

# Alfonso MondragÃ³n

## List of Publications by Year in descending order

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54  
papers

3,764  
citations

159585

30  
h-index

168389

53  
g-index

61  
all docs

61  
docs citations

61  
times ranked

2917  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures of an active type III-A CRISPR effector complex. <i>Structure</i> , 2022, , .	3.3	4
2	Mechanisms of catalytic RNA molecules. <i>Biochemical Society Transactions</i> , 2021, 49, 1529-1535.	3.4	7
3	Basic residues at the C-gate of DNA gyrase are involved in DNA supercoiling. <i>Journal of Biological Chemistry</i> , 2021, 297, 101000.	3.4	2
4	Crystal structures of an unmodified bacterial tRNA reveal intrinsic structural flexibility and plasticity as general properties of unbound tRNAs. <i>Rna</i> , 2020, 26, 278-289.	3.5	18
5	Crystal structure of an atypical cobalamin riboswitch reveals RNA structural adaptability as basis for promiscuous ligand binding. <i>Nucleic Acids Research</i> , 2020, 48, 7569-7583.	14.5	13
6	Structural organization of a Type III-A CRISPR effector subcomplex determined by X-ray crystallography and cryo-EM. <i>Nucleic Acids Research</i> , 2019, 47, 3765-3783.	14.5	7
7	Crystal Structure of Human Rpp20/Rpp25 Reveals Quaternary Level Adaptation of the Alba Scaffold as Structural Basis for Single-stranded RNA Binding. <i>Journal of Molecular Biology</i> , 2018, 430, 1403-1416.	4.2	4
8	Single-Molecule Magnetic Tweezer Analysis of Topoisomerases. <i>Methods in Molecular Biology</i> , 2018, 1703, 139-152.	0.9	4
9	Specific structural elements of the T-box riboswitch drive the two-step binding of the tRNA ligand. <i>ELife</i> , 2018, 7, .	6.0	24
10	CryoEM structures of open dimers of gyrase A in complex with DNA illuminate mechanism of strand passage. <i>ELife</i> , 2018, 7, .	6.0	26
11	An orthogonal single-molecule experiment reveals multiple-attempt dynamics of type IA topoisomerases. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 484-490.	8.2	21
12	Molecular envelope and atomic model of an anti-terminated glyQS T-box regulator in complex with tRNA <sup>Gly</sup> . <i>Nucleic Acids Research</i> , 2017, 45, 8079-8090.	14.5	10
13	Nucleation of Multiple Buckled Structures in Intertwined DNA Double Helices. <i>Physical Review Letters</i> , 2017, 119, 188103.	7.8	7
14	<i>Methanopyrus kandleri</i> topoisomerase V contains three distinct AP lyase active sites in addition to the topoisomerase active site. <i>Nucleic Acids Research</i> , 2016, 44, 3464-3474.	14.5	9
15	Allosteric transcriptional regulation via changes in the overall topology of the core promoter. <i>Science</i> , 2015, 349, 877-881.	12.6	118
16	Single-molecule analysis uncovers the difference between the kinetics of DNA decatenation by bacterial topoisomerases I and III. <i>Nucleic Acids Research</i> , 2014, 42, 11657-11667.	14.5	29
17	Biochemical Characterization of the Topoisomerase Domain of <i>Methanopyrus kandleri</i> Topoisomerase V. <i>Journal of Biological Chemistry</i> , 2014, 289, 28898-28909.	3.4	6
18	Structure and function of the Tâ€loop structural motif in noncoding <sc>RNAs</sc>. <i>Wiley Interdisciplinary Reviews RNA</i> , 2013, 4, 507-522.	6.4	61

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19	Studies of bacterial topoisomerases I and III at the single-molecule level. <i>Biochemical Society Transactions</i> , 2013, 41, 571-575.	3.4	14
20	Structural Studies of RNase P. <i>Annual Review of Biophysics</i> , 2013, 42, 537-557.	10.0	67
21	Identification of one of the apurinic/aprimidinic lyase active sites of topoisomerase V by structural and functional studies. <i>Nucleic Acids Research</i> , 2013, 41, 657-666.	14.5	8
22	Bacterial topoisomerase I and topoisomerase III relax supercoiled DNA via distinct pathways. <i>Nucleic Acids Research</i> , 2012, 40, 10432-10440.	14.5	47
23	The bacterial ribonuclease P holoenzyme requires specific, conserved residues for efficient catalysis and substrate positioning. <i>Nucleic Acids Research</i> , 2012, 40, 10384-10393.	14.5	16
24	Emerging structural themes in large RNA molecules. <i>Current Opinion in Structural Biology</i> , 2011, 21, 319-326.	5.7	45
25	Solution structures of DNA-bound gyrase. <i>Nucleic Acids Research</i> , 2011, 39, 755-766.	14.5	36
26	Structural basis for spectrin recognition by ankyrin. <i>Blood</i> , 2010, 115, 4093-4101.	1.4	78
27	Crystal structure and functional interpretation of the erythrocyte spectrin tetramerization domain complex. <i>Blood</i> , 2010, 115, 4843-4852.	1.4	66
28	Structures of Minimal Catalytic Fragments of Topoisomerase V Reveals Conformational Changes Relevant for DNA Binding. <i>Structure</i> , 2010, 18, 829-838.	3.3	11
29	Structure of a bacterial ribonuclease P holoenzyme in complex with tRNA. <i>Nature</i> , 2010, 468, 784-789.	27.8	266
30	Structural studies of type I topoisomerases. <i>Nucleic Acids Research</i> , 2009, 37, 693-701.	14.5	102
31	Structures of the spectrin-ankyrin interaction binding domains. <i>Blood</i> , 2009, 113, 5385-5393.	1.4	96
32	Topoisomerase V relaxes supercoiled DNA by a constrained swiveling mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14670-14675.	7.1	57
33	Structural Studies of E. coli Topoisomerase III-DNA Complexes Reveal a Novel Type IA Topoisomerase-DNA Conformational Intermediate. <i>Journal of Molecular Biology</i> , 2007, 368, 105-118.	4.2	32
34	Structure of the N-terminal fragment of topoisomerase V reveals a new family of topoisomerases. <i>EMBO Journal</i> , 2006, 25, 398-408.	7.8	50
35	Structure of ribonuclease P is a universal ribozyme. <i>Current Opinion in Structural Biology</i> , 2006, 16, 327-335.	5.7	76
36	Crystal structure of the RNA component of bacterial ribonuclease P. <i>Nature</i> , 2005, 437, 584-587.	27.8	202

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37	Basis for Structural Diversity in Homologous RNAs. <i>Science</i> , 2004, 306, 104-107.	12.6	136
38	Structural Insights into the Stability and Flexibility of Unusual Erythroid Spectrin Repeats. <i>Structure</i> , 2004, 12, 645-656.	3.3	70
39	Independent Movement, Dimerization and Stability of Tandem Repeats of Chicken Brain $\hat{\iota}$ -Spectrin. <i>Journal of Molecular Biology</i> , 2004, 344, 495-511.	4.2	97
40	DNA manipulators: caught in the act. <i>Current Opinion in Structural Biology</i> , 2003, 13, 15-22.	5.7	8
41	Structure of a Complex between <i>E. coli</i> DNA Topoisomerase I and Single-Stranded DNA. <i>Structure</i> , 2003, 11, 1349-1358.	3.3	42
42	Structure of the bacillus subtilis YCN protein: A putative N-acetyltransferase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 950-952.	2.6	0
43	Crystal structure of the specificity domain of ribonuclease P. <i>Nature</i> , 2003, 421, 760-764.	27.8	222
44	Molecular Basis of Metal-Ion Selectivity and Zeptomolar Sensitivity by CueR. <i>Science</i> , 2003, 301, 1383-1387.	12.6	598
45	On the occurrence of the T-loop RNA folding motif in large RNA molecules. <i>Rna</i> , 2003, 9, 640-643.	3.5	81
46	Biochemical Characterization of an Invariant Histidine Involved in <i>Escherichia coli</i> DNA Topoisomerase I Catalysis. <i>Journal of Biological Chemistry</i> , 2002, 277, 13237-13245.	3.4	25
47	The Mechanism of Type IA Topoisomerase-Mediated DNA Topological Transformations. <i>Molecular Cell</i> , 2001, 7, 301-307.	9.7	48
48	Crystal structure of a complex of a type IA DNA topoisomerase with a single-stranded DNA molecule. <i>Nature</i> , 2001, 411, 1077-1081.	27.8	100
49	Identification of a unique domain essential for <i>Escherichia coli</i> DNA topoisomerase III-catalysed decatenation of replication intermediates. <i>Molecular Microbiology</i> , 2000, 35, 888-895.	2.5	42
50	Conformational changes in <i>E. coli</i> DNA topoisomerase I. <i>Nature Structural Biology</i> , 1999, 6, 918-922.	9.7	46
51	The structure of <i>Escherichia coli</i> DNA topoisomerase III. <i>Structure</i> , 1999, 7, 1373-1383.	3.3	75
52	Structures of Two Repeats of Spectrin Suggest Models of Flexibility. <i>Cell</i> , 1999, 98, 523-535.	28.9	228
53	Solving the cis/trans paradox in the Int family of recombinases. <i>Nature Structural Biology</i> , 1997, 4, 427-429.	9.7	5
54	Three-dimensional structure of the 67K N-terminal fragment of <i>E. coli</i> DNA topoisomerase I. <i>Nature</i> , 1994, 367, 138-146.	27.8	302