Simon Mitternacht

List of Publications by Year
in descending order

18	978	623188 14	839053 18
papers	citations	h-index	g-index

18	18	18	1391
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	FreeSASA: An open source C library for solvent accessible surface area calculations. F1000Research, 2016, 5, 189.	0.8	294
2	Unraveling Hidden Regulatory Sites in Structurally Homologous Metalloproteases. Journal of Molecular Biology, 2013, 425, 2330-2346.	2.0	52
3	Mechanical Resistance in Unstructured Proteins. Biophysical Journal, 2013, 104, 2725-2732.	0.2	15
4	SPACER: server for predicting allosteric communication and effects of regulation. Nucleic Acids Research, 2013, 41, W266-W272.	6.5	88
5	Monte Carlo Study of the Formation and Conformational Properties of Dimers of AÎ²42 Variants. Journal of Molecular Biology, 2011, 410, 357-367.	2.0	50
6	On the Importance of Amino Acid Sequence and Spatial Proximity of Interacting Residues for Protein Folding. Journal of Biomolecular Structure and Dynamics, 2011, 28, 607-609.	2.0	2
7	Coherent Conformational Degrees of Freedom as a Structural Basis for Allosteric Communication. PLoS Computational Biology, 2011, 7, e1002301.	1.5	44
8	A geometry-based generic predictor for catalytic and allosteric sites. Protein Engineering, Design and Selection, 2011, 24, 405-409.	1.0	29
9	Binding Leverage as a Molecular Basis for Allosteric Regulation. PLoS Computational Biology, 2011, 7, e1002148.	1.5	76
10	Protein folding, aggregation and unfolding in Monte Carlo simulations. Physics Procedia, 2010, 7, 68-71.	1.2	1
11	Comparing the folding freeâ€energy landscapes of AÎ²42 variants with different aggregation properties. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2600-2608.	1.5	45
12	Unfolding times for proteins in a force clamp. Physical Review E, 2010, 81, 010902.	0.8	16
13	An effective all-atom potential for proteins. PMC Biophysics, 2009, 2, 2.	2.2	63
14	Changing the Mechanical Unfolding Pathway of FnIII10 by Tuning the Pulling Strength. Biophysical Journal, 2009, 96, 429-441.	0.2	42
15	Spontaneous Î²â€barrel formation: An allâ€atom Monte Carlo study of AÎ²_{16â€“22} oligomerization. Proteins: Structure, Function and Bioinformatics, 2008, 71, 207-214.	1.5	52
16	Differences in Solution Behavior among Four Semiconductor-Binding Peptides. Journal of Physical Chemistry B, 2007, 111, 4355-4360.	1.2	11
17	Thermal versus mechanical unfolding of ubiquitin. Proteins: Structure, Function and Bioinformatics, 2006, 65, 759-766.	1.5	28
18	Dissecting the mechanical unfolding of ubiquitin. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13427-13432.	3.3	70