James T Macdonald

List of Publications by Year
in descending order

23 papers	1,101 citations	471509 17 h-index	642732 23 g-index
25 all docs	25 docs citations	25 times ranked	1583 citing authors

#	Article	IF	Citations
1	Rapid acquisition and model-based analysis of cell-free transcription–translation reactions from nonmodel bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4340-E4349.	7.1	162
2	Development of a Bacillus subtilis cell-free transcription-translation system for prototyping regulatory elements. Metabolic Engineering, 2016, 38, 370-381.	7.0	112
3	One-pot DNA construction for synthetic biology: the Modular Overlap-Directed Assembly with Linkers (MODAL) strategy. Nucleic Acids Research, 2014, 42, e7-e7.	14.5	99
4	Probing the "Dark Matter" of Protein Fold Space. Structure, 2009, 17, 1244-1252.	3.3	85
5	Developments in the Tools and Methodologies of Synthetic Biology. Frontiers in Bioengineering and Biotechnology, 2014, 2, 60.	4.1	78
6	Computational design approaches and tools for synthetic biology. Integrative Biology (United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542	1.3	74
7	Delineation of metabolic gene clusters in plant genomes by chromatin signatures. Nucleic Acids Research, 2016, 44, 2255-2265.	14.5	66
8	R2oDNA Designer: Computational Design of Biologically Neutral Synthetic DNA Sequences. ACS Synthetic Biology, 2014, 3, 525-528.	3.8	63
9	High–quality protein backbone reconstruction from alpha carbons using Gaussian mixture models. Journal of Computational Chemistry, 2013, 34, 1881-1889.	3.3	52
10	*De novo* backbone scaffolds for protein design. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1311-1325.	2.6	37
11	Cell-free synthetic biology for *in vitro* prototype engineering. Biochemical Society Transactions, 2017, 45, 785-791.	3.4	37
12	Cell-Free Protein Synthesis as a Prototyping Platform for Mammalian Synthetic Biology. ACS Synthetic Biology, 2020, 9, 144-156.	3.8	31
13	Unfolding crystallins: The destabilizing role of a β-hairpin cysteine in βB2-crystallin by simulation and experiment. Protein Science, 2005, 14, 1282-1292.	7.6	30
14	Atomic Structure of Type VI Contractile Sheath from Pseudomonas aeruginosa. Structure, 2018, 26, 329-336.e3.	3.3	29
15	Synthetic beta-solenoid proteins with the fragment-free computational design of a beta-hairpin extension. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10346-10351.	7.1	28
16	Structural and Mechanistic Insight into the Listeria monocytogenes Two-enzyme Lipoteichoic Acid Synthesis System. Journal of Biological Chemistry, 2014, 289, 28054-28069.	3.4	25
17	Electron momentum states and bremsstrahlung radiation from the ultraintense field ionization of atoms. Optics Express, 2004, 12, 3911.	3.4	19
18	Structural basis for the recognition and cleavage of abasic DNA in *Neisseria meningitidis*. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16852-16857.	7.1	19

#	Article	IF	Citations
19	Computational protein design with backbone plasticity. Biochemical Society Transactions, 2016, 44, 1523-1529.	3.4	16
20	Validating a Coarse-Grained Potential Energy Function through Protein Loop Modelling. PLoS ONE, 2013, 8, e65770.	2.5	14
21	Computational Sequence Design with R2oDNA Designer. Methods in Molecular Biology, 2017, 1651, 249-262.	0.9	12
22	Analytic Markovian Rates for Generalized Protein Structure Evolution. PLoS ONE, 2012, 7, e34228.	2.5	7
23	Comparison of Generalised Born/Surface Area with Periodic Boundary Simulations to Study Protein Unfolding. Molecular Simulation, 2004, 30, 333-340.	2.0	2