

# Sarah Rauscher

## List of Publications by Citations

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**Version:** 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

18  
papers

2,867  
citations

12  
h-index

22  
g-index

22  
ext. papers

4,119  
ext. citations

5.9  
avg. IF

5.27  
L-index

#	Paper	IF	Citations
18	CHARMM36m: an improved force field for folded and intrinsically disordered proteins. <i>Nature Methods</i> , <b>2017</b> , 14, 71-73	21.6	1819
17	Structural Ensembles of Intrinsically Disordered Proteins Depend Strongly on Force Field: A Comparison to Experiment. <i>Journal of Chemical Theory and Computation</i> , <b>2015</b> , 11, 5513-24	6.4	281
16	Proline and glycine control protein self-organization into elastomeric or amyloid fibrils. <i>Structure</i> , <b>2006</b> , 14, 1667-76	5.2	274
15	The liquid structure of elastin. <i>ELife</i> , <b>2017</b> , 6,	8.9	83
14	Accelerating Convergence in Molecular Dynamics Simulations of Solutes in Lipid Membranes by Conducting a Random Walk along the Bilayer Normal. <i>Journal of Chemical Theory and Computation</i> , <b>2013</b> , 9, 3686-703	6.4	73
13	Molecular simulations of protein disorder. <i>Biochemistry and Cell Biology</i> , <b>2010</b> , 88, 269-90	3.6	65
12	Improving Internal Peptide Dynamics in the Coarse-Grained MARTINI Model: Toward Large-Scale Simulations of Amyloid- and Elastin-like Peptides. <i>Journal of Chemical Theory and Computation</i> , <b>2012</b> , 8, 1774-1785	6.4	63
11	Structural disorder and protein elasticity. <i>Advances in Experimental Medicine and Biology</i> , <b>2012</b> , 725, 159-88	3.8	59
10	Simulated Tempering Distributed Replica Sampling, Virtual Replica Exchange, and Other Generalized-Ensemble Methods for Conformational Sampling. <i>Journal of Chemical Theory and Computation</i> , <b>2009</b> , 5, 2640-62	6.4	47
9	Molecular mechanism of $\beta$ -sheet self-organization at water-hydrophobic interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 1-22	4.2	42
8	Structural and functional consequences of the STAT5B driver mutation. <i>Nature Communications</i> , <b>2019</b> , 10, 2517	17.4	27
7	Binding of inositol stereoisomers to model amyloidogenic peptides. <i>Journal of Physical Chemistry B</i> , <b>2012</b> , 116, 1111-9	3.4	14
6	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , <b>2020</b> , 118, 2952-2965	2.9	6
5	Structural diversity of lithium sulfenamides: $^7\text{Li}$ NMR studies in solution and crystal structures of $[\text{Li}_2(\text{eta}^2\text{-}(\text{CH}_3)_3\text{C-NS-C}_6\text{H}_4\text{CH}(3)\text{-}4)_2(\text{THF})_2]$ and $[\text{Li}_2(\text{eta}^1\text{-}4\text{-CH}_3\text{C}_6\text{H}_4\text{-NS-C}_6\text{H}_4\text{CH}(3)\text{-}4)_2(\text{THF})_4]$ . <i>Inorganic Chemistry</i> , <b>2003</b> , 42, 3849-55	5.1	5
4	A Novel Polar Core and Weakly Fixed C-Tail in Squid Arrestin Provide New Insight into Interaction with Rhodopsin. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 4102-4118	6.5	4
3	Simulated tempering distributed replica sampling: A practical guide to enhanced conformational sampling. <i>Journal of Physics: Conference Series</i> , <b>2010</b> , 256, 012011	0.3	2
2	Atomistic Simulation Tools to Study Protein Self-Aggregation. <i>Methods in Molecular Biology</i> , <b>2019</b> , 2039, 243-262	1.4	1

1 The Liquid Structure of Elastin

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