## James T Macdonald

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2238951/publications.pdf

Version: 2024-02-01

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

#	Article	IF	CITATIONS
1	Cell-Free Protein Synthesis as a Prototyping Platform for Mammalian Synthetic Biology. ACS Synthetic Biology, 2020, 9, 144-156.	3.8	31
2	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
3	Atomic Structure of Type VI Contractile Sheath from Pseudomonas aeruginosa. Structure, 2018, 26, 329-336.e3.	3.3	29
4	Cell-free synthetic biology for <i>in vitro</i> prototype engineering. Biochemical Society Transactions, 2017, 45, 785-791.	3 <b>.</b> 4	37
5	Computational Sequence Design with R2oDNA Designer. Methods in Molecular Biology, 2017, 1651, 249-262.	0.9	12
6	Delineation of metabolic gene clusters in plant genomes by chromatin signatures. Nucleic Acids Research, 2016, 44, 2255-2265.	14.5	66
7	Development of a Bacillus subtilis cell-free transcription-translation system for prototyping regulatory elements. Metabolic Engineering, 2016, 38, 370-381.	7.0	112
8	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
9	Computational protein design with backbone plasticity. Biochemical Society Transactions, 2016, 44, 1523-1529.	3.4	16
10	Developments in the Tools and Methodologies of Synthetic Biology. Frontiers in Bioengineering and Biotechnology, 2014, 2, 60.	4.1	78
11	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
12	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
13	R2oDNA Designer: Computational Design of Biologically Neutral Synthetic DNA Sequences. ACS Synthetic Biology, 2014, 3, 525-528.	3.8	63
14	High–quality protein backbone reconstruction from alpha carbons using Gaussian mixture models. Journal of Computational Chemistry, 2013, 34, 1881-1889.	3.3	52
15	Validating a Coarse-Grained Potential Energy Function through Protein Loop Modelling. PLoS ONE, 2013, 8, e65770.	2.5	14
16	Structural basis for the recognition and cleavage of abasic DNA in <i>Neisseria meningitidis</i> Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16852-16857.	7.1	19
17	Analytic Markovian Rates for Generalized Protein Structure Evolution. PLoS ONE, 2012, 7, e34228.	2.5	7

 $Computational\ design\ approaches\ and\ tools\ for\ synthetic\ biology.\ Integrative\ Biology\ (United)\ Tj\ ETQq0\ 0\ 0\ rgBT\ / Overlock\ 10\ Tf\ 50\ 62$ 

18

#	Article	IF	CITATIONS
19	<i>De novo</i> backbone scaffolds for protein design. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1311-1325.	2.6	37
20	Probing the "Dark Matter―of Protein Fold Space. Structure, 2009, 17, 1244-1252.	3.3	85
21	Unfolding crystallins: The destabilizing role of a $\hat{l}^2$ -hairpin cysteine in $\hat{l}^2$ B2-crystallin by simulation and experiment. Protein Science, 2005, 14, 1282-1292.	7.6	30
22	Comparison of Generalised Born/Surface Area with Periodic Boundary Simulations to Study Protein Unfolding. Molecular Simulation, 2004, 30, 333-340.	2.0	2
23	Electron momentum states and bremsstrahlung radiation from the ultraintense field ionization of atoms. Optics Express, 2004, 12, 3911.	3.4	19