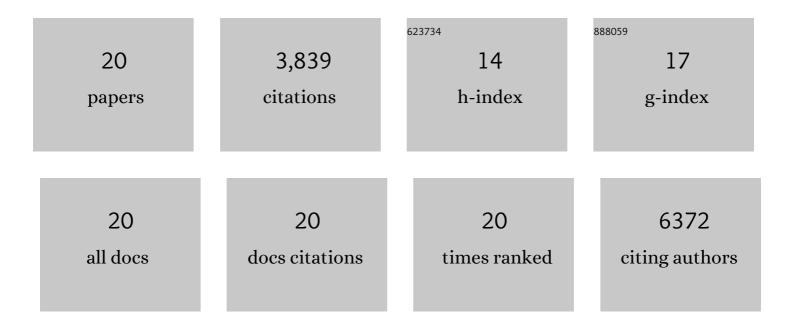
Joel R Gillespie

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Why are ?natively unfolded? proteins unstructured under physiologic conditions?. Proteins: Structure, Function and Bioinformatics, 2000, 41, 415-427.	2.6	1,931
2	Partially Folded Intermediates as Critical Precursors of Light Chain Amyloid Fibrils and Amorphous Aggregatesâ€. Biochemistry, 2001, 40, 3525-3535.	2.5	306
3	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.	4.2	299
4	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.	4.2	281
5	Monitoring the assembly of Ig light-chain amyloid fibrils by atomic force microscopy. Proceedings of the United States of America, 1999, 96, 13175-13179.	7.1	198
6	Closing the Folding Chamber of the Eukaryotic Chaperonin Requires the Transition State of ATP Hydrolysis. Cell, 2003, 113, 369-381.	28.9	195
7	Natively Unfolded Human Prothymosin α Adopts Partially Folded Collapsed Conformation at Acidic pH. Biochemistry, 1999, 38, 15009-15016.	2.5	145
8	uShuffle: A useful tool for shuffling biological sequences while preserving the k-let counts. BMC Bioinformatics, 2008, 9, 192.	2.6	139
9	Structure and function of $\hat{l}\pm$ -fetoprotein: a biophysical overview. BBA - Proteins and Proteomics, 2000, 1480, 41-56.	2.1	79
10	Zn2+-Mediated Structure Formation and Compaction of the "Natively Unfolded―Human Prothymosin α. Biochemical and Biophysical Research Communications, 2000, 267, 663-668.	2.1	72
11	The Second Cu(II)-Binding Site in a Proton-Rich Environment Interferes with the Aggregation of Amyloid-β(1â~40) into Amyloid Fibrils. Biochemistry, 2009, 48, 10724-10732.	2.5	50
12	Protein folding for realists: A timeless phenomenon. Protein Science, 1996, 5, 991-1000.	7.6	37
13	Why are $\hat{a}\in \hat{c}$ and \hat{c}		29
14	Structural and Functional Similarity between Yersinia pestis Capsular Protein Caf1 and Human Interleukin-1β. Biochemistry, 2001, 40, 6076-6084.	2.5	20
15	Why are "natively unfolded―proteins unstructured under physiologic conditions?. Proteins: Structure, Function and Bioinformatics, 2000, 41, 415-427.	2.6	18
16	RNA folding on the 3D triangular lattice. BMC Bioinformatics, 2009, 10, 369.	2.6	14
17	Structural and Functional Properties ofYersinia pestisCaf1 Capsular Antigen and Their Possible Role in Fulminant Development of Primary Pneumonic Plague. Journal of Proteome Research, 2002, 1, 307-315.	3.7	12
18	Engineering the Divide-and-Conquer Closest Pair Algorithm. Journal of Computer Science and Technology, 2007, 22, 532-540.	1.5	7

#	Article	IF	CITATIONS
19	Why are "natively unfolded―proteins unstructured under physiologic conditions?. , 2000, 41, 415.		4
20	Delta: A Toolset for the Structural Analysis of Biological Sequences on a 3D Triangular Lattice. , 2007, , 518-529.		3