

# Sophie Sacquin-Mora

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

1,104  
citations

394421

19  
h-index

454955

30  
g-index

52  
all docs

52  
docs citations

52  
times ranked

1081  
citing authors

#	ARTICLE	IF	CITATIONS
1	Locating the active sites of enzymes using mechanical properties. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 350-359.	2.6	96
2	Investigating the Local Flexibility of Functional Residues in Hemoproteins. <i>Biophysical Journal</i> , 2006, 90, 2706-2717.	0.5	92
3	Joint Evolutionary Trees: A Large-Scale Method To Predict Protein Interfaces Based on Sequence Sampling. <i>PLoS Computational Biology</i> , 2009, 5, e1000267.	3.2	79
4	Controlling Redox Enzyme Orientation at Planar Electrodes. <i>Catalysts</i> , 2018, 8, 192.	3.5	78
5	Protein mechanics: a route from structure to function. <i>Journal of Biosciences</i> , 2007, 32, 891-898.	1.1	73
6	Probing the Flexibility of the Bacterial Reaction Center: The Wild-Type Protein Is More Rigid Than Two Site-Specific Mutants. <i>Biochemistry</i> , 2007, 46, 14960-14968.	2.5	54
7	Identification of Protein Interaction Partners and Protein-Protein Interaction Sites. <i>Journal of Molecular Biology</i> , 2008, 382, 1276-1289.	4.2	52
8	Protein-Protein Interactions in a Crowded Environment: An Analysis via Cross-Docking Simulations and Evolutionary Information. <i>PLoS Computational Biology</i> , 2013, 9, e1003369.	3.2	48
9	Relating the Diffusion of Small Ligands in Human Neuroglobin to Its Structural and Mechanical Properties. <i>Journal of Physical Chemistry B</i> , 2009, 113, 16257-16267.	2.6	45
10	Thermal fluctuations of haemoglobin from different species: adaptation to temperature via conformational dynamics. <i>Journal of the Royal Society Interface</i> , 2012, 9, 2845-2855.	3.4	37
11	Charge Recombination Kinetics and Protein Dynamics in Wild Type and Carotenoid-less Bacterial Reaction Centers: Studies in Trehalose Glasses. <i>Journal of Physical Chemistry B</i> , 2009, 113, 10389-10398.	2.6	33
12	Frontier Residues Lining Globin Internal Cavities Present Specific Mechanical Properties. <i>Journal of the American Chemical Society</i> , 2011, 133, 8753-8761.	13.7	32
13	The weak, fluctuating, dipole moment of membrane-bound hydrogenase from <i>Aquifex aeolicus</i> accounts for its adaptability to charged electrodes. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 11318-11322.	2.8	31
14	Multiscale Simulations Give Insight into the Hydrogen In and Out Pathways of [NiFe]-Hydrogenases from <i>Aquifex aeolicus</i> and <i>Desulfovibrio fructosovorans</i> . <i>Journal of Physical Chemistry B</i> , 2014, 118, 13800-13811.	2.6	26
15	Fold and flexibility: what can proteins' mechanical properties tell us about their folding nucleus?. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150876.	3.4	26
16	Fluid phase transitions at chemically heterogeneous, nonplanar solid substrates: Surface versus confinement effects. <i>Journal of Chemical Physics</i> , 2003, 118, 1453-1465.	3.0	25
17	Heme orientation modulates histidine dissociation and ligand binding kinetics in the hexacoordinated human neuroglobin. <i>Journal of Biological Inorganic Chemistry</i> , 2013, 18, 111-122.	2.6	24
18	Motions and mechanics: investigating conformational transitions in multi-domain proteins with coarse-grain simulations. <i>Molecular Simulation</i> , 2014, 40, 229-236.	2.0	24

#	ARTICLE	IF	CITATIONS
19	Functional Modes and Residue Flexibility Control the Anisotropic Response of Guanylate Kinase to Mechanical Stress. <i>Biophysical Journal</i> , 2010, 99, 3412-3419.	0.5	22
20	Modeling the Mechanical Response of Proteins to Anisotropic Deformation. <i>ChemPhysChem</i> , 2009, 10, 115-118.	2.1	21
21	Bridging Enzymatic Structure Function via Mechanics. <i>Methods in Enzymology</i> , 2016, 578, 227-248.	1.0	21
22	Great interactions: How binding incorrect partners can teach us about protein recognition and function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1408-1421.	2.6	18
23	Enzyme Closure and Nucleotide Binding Structurally Lock Guanylate Kinase. <i>Biophysical Journal</i> , 2011, 101, 1440-1449.	0.5	16
24	Mobility and Core-Protein Binding Patterns of Disordered C-Terminal Tails in $\beta^2$ -Tubulin Isoforms. <i>Biochemistry</i> , 2017, 56, 1746-1756.	2.5	15
25	Hidden partners: Using cross-docking calculations to predict binding sites for proteins with multiple interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 723-737.	2.6	14
26	Fluids confined by nanopatterned substrates of low symmetry. <i>Molecular Physics</i> , 2002, 100, 2971-2982.	1.7	11
27	Protein Interaction Energy Landscapes are Shaped by Functional and also Non-functional Partners. <i>Journal of Molecular Biology</i> , 2020, 432, 1183-1198.	4.2	10
28	Investigating the Structural Variability and Binding Modes of the Glioma Targeting NFL-TBS.40-63 Peptide on Tubulin. <i>Biochemistry</i> , 2015, 54, 3660-3669.	2.5	8
29	Implicit Modeling of the Impact of Adsorption on Solid Surfaces for Protein Mechanics and Activity with a Coarse-Grained Representation. <i>Journal of Physical Chemistry B</i> , 2020, 124, 8516-8523.	2.6	8
30	Docking Peptides on Proteins: How to Open a Lock, in the Dark, with a Flexible Key. <i>Structure</i> , 2015, 23, 1373-1374.	3.3	7
31	Determinants of neuroglobin plasticity highlighted by joint coarse-grained simulations and high pressure crystallography. <i>Scientific Reports</i> , 2017, 7, 1858.	3.3	7
32	Mechanical variations in proteins with large-scale motions highlight the formation of structural locks. <i>Journal of Structural Biology</i> , 2018, 203, 195-204.	2.8	7
33	Moving pictures: Reassessing docking experiments with a dynamic view of protein interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1315-1323.	2.6	7
34	Assessing the effect of dynamics on the closed-loop protein-folding hypothesis. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20130935.	3.4	6
35	Nanoscope liquid bridges exposed to a torsional strain. <i>Physical Review E</i> , 2003, 68, 066103.	2.1	5
36	Torsion-induced phase transitions in fluids confined between chemically decorated substrates. <i>Journal of Chemical Physics</i> , 2004, 121, 9077-9086.	3.0	5

#	ARTICLE	IF	CITATIONS
37	Conformational Stability Adaptation of a Double-Stranded RNA-Binding Domain to Transfer RNA Ligand. <i>Biochemistry</i> , 2019, 58, 2463-2473.	2.5	5
38	Meet-U: Educating through research immersion. <i>PLoS Computational Biology</i> , 2018, 14, e1005992.	3.2	4
39	When Order Meets Disorder: Modeling and Function of the Protein Interface in Fuzzy Complexes. <i>Biomolecules</i> , 2021, 11, 1529.	4.0	4
40	Modeling the Dynamics of Protein-Protein Interfaces, How and Why?. <i>Molecules</i> , 2022, 27, 1841.	3.8	4
41	Between Two Walls: Modeling the Adsorption Behavior of Î²-Glucosidase A on Bare and SAM-Functionalized Gold Surfaces. <i>Langmuir</i> , 2022, 38, 1313-1323.	3.5	2
42	The Closure Mechanism Of M. Tuberculosis Guanylate Kinase Relates Structural Fluctuations To Enzymatic Function. <i>Biophysical Journal</i> , 2009, 96, 70a.	0.5	0
43	Great Interactions: Binding Incorrect Partners to Learn about Protein Recognition and Function. <i>Biophysical Journal</i> , 2017, 112, 200a-201a.	0.5	0
44	Coarse-grain simulations on NMR conformational ensembles highlight functional residues in proteins. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20190075.	3.4	0
45	Coarse-Graining Protein Mechanics. , 2008, , 317-327.		0