

Francois Major

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

4,175
citations

218381

26
h-index

189595

50
g-index

58
all docs

58
docs citations

58
times ranked

4704
citing authors

#	ARTICLE	IF	CITATIONS
1	The MC-Fold and MC-Sym pipeline infers RNA structure from sequence data. <i>Nature</i> , 2008, 452, 51-55.	13.7	726
2	An E2F/miR-20a Autoregulatory Feedback Loop. <i>Journal of Biological Chemistry</i> , 2007, 282, 2135-2143.	1.6	521
3	Autism-related deficits via dysregulated eIF4E-dependent translational control. <i>Nature</i> , 2013, 493, 371-377.	13.7	451
4	<i>RNA-Puzzles</i> : A CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012, 18, 610-625.	1.6	241
5	Quantitative analysis of nucleic acid three-dimensional structures. <i>Journal of Molecular Biology</i> , 2001, 308, 919-936.	2.0	161
6	<i>RNA-Puzzles</i> Round II: assessment of RNA structure prediction programs applied to three large RNA structures. <i>Rna</i> , 2015, 21, 1066-1084.	1.6	161
7	<i>RNA-Puzzles</i> Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	1.6	158
8	Function of Hexameric RNA in Packaging of Bacteriophage ϕ 29 DNA In Vitro. <i>Molecular Cell</i> , 1998, 2, 141-147.	4.5	153
9	New metrics for comparing and assessing discrepancies between RNA 3D structures and models. <i>Rna</i> , 2009, 15, 1875-1885.	1.6	138
10	RNA canonical and non-canonical base pairing types: a recognition method and complete repertoire. <i>Nucleic Acids Research</i> , 2002, 30, 4250-4263.	6.5	133
11	<i>RNA-Puzzles</i> Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	1.6	100
12	RNAML: A standard syntax for exchanging RNA information. <i>Rna</i> , 2002, 8, 707-717.	1.6	91
13	Identification of a Conserved RNA Motif Essential for She2p Recognition and mRNA Localization to the Yeast Bud. <i>Molecular and Cellular Biology</i> , 2005, 25, 4752-4766.	1.1	89
14	Modeling the Three-dimensional Structure of RNA Using Discrete Nucleotide Conformational Sets. <i>Journal of Molecular Biology</i> , 1993, 229, 1049-1064.	2.0	85
15	Pattern searching/alignment with RNA primary and secondary structures: an effective descriptor for tRNA. <i>Bioinformatics</i> , 1990, 6, 325-331.	1.8	62
16	NMR structure of the active conformation of the Varkud satellite ribozyme cleavage site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7003-7008.	3.3	61
17	Structural Basis for the Guanosine Requirement of the Hairpin Ribozyme. <i>Biochemistry</i> , 1999, 38, 16035-16039.	1.2	60
18	The RNA Ontology Consortium: An open invitation to the RNA community. <i>Rna</i> , 2006, 12, 533-541.	1.6	59

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19	RNA Structure Determination Using SAXS Data. <i>Journal of Physical Chemistry B</i> , 2010, 114, 10039-10048.	1.2	58
20	Automated extraction and classification of RNA tertiary structure cyclic motifs. <i>Nucleic Acids Research</i> , 2006, 34, 2340-2346.	6.5	52
21	Recognition and coupling of A-to-I edited sites are determined by the tertiary structure of the RNA. <i>Nucleic Acids Research</i> , 2009, 37, 6916-6926.	6.5	47
22	Apoptotic endothelial cells release small extracellular vesicles loaded with immunostimulatory viral-like RNAs. <i>Scientific Reports</i> , 2019, 9, 7203.	1.6	46
23	The ERPIN server: an interface to profile-based RNA motif identification. <i>Nucleic Acids Research</i> , 2004, 32, W160-W165.	6.5	43
24	Towards 3D structure prediction of large RNA molecules: an integer programming framework to insert local 3D motifs in RNA secondary structure. <i>Bioinformatics</i> , 2012, 28, i207-i214.	1.8	41
25	Designing small multiple-target artificial RNAs. <i>Nucleic Acids Research</i> , 2010, 38, e140-e140.	6.5	36
26	Modeling active RNA structures using the intersection of conformational space: Application to the lead-activated ribozyme. <i>Rna</i> , 1998, 4, 739-749.	1.6	27
27	The hairpin ribozyme substrate binding-domain: A highly constrained D-shaped conformation. <i>Journal of Molecular Biology</i> , 2001, 307, 51-65.	2.0	27
28	Computational methods for RNA structure determination. <i>Current Opinion in Structural Biology</i> , 2001, 11, 282-286.	2.6	27
29	A comparative analysis of the triloops in all high-resolution RNA structures reveals sequence-structure relationships. <i>Rna</i> , 2007, 13, 1537-1545.	1.6	25
30	Modeling RNA tertiary structure motifs by graph-grammars. <i>Nucleic Acids Research</i> , 2007, 35, 1726-1736.	6.5	24
31	Role of SLV in SLI substrate recognition by the <i>Neurospora</i> VS ribozyme. <i>Rna</i> , 2008, 14, 736-748.	1.6	24
32	NMR structure of a 4 Å— 4 nucleotide RNA internal loop from an R2 retrotransposon: Identification of a three purine-purine sheared pair motif and comparison to MC-SYM predictions. <i>Rna</i> , 2011, 17, 1664-1677.	1.6	24
33	Determining RNA three-dimensional structures using low-resolution data. <i>Journal of Structural Biology</i> , 2012, 179, 252-260.	1.3	24
34	Structural messenger RNA contains cytoke- ratin polymerization and depolymerization signals. <i>Cell and Tissue Research</i> , 2011, 346, 209-222.	1.5	19
35	A new catalog of protein β^2 -sheets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 545-558.	1.5	18
36	MIRBooking simulates the stoichiometric mode of action of microRNAs. <i>Nucleic Acids Research</i> , 2015, 43, 6730-6738.	6.5	18

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37	Ranking the factors that contribute to protein β -sheet folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 824-829.	1.5	17
38	Structural dynamics control the MicroRNA maturation pathway. <i>Nucleic Acids Research</i> , 2016, 44, gkw793.	6.5	17
39	RNA-MolIP: prediction of RNA secondary structure and local 3D motifs from sequence data. <i>Nucleic Acids Research</i> , 2017, 45, W440-W444.	6.5	17
40	Implication of the prohead RNA in phage ϕ 29 DNA packaging. <i>Biochimie</i> , 2002, 84, 945-951.	1.3	14
41	Exploring Alternative RNA Structure Sets Using MC-Flashfold and db2cm. <i>Methods in Molecular Biology</i> , 2016, 1490, 237-251.	0.4	13
42	Noncoding regions of <i>C. elegans</i> mRNA undergo selective adenosine to inosine deamination and contain a small number of editing sites per transcript. <i>RNA Biology</i> , 2015, 12, 162-174.	1.5	12
43	Leadzyme. <i>Methods in Enzymology</i> , 2001, 341, 518-540.	0.4	9
44	Molecular basis of TRAP σ 54 ^{SL} RNA interaction in the <i>Bacillus subtilis</i> <i>trp</i> operon transcription attenuation mechanism. <i>Rna</i> , 2009, 15, 55-66.	1.6	9
45	RKB: a Semantic Web knowledge base for RNA. <i>Journal of Biomedical Semantics</i> , 2010, 1, S2.	0.9	5
46	The sequence features that define efficient and specific hAGO2-dependent miRNA silencing guides. <i>Nucleic Acids Research</i> , 2018, 46, 8181-8196.	6.5	5
47	Domain generating functions for solving constraint satisfaction problems. <i>Journal of Functional Programming</i> , 1991, 1, 213-227.	0.5	4
48	Computational identification of RNA functional determinants by three-dimensional quantitative structure-activity relationships. <i>Nucleic Acids Research</i> , 2014, 42, 11261-11271.	6.5	4
49	Modifications and deletions of helices within the hairpin ribozyme-substrate complex: An active ribozyme lacking helix 1. <i>Rna</i> , 2004, 10, 395-402.	1.6	3
50	Exploring the conformations of nucleic acids. <i>Journal of Functional Programming</i> , 1995, 5, 443-460.	0.5	1