

William M Jacobs

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

1,325
citations

516710

16
h-index

794594

19
g-index

25
all docs

25
docs citations

25
times ranked

1745
citing authors

#	ARTICLE	IF	CITATIONS
1	Competing Protein-RNA Interaction Networks Control Multiphase Intracellular Organization. <i>Cell</i> , 2020, 181, 306-324.e28.	28.9	543
2	Phase Transitions in Biological Systems with Many Components. <i>Biophysical Journal</i> , 2017, 112, 683-691.	0.5	121
3	Rational design of self-assembly pathways for complex multicomponent structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6313-6318.	7.1	97
4	Evidence of evolutionary selection for cotranslational folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11434-11439.	7.1	90
5	Self-Assembly of Structures with Addressable Complexity. <i>Journal of the American Chemical Society</i> , 2016, 138, 2457-2467.	13.7	73
6	Accessibility of the Shine-Dalgarno Sequence Dictates N-Terminal Codon Bias in <i>E. coli</i> . <i>Molecular Cell</i> , 2018, 70, 894-905.e5.	9.7	58
7	Predicting phase behavior in multicomponent mixtures. <i>Journal of Chemical Physics</i> , 2013, 139, 024108.	3.0	46
8	Cotranslational folding allows misfolding-prone proteins to circumvent deep kinetic traps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1485-1495.	7.1	44
9	Self-Assembly of Biomolecular Condensates with Shared Components. <i>Physical Review Letters</i> , 2021, 126, 258101.	7.8	43
10	Communication: Theoretical prediction of free-energy landscapes for complex self-assembly. <i>Journal of Chemical Physics</i> , 2015, 142, 021101.	3.0	34
11	Phase separation in solutions with specific and nonspecific interactions. <i>Journal of Chemical Physics</i> , 2014, 140, 204109.	3.0	29
12	Self-assembly of photonic crystals by controlling the nucleation and growth of DNA-coated colloids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	28
13	Structure-Based Prediction of Protein-Folding Transition Paths. <i>Biophysical Journal</i> , 2016, 111, 925-936.	0.5	27
14	Direct observation and rational design of nucleation behavior in addressable self-assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5877-E5886.	7.1	22
15	Effect of Protein Structure on Evolution of Cotranslational Folding. <i>Biophysical Journal</i> , 2020, 119, 1123-1134.	0.5	19
16	Self-assembly protocol design for periodic multicomponent structures. <i>Soft Matter</i> , 2015, 11, 8930-8938.	2.7	17
17	Accurate Protein-Folding Transition-Path Statistics from a Simple Free-Energy Landscape. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11126-11136.	2.6	13
18	Validation of DBFOLD: An efficient algorithm for computing folding pathways of complex proteins. <i>PLoS Computational Biology</i> , 2020, 16, e1008323.	3.2	11

#	ARTICLE	IF	CITATIONS
19	Oligomers of Heat-Shock Proteins: Structures That Donâ€™t Imply Function. PLoS Computational Biology, 2016, 12, e1004756.	3.2	9
20	Validation of DBFOLD: An efficient algorithm for computing folding pathways of complex proteins. , 2020, 16, e1008323.		0
21	Validation of DBFOLD: An efficient algorithm for computing folding pathways of complex proteins. , 2020, 16, e1008323.		0
22	Validation of DBFOLD: An efficient algorithm for computing folding pathways of complex proteins. , 2020, 16, e1008323.		0
23	Validation of DBFOLD: An efficient algorithm for computing folding pathways of complex proteins. , 2020, 16, e1008323.		0
24	Validation of DBFOLD: An efficient algorithm for computing folding pathways of complex proteins. , 2020, 16, e1008323.		0