Giovanni Settanni

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7821839/publications.pdf

Version: 2024-02-01

40 papers	1,577 citations	411340 20 h-index	466096 32 g-index
40 all docs	40 docs citations	40 times ranked	2368 citing authors

#	Article	IF	Citations
1	pHâ€Dependent Behavior of Ionizable Cationic Lipids in mRNAâ€Carrying Lipoplexes Investigated by Molecular Dynamics Simulations. Macromolecular Rapid Communications, 2022, 43, e2100683.	2.0	12
2	Thermodynamics and Kinetics of the Interactions Between Proteins and Hydrophilic Polymers. , 2021, , 65-76.		0
3	Data Reweighting in Metadynamics Simulations. Journal of Chemical Theory and Computation, 2020, 16, 2042-2052.	2.3	21
4	Targeting Cavity-Creating p53 Cancer Mutations with Small-Molecule Stabilizers: the Y220X Paradigm. ACS Chemical Biology, 2020, 15, 657-668.	1.6	45
5	Interactions Between Blood Proteins and Nanoparticles Investigated Using Molecular Dynamics Simulations. , 2019, , 63-74.		2
6	Blood Proteins and Their Interactions with Nanoparticles Investigated Using Molecular Dynamics Simulations. , 2018, , 5-19.		0
7	Poly-sarcosine and Poly(Ethylene-Glycol) Interactions with Proteins Investigated Using Molecular Dynamics Simulations. Computational and Structural Biotechnology Journal, 2018, 16, 543-550.	1.9	32
8	Protein corona composition of poly(ethylene glycol)- and poly(phosphoester)-coated nanoparticles correlates strongly with the amino acid composition of the protein surface. Nanoscale, 2017, 9, 2138-2144.	2.8	76
9	Potassium Triggers a Reversible Specific Stiffness Transition of Polyethylene Glycol. Journal of Physical Chemistry C, 2017, 121, 22396-22402.	1.5	10
10	Interactions between proteins and poly(ethylene-glycol) investigated using molecular dynamics simulations. Journal of Physics: Conference Series, 2017, 921, 012002.	0.3	17
11	The Internal Dynamics and Early Adsorption Stages of Fibrinogen Investigated by Molecular Dynamics Simulations. , 2016, , 61-78.		0
12	The Internal Dynamics of Fibrinogen and Its Implications for Coagulation and Adsorption. PLoS Computational Biology, 2015, 11, e1004346.	1.5	44
13	Molecular Dynamics Simulations of the Initial Adsorption Stages of Fibrinogen on Mica and Graphite Surfaces. Langmuir, 2015, 31, 13180-13190.	1.6	34
14	Simulations and Experiments in Protein Folding. Methods in Molecular Biology, 2015, 1215, 289-306.	0.4	0
15	Effects of Ligand Binding on the Mechanical Properties of Ankyrin Repeat Protein Gankyrin. PLoS Computational Biology, 2013, 9, e1002864.	1.5	18
16	Combination of Markov State Models and Kinetic Networks for the Analysis of Molecular Dynamics Simulations of Peptide Folding. Journal of Physical Chemistry B, 2011, 115, 7459-7471.	1.2	8
17	Toward the Rational Design of p53-Stabilizing Drugs: Probing the Surface of the Oncogenic Y220C Mutant. Chemistry and Biology, 2010, 17, 46-56.	6.2	97
18	Mechanical Unfolding of an Ankyrin Repeat Protein. Biophysical Journal, 2010, 98, 1294-1301.	0.2	56

#	Article	IF	Citations
19	Residue-Resolved Stability of Full-Consensus Ankyrin Repeat Proteins Probed by NMR. Journal of Molecular Biology, 2010, 402, 241-258.	2.0	33
20	Multiple conformations of full-length p53 detected with single-molecule fluorescence resonance energy transfer. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20758-20763.	3.3	96
21	Downhill versus Barrier-Limited Folding of BBL. Journal of Molecular Biology, 2009, 387, 993-1001.	2.0	15
22	Structure of Human MDM4 N-Terminal Domain Bound to a Single-Domain Antibody. Journal of Molecular Biology, 2009, 385, 1578-1589.	2.0	13
23	High Temperature Unfolding Simulations of the TRPZ1 Peptide. Biophysical Journal, 2008, 94, 4444-4453.	0.2	41
24	Characterization and Further Stabilization of Designed Ankyrin Repeat Proteins by Combining Molecular Dynamics Simulations and Experiments. Journal of Molecular Biology, 2008, 375, 837-854.	2.0	77
25	Folding and Unfolding Mechanism of Highly Stable Full-Consensus Ankyrin Repeat Proteins. Journal of Molecular Biology, 2008, 376, 241-257.	2.0	161
26	Fluorescence resonance energy transfer analysis of the folding pathway of Engrailed Homeodomain. Protein Engineering, Design and Selection, 2008, 21, 131-146.	1.0	18
27	Estimation of Folding Probabilities and Î¦ Values From Molecular Dynamics Simulations of Reversible Peptide Folding. , 2007, 350, 225-250.		6
28	Wordom: a program for efficient analysis of molecular dynamics simulations. Bioinformatics, 2007, 23, 2625-2627.	1.8	251
29	Unfolding transition state and intermediates of the tumor suppressor p16 INK4a investigated by molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2006, 64, 178-192.	1.5	15
30	Estimation of protein folding probability from equilibrium simulations. Journal of Chemical Physics, 2005, 122, 184901.	1.2	35
31	Â-Value analysis by molecular dynamics simulations of reversible folding. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 628-633.	3.3	67
32	Formation of the Folding Nucleus of an SH3 Domain Investigated by Loosely Coupled Molecular Dynamics Simulations. Biophysical Journal, 2004, 86, 1691-1701.	0.2	27
33	Molecular Dynamics Simulations of the NGF-TrkA Domain 5 Complex and Comparison with Biological Data. Biophysical Journal, 2003, 84, 2282-2292.	0.2	26
34	Combining task- and data parallelism to speed up protein folding on a desktop grid platform. , 2003, , .		7
35	The intracellular antibody capture technology (IACT): towards a consensus sequence for intracellular antibodies. Journal of Molecular Biology, 2002, 317, 73-83.	2.0	130
36	Folding Pathways of Prion and Doppel. Biophysical Journal, 2002, 83, 3533-3541.	0.2	40

#	Article	IF	Citations
37	Role of Native-State Topology in the Stabilization of Intracellular Antibodies. Biophysical Journal, 2001, 81, 2935-2945.	0.2	10
38	Analytical Model for the Effects of Learning on Spike Count Distributions. Neural Computation, 2000, 12, 1773-1787.	1.3	3
39	Extraction of interaction potentials between amino acids from native protein structures. Journal of Chemical Physics, 2000, 112, 9151-9166.	1.2	32
40	Implementation and characterization of protein folding on a desktop computational grid. Is CHARMM a suitable candidate for the United Devices MetaProcessor?. , 0, , .		2