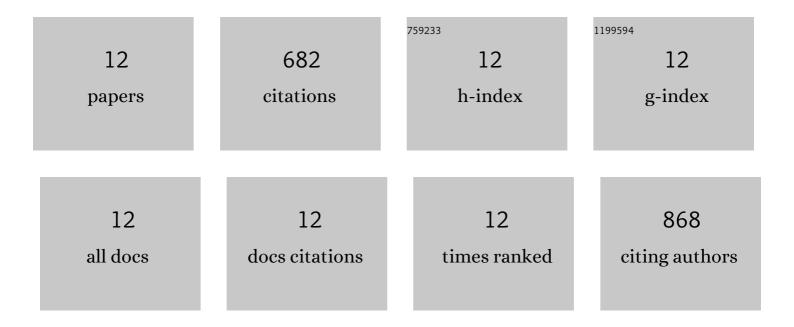
Michael J Bradley

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	ATP Utilization and RNA Conformational Rearrangement by DEAD-Box Proteins. Annual Review of Biophysics, 2012, 41, 247-267.	10.0	97
2	Discovery and Characterization of SY-1365, a Selective, Covalent Inhibitor of CDK7. Cancer Research, 2019, 79, 3479-3491.	0.9	91
3	Identification of cation-binding sites on actin that drive polymerization and modulate bending stiffness. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16923-16927.	7.1	79
4	Nickel-Specific Response in the Transcriptional Regulator,EscherichiacoliNikR. Journal of the American Chemical Society, 2007, 129, 5085-5095.	13.7	72
5	Molecular Dynamics Simulation of the Escherichia coli NikR Protein: Equilibrium Conformational Fluctuations Reveal Interdomain Allosteric Communication Pathways. Journal of Molecular Biology, 2008, 378, 1155-1173.	4.2	63
6	Mechanism of Mss116 ATPase Reveals Functional Diversity of DEAD-Box Proteins. Journal of Molecular Biology, 2011, 409, 399-414.	4.2	63
7	Selective inhibition of CDK7 reveals high-confidence targets and new models for TFIIH function in transcription. Genes and Development, 2020, 34, 1452-1473.	5.9	47
8	Site-specific cation release drives actin filament severing by vertebrate cofilin. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17821-17826.	7.1	45
9	Cations Stiffen Actin Filaments by Adhering a Key Structural Element to Adjacent Subunits. Journal of Physical Chemistry B, 2016, 120, 4558-4567.	2.6	39
10	Regulation of Actin by Ion-Linked Equilibria. Biophysical Journal, 2013, 105, 2621-2628.	0.5	37
11	Discovery of SY-5609: A Selective, Noncovalent Inhibitor of CDK7. Journal of Medicinal Chemistry, 2022, 65, 1458-1480.	6.4	31
12	Analyzing ATP Utilization by DEAD-Box RNA Helicases Using Kinetic and Equilibrium Methods. Methods in Enzymology, 2012, 511, 29-63.	1.0	18