Sophie Sacquin-Mora

List of Publications by Year
in descending order

45	1,104	394421	454955
papers	citations	19 h-index	30 g-index

52	52	52	1081
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Between Two Walls: Modeling the Adsorption Behavior of Î²-Glucosidase A on Bare and SAM-Functionalized Gold Surfaces. Langmuir, 2022, 38, 1313-1323.	3.5	2
2	Modeling the Dynamics of Proteinâ€“Protein Interfaces, How and Why?. Molecules, 2022, 27, 1841.	3.8	4
3	Moving pictures: Reassessing docking experiments with a dynamic view of protein interfaces. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1315-1323.	2.6	7
4	When Order Meets Disorder: Modeling and Function of the Protein Interface in Fuzzy Complexes. Biomolecules, 2021, 11, 1529.	4.0	4
5	Implicit Modeling of the Impact of Adsorption on Solid Surfaces for Protein Mechanics and Activity with a Coarse-Grained Representation. Journal of Physical Chemistry B, 2020, 124, 8516-8523.	2.6	8
6	Protein Interaction Energy Landscapes are Shaped by Functional and also Non-functional Partners. Journal of Molecular Biology, 2020, 432, 1183-1198.	4.2	10
7	Conformational Stability Adaptation of a Double-Stranded RNA-Binding Domain to Transfer RNA Ligand. Biochemistry, 2019, 58, 2463-2473.	2.5	5
8	Coarse-grain simulations on NMR conformational ensembles highlight functional residues in proteins. Journal of the Royal Society Interface, 2019, 16, 20190075.	3.4	0
9	Hidden partners: Using crossâ€docking calculations to predict binding sites for proteins with multiple interactions. Proteins: Structure, Function and Bioinformatics, 2018, 86, 723-737.	2.6	14
10	Mechanical variations in proteins with large-scale motions highlight the formation of structural locks. Journal of Structural Biology, 2018, 203, 195-204.	2.8	7
11	Controlling Redox Enzyme Orientation at Planar Electrodes. Catalysts, 2018, 8, 192.	3.5	78
12	Meet-U: Educating through research immersion. PLoS Computational Biology, 2018, 14, e1005992.	3.2	4
13	Great Interactions: Binding Incorrect Partners to Learn about Protein Recognition and Function. Biophysical Journal, 2017, 112, 200a-201a.	0.5	0
14	Mobility and Core-Protein Binding Patterns of Disordered C-Terminal Tails in Î²-Tubulin Isotypes. Biochemistry, 2017, 56, 1746-1756.	2.5	15
15	Determinants of neuroglobin plasticity highlighted by joint coarse-grained simulations and high pressure crystallography. Scientific Reports, 2017, 7, 1858.	3.3	7
16	Great interactions: How binding incorrect partners can teach us about protein recognition and function. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1408-1421.	2.6	18
17	Bridging Enzymatic Structure Function via Mechanics. Methods in Enzymology, 2016, 578, 227-248.	1.0	21
18	Investigating the Structural Variability and Binding Modes of the Glioma Targeting NFL-TBS.40â€“63 Peptide on Tubulin. Biochemistry, 2015, 54, 3660-3669.	2.5	8

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19	Docking Peptides on Proteins: How to Open a Lock, in the Dark, with a Flexible Key. Structure, 2015, 23, 1373-1374.	3.3	7
20	Fold and flexibility: what can proteins' mechanical properties tell us about their folding nucleus?. Journal of the Royal Society Interface, 2015, 12, 20150876.	3.4	26
21	Motions and mechanics: investigating conformational transitions in multi-domain proteins with coarse-grain simulations. Molecular Simulation, 2014, 40, 229-236.	2.0	24
22	Multiscale Simulations Give Insight into the Hydrogen In and Out Pathways of [NiFe]-Hydrogenases from Aquifex aeolicus and Desulfovibrio fructosovorans. Journal of Physical Chemistry B, 2014, 118, 13800-13811.	2.6	26
23	Assessing the effect of dynamics on the closed-loop protein-folding hypothesis. Journal of the Royal Society Interface, 2014, 11, 20130935.	3.4	6
24	The weak, fluctuating, dipole moment of membrane-bound hydrogenase from Aquifex aeolicus accounts for its adaptability to charged electrodes. Physical Chemistry Chemical Physics, 2014, 16, 11318-11322.	2.8	31
25	Heme orientation modulates histidine dissociation and ligand binding kinetics in the hexacoordinated human neuroglobin. Journal of Biological Inorganic Chemistry, 2013, 18, 111-122.	2.6	24
26	Protein-Protein Interactions in a Crowded Environment: An Analysis via Cross-Docking Simulations and Evolutionary Information. PLoS Computational Biology, 2013, 9, e1003369.	3.2	48
27	Thermal fluctuations of haemoglobin from different species: adaptation to temperature via conformational dynamics. Journal of the Royal Society Interface, 2012, 9, 2845-2855.	3.4	37
28	Enzyme Closure and Nucleotide Binding Structurally Lock Guanylate Kinase. Biophysical Journal, 2011, 101, 1440-1449.	0.5	16
29	Frontier Residues Lining Globin Internal Cavities Present Specific Mechanical Properties. Journal of the American Chemical Society, 2011, 133, 8753-8761.	13.7	32
30	Functional Modes and Residue Flexibility Control the Anisotropic Response of Guanylate Kinase to Mechanical Stress. Biophysical Journal, 2010, 99, 3412-3419.	0.5	22
31	Joint Evolutionary Trees: A Large-Scale Method To Predict Protein Interfaces Based on Sequence Sampling. PLoS Computational Biology, 2009, 5, e1000267.	3.2	79
32	Modeling the Mechanical Response of Proteins to Anisotropic Deformation. ChemPhysChem, 2009, 10, 115-118.	2.1	21
33	Charge Recombination Kinetics and Protein Dynamics in Wild Type and Carotenoid-less Bacterial Reaction Centers: Studies in Trehalose Glasses. Journal of Physical Chemistry B, 2009, 113, 10389-10398.	2.6	33
34	Relating the Diffusion of Small Ligands in Human Neuroglobin to Its Structural and Mechanical Properties. Journal of Physical Chemistry B, 2009, 113, 16257-16267.	2.6	45
35	The Closure Mechanism Of M. Tuberculosis Guanylate Kinase Relates Structural Fluctuations To Enzymatic Function. Biophysical Journal, 2009, 96, 70a.	0.5	0
36	Identification of Protein Interaction Partners and Proteinâ€“Protein Interaction Sites. Journal of Molecular Biology, 2008, 382, 1276-1289.	4.2	52

#	Article	IF	Citations
37	Coarse-Graining Protein Mechanics. , 2008, , 317-327.		0
38	Probing the Flexibility of the Bacterial Reaction Center:â€‰ The Wild-Type Protein Is More Rigid Than Two Site-Specific Mutants. Biochemistry, 2007, 46, 14960-14968.	2.5	54
39	Locating the active sites of enzymes using mechanical properties. Proteins: Structure, Function and Bioinformatics, 2007, 67, 350-359.	2.6	96
40	Protein mechanics: a route from structure to function. Journal of Biosciences, 2007, 32, 891-898.	1.1	73
41	Investigating the Local Flexibility of Functional Residues in Hemoproteins. Biophysical Journal, 2006, 90, 2706-2717.	0.5	92
42	Torsion-induced phase transitions in fluids confined between chemically decorated substrates. Journal of Chemical Physics, 2004, 121, 9077-9086.	3.0	5
43	Fluid phase transitions at chemically heterogeneous, nonplanar solid substrates: Surface versus confinement effects. Journal of Chemical Physics, 2003, 118, 1453-1465.	3.0	25
44	Nanoscopic liquid bridges exposed to a torsional strain. Physical Review E, 2003, 68, 066103.	2.1	5
45	Fluids confined by nanopatterned substrates of low symmetry. Molecular Physics, 2002, 100, 2971-2982.	1.7	11