## Joel R Gillespie

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4825378/publications.pdf

Version: 2024-02-01

20 papers 3,839 citations

623188 14 h-index 940134 16 g-index

20 all docs

20 docs citations

times ranked

20

6372 citing authors

#	Article	IF	CITATIONS
1	RNA folding on the 3D triangular lattice. BMC Bioinformatics, 2009, 10, 369.	1.2	14
2	The Second Cu(II)-Binding Site in a Proton-Rich Environment Interferes with the Aggregation of Amyloid- $\hat{l}^2(1\hat{a}^340)$ into Amyloid Fibrils. Biochemistry, 2009, 48, 10724-10732.	1.2	50
3	uShuffle: A useful tool for shuffling biological sequences while preserving the k-let counts. BMC Bioinformatics, 2008, 9, 192.	1.2	139
4	Engineering the Divide-and-Conquer Closest Pair Algorithm. Journal of Computer Science and Technology, 2007, 22, 532-540.	0.9	7
5	Delta: A Toolset for the Structural Analysis of Biological Sequences on a 3D Triangular Lattice. , 2007, , 518-529.		3
6	Closing the Folding Chamber of the Eukaryotic Chaperonin Requires the Transition State of ATP Hydrolysis. Cell, 2003, 113, 369-381.	13.5	195
7	Structural and Functional Properties of Yersinia pestis Caf1 Capsular Antigen and Their Possible Role in Fulminant Development of Primary Pneumonic Plague. Journal of Proteome Research, 2002, 1, 307-315.	1.8	12
8	Partially Folded Intermediates as Critical Precursors of Light Chain Amyloid Fibrils and Amorphous Aggregatesâ€. Biochemistry, 2001, 40, 3525-3535.	1.2	306
9	Structural and Functional Similarity between Yersinia pestis Capsular Protein Caf1 and Human Interleukin- $1\hat{l}^2$ . Biochemistry, 2001, 40, 6076-6084.	1.2	20
10	Why are ?natively unfolded? proteins unstructured under physiologic conditions?. Proteins: Structure, Function and Bioinformatics, 2000, 41, 415-427.	1.5	1,931
11	Structure and function of α-fetoprotein: a biophysical overview. BBA - Proteins and Proteomics, 2000, 1480, 41-56.	2.1	79
12	Zn2+-Mediated Structure Formation and Compaction of the "Natively Unfolded―Human Prothymosin α. Biochemical and Biophysical Research Communications, 2000, 267, 663-668.	1.0	72
13	Why are "natively unfolded―proteins unstructured under physiologic conditions?. , 2000, 41, 415.		4
14	Why are "natively unfolded―proteins unstructured under physiologic conditions?. , 2000, 41, 415.		18
15	Monitoring the assembly of Ig light-chain amyloid fibrils by atomic force microscopy. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 13175-13179.	3.3	198
16	Natively Unfolded Human Prothymosin α Adopts Partially Folded Collapsed Conformation at Acidic pHâ€. Biochemistry, 1999, 38, 15009-15016.	1.2	145
17	Characterization of long-range structure in the denatured state of staphylococcal nuclease. II. distance restraints from paramagnetic relaxation and calculation of an ensemble of structures. Journal of Molecular Biology, 1997, 268, 170-184.	2.0	281
18	Characterization of long-range structure in the denatured state of staphylococcal nuclease. I. paramagnetic relaxation enhancement by nitroxide spin labels. Journal of Molecular Biology, 1997, 268, 158-169.	2.0	299

#	Article	IF	CITATIONS
19	Protein folding for realists: A timeless phenomenon. Protein Science, 1996, 5, 991-1000.	3.1	37
20	Why are "natively unfolded―proteins unstructured under physiologic conditions?. , 0, .		29