methyltransferase complex. <i>Genes and Development</i> , 2016, 30, 149-163.	5.9	27
38	Characterization of the NTPR and BD1 interacting domains of the human PICH-BEND3 complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 646-651.	0.8	5
39	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
40	Engineering a Nickase on the Homing Endonuclease I-Dmol Scaffold. <i>Journal of Biological Chemistry</i> , 2015, 290, 18534-18544.	3.4	7
41	Visualizing phosphodiester-bond hydrolysis by an endonuclease. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 65-72.	8.2	30
42	XTACC3-XMAP215 association reveals an asymmetric interaction promoting microtubule elongation. <i>Nature Communications</i> , 2014, 5, 5072.	12.8	19
43	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
44	Purification, crystallization and preliminary X-ray diffraction analysis of the kinase domain of human tousel-like kinase 2. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 354-357.	0.8	3
45	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
46	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
47	Non-specific protein-DNA interactions control I-Crel target binding and cleavage. <i>Nucleic Acids Research</i> , 2012, 40, 6936-6945.	14.5	24
48	Molecular architecture of a multifunctional MCM complex. <i>Nucleic Acids Research</i> , 2012, 40, 1366-1380.	14.5	22
49	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
50	Crystal structure of the open conformation of the mammalian chaperonin CCT in complex with tubulin. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 14-19.	8.2	128
51	Chaperonins: two rings for folding. <i>Trends in Biochemical Sciences</i> , 2011, 36, 424-432.	7.5	140
52	Molecular basis of engineered meganuclease targeting of the endogenous human RAG1 locus. <i>Nucleic Acids Research</i> , 2011, 39, 729-743.	14.5	63
53	Homing endonucleases: from basics to therapeutic applications. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 727-748.	5.4	73
54	Efficient targeting of a SCID gene by an engineered single-chain homing endonuclease. <i>Nucleic Acids Research</i> , 2009, 37, 5405-5419.	14.5	146

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55	Molecular basis of xeroderma pigmentosum group C DNA recognition by engineered meganucleases. <i>Nature</i> , 2008, 456, 107-111.	27.8	150
56	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
57	Generation and Analysis of Mesophilic Variants of the Thermostable Archaeal I-Dmol Homing Endonuclease. <i>Journal of Biological Chemistry</i> , 2008, 283, 4364-4374.	3.4	17
58	The C-terminal loop of the homing endonuclease I-Crel is essential for site recognition, DNA binding and cleavage. <i>Nucleic Acids Research</i> , 2007, 35, 3262-3271.	14.5	25
59	Engineering of Large Numbers of Highly Specific Homing Endonucleases that Induce Recombination on Novel DNA Targets. <i>Journal of Molecular Biology</i> , 2006, 355, 443-458.	4.2	175