

Claire Lesieur

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

316
citations

1040056

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1058476

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19
all docs

19
docs citations

19
times ranked

344
citing authors

#	ARTICLE	IF	CITATIONS
1	A protocol to measure slow protein dynamics of the cholera toxin B pentamers using broadband dielectric spectroscopy. STAR Protocols, 2022, 3, 101561.	1.2	0
2	Experimental diagnostic of sequence-variant dynamic perturbations revealed by broadband dielectric spectroscopy. Structure, 2021, 29, 1419-1429.e3.	3.3	4
3	A computational methodology to diagnose sequence-variant dynamic perturbations by comparing atomic protein structures. Bioinformatics, 2021, , .	4.1	0
4	Mapping Function from Dynamics: Future Challenges for Network-Based Models of Protein Structures. Frontiers in Molecular Biosciences, 2021, 8, 744646.	3.5	1
5	Topology Results on of Oligomeric Proteins. Methods in Molecular Biology, 2021, 2253, 113-135.	0.9	0
6	Analysis of Nanoconfined Protein Dielectric Signals Using Charged Amino Acid Network Models. Australian Journal of Chemistry, 2020, 73, 803.	0.9	3
7	Induced Perturbation Network and tiling for modeling the L55P Transthyretin amyloid fiber. Procedia Computer Science, 2020, 178, 8-17.	2.0	3
8	Exploring Allosteric Pathways of a V-Type Enzyme with Dynamical Perturbation Networks. Journal of Physical Chemistry B, 2019, 123, 3452-3461.	2.6	29
9	Experimental Protein Molecular Dynamics: Broadband Dielectric Spectroscopy coupled with nanoconfinement. Scientific Reports, 2019, 9, 17988.	3.3	11
10	In proteins, the structural responses of a position to mutation rely on the Goldilocks principle: not too many links, not too few. Physical Chemistry Chemical Physics, 2018, 20, 25399-25410.	2.8	18
11	Protein structural robustness to mutations: an in silico investigation. Physical Chemistry Chemical Physics, 2016, 18, 13770-13780.	2.8	24
12	Editorial overview: Theory and simulation. Current Opinion in Structural Biology, 2015, 31, v-vi.	5.7	4
13	From local to global changes in proteins: a network view. Current Opinion in Structural Biology, 2015, 31, 1-8.	5.7	54
14	Intermolecular \hat{I}^2 -Strand Networks Avoid Hub Residues and Favor Low Interconnectedness: A Potential Protection Mechanism against Chain Dissociation upon Mutation. PLoS ONE, 2014, 9, e94745.	2.5	7
15	The Assembly of Protein Oligomers " Old Stories and New Perspectives with Graph Theory. , 2014, , .		6
16	Cholera Toxin B Subunits Assemble into Pentamers - Proposition of a Fly-Casting Mechanism. PLoS ONE, 2010, 5, e15347.	2.5	21
17	A Kinetic Model of Intermediate Formation during Assembly of Cholera Toxin B-subunit Pentamers. Journal of Biological Chemistry, 2002, 277, 16697-16704.	3.4	34
18	Conformational Changes Due to Membrane Binding and Channel Formation by Staphylococcal \hat{I}^2 -Toxin. Journal of Biological Chemistry, 1997, 272, 5709-5717.	3.4	47

#	ARTICLE	IF	CITATIONS
19	Protonation of Histidine-132 Promotes Oligomerization of the Channel-Forming Toxin Aerolysin. <i>Biochemistry</i> , 1995, 34, 16450-16455.	2.5	50