

Xiang-Jun Lu

List of Publications by Year in descending order

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37
papers

4,662
citations

304743

22
h-index

330143

37
g-index

40
all docs

40
docs citations

40
times ranked

4827
citing authors

#	ARTICLE	IF	CITATIONS
1	3DNA: a software package for the analysis, rebuilding and visualization of three-dimensional nucleic acid structures. <i>Nucleic Acids Research</i> , 2003, 31, 5108-5121.	14.5	1,470
2	3DNA: a versatile, integrated software system for the analysis, rebuilding and visualization of three-dimensional nucleic-acid structures. <i>Nature Protocols</i> , 2008, 3, 1213-1227.	12.0	572
3	A standard reference frame for the description of nucleic acid base-pair geometry 1 Edited by P. E. Wright 2 This is a document of the Nomenclature Committee of IUBMB (NC-IUBMB)/IUPAC-IUBMB Joint Commission on Biochemical Nomenclature (JCBN), whose members are R. Cammack (chairman), A. Bairoch, H.M. Berman, S. Boyce, C.R. Cantor, K. Elliott, D. Horton, M. Kanehisa, A. Kotyk, G.P. Moss, N. Sharon and K.F. Tipton. <i>Journal of Molecular Biology</i> , 2001, 313, 229-237.	4.2	533
4	A-form Conformational Motifs in Ligand-bound DNA Structures. <i>Journal of Molecular Biology</i> , 2000, 300, 819-840.	4.2	326
5	Web 3DNA—a web server for the analysis, reconstruction, and visualization of three-dimensional nucleic-acid structures. <i>Nucleic Acids Research</i> , 2009, 37, W240-W246.	14.5	276
6	DSSR: an integrated software tool for dissecting the spatial structure of RNA. <i>Nucleic Acids Research</i> , 2015, 43, gkv716.	14.5	204
7	Web 3DNA 2.0 for the analysis, visualization, and modeling of 3D nucleic acid structures. <i>Nucleic Acids Research</i> , 2019, 47, W26-W34.	14.5	189
8	Hotspots of transcription factor colocalization in the genome of <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12027-12032.	7.1	182
9	DNA base-stacking interactions: a comparison of theoretical calculations with oligonucleotide X-ray crystal structures. <i>Journal of Molecular Biology</i> , 1997, 265, 603-619.	4.2	114
10	Resolving the discrepancies among nucleic acid conformational analyses 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1999, 285, 1563-1575.	4.2	91
11	Structure and conformation of helical nucleic acids: analysis program (SCHNAaP) 1 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1997, 273, 668-680.	4.2	75
12	Bending of DNA by Asymmetric Charge Neutralization: All-Atom Energy Simulations. <i>Journal of the American Chemical Society</i> , 2002, 124, 4838-4847.	13.7	61
13	Toward A Mechanistic Understanding of DNA Methylation Readout by Transcription Factors. <i>Journal of Molecular Biology</i> , 2020, 432, 1801-1815.	4.2	54
14	Structure and conformation of helical nucleic acids: rebuilding program (SCHNArP) 1 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1997, 273, 681-691.	4.2	50
15	Analyzing and Building Nucleic Acid Structures with 3DNA. <i>Journal of Visualized Experiments</i> , 2013, , e4401.	0.3	43
16	DSSR-enhanced visualization of nucleic acid structures in Jmol. <i>Nucleic Acids Research</i> , 2017, 45, W528-W533.	14.5	42
17	Linking tumor cell cytotoxicity to mechanism of drug action: An integrated analysis of gene expression, small-molecule screening and structural databases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 403-433.	2.6	39
18	Transitions of Double-Stranded DNA Between the A- and B-Forms. <i>Journal of Physical Chemistry B</i> , 2016, 120, 8449-8456.	2.6	38

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19	Overview of Nucleic Acid Analysis Programs. Journal of Biomolecular Structure and Dynamics, 1999, 16, 833-843.	3.5	37
20	Inferring Condition-Specific Modulation of Transcription Factor Activity in Yeast through Regulon-Based Analysis of Genomewide Expression. PLoS ONE, 2008, 3, e3112.	2.5	35
21	The RNA backbone plays a crucial role in mediating the intrinsic stability of the GpU dinucleotide platform and the GpUpA/CpA miniduplex. Nucleic Acids Research, 2010, 38, 4868-4876.	14.5	32
22	New information content in RNA base pairing deduced from quantitative analysis of high-resolution structures. Methods, 2009, 47, 177-186.	3.8	25
23	Understanding the Sequence Preference of Recurrent RNA Building Blocks Using Quantum Chemistry: The Intrastrand RNA Dinucleotide Platform. Journal of Chemical Theory and Computation, 2012, 8, 335-347.	5.3	25
24	Detecting transcriptionally active regions using genomic tiling arrays. Genome Biology, 2006, 7, R59.	9.6	19
25	DSSR-enabled innovative schematics of 3D nucleic acid structures with PyMOL. Nucleic Acids Research, 2020, 48, e74.	14.5	19
26	Effects of Noncanonical Base Pairing on RNA Folding: Structural Context and Spatial Arrangements of GÂ·A Pairs. Biochemistry, 2019, 58, 2474-2487.	2.5	18
27	Construction of Double-helical DNA Structures Based on Dinucleotide Building Blocks. Journal of Biomolecular Structure and Dynamics, 1997, 14, 747-756.	3.5	14
28	A Structural Similarity Analysis of Double-helical DNA. Journal of Molecular Biology, 2004, 343, 879-889.	4.2	14
29	DNA Conformational Changes Play a Force-Generating Role during Bacteriophage Genome Packaging. Biophysical Journal, 2019, 116, 2172-2180.	0.5	13
30	3DNALandscapes: a database for exploring the conformational features of DNA. Nucleic Acids Research, 2010, 38, D267-D274.	14.5	12
31	Weak operator binding enhances simulated lac repressor-mediated DNA looping. Biopolymers, 2013, 99, n/a-n/a.	2.4	11
32	DNA Scrunching in the Packaging of Viral Genomes. Journal of Physical Chemistry B, 2016, 120, 6200-6207.	2.6	10
33	New restraints and validation approaches for nucleic acid structures in <i>PDB-REDO</i>. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1127-1141.	2.3	6
34	Feature Extraction Using Molecular Planes for Fuzzy Relational Clustering of a Flexible Dopamine Reuptake Inhibitor. Journal of Chemical Information and Modeling, 2007, 47, 2216-2227.	5.4	5
35	Parallels between DNA and collagen â€“ comparing elastic models of the double and triple helix. Scientific Reports, 2017, 7, 12802.	3.3	4
36	Algorithm for rapid retrieval of elemental information. Computers & Chemistry, 1993, 17, 331-333.	1.2	1

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37	A structure-based method for identifying DNA-binding proteins and their sites of DNA-interaction. Journal of Structural and Functional Genomics, 2004, 5, 255-265.	1.2	1