Leonor Saiz

List of Publications by Year in descending order

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48 papers	2,445 citations	257450 24 h-index	206112 48 g-index
53 all docs	53 docs citations	53 times ranked	2800 citing authors

#	Article	IF	Citations
1	Computational design of single-stranded DNA hairpin aptamers immobilized on a biosensor substrate. Scientific Reports, 2021, 11, 10984.	3.3	9
2	All-or-none amyloid disassembly via chaperone-triggered fibril unzipping favors clearance of Î±-synuclein toxic species. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	15
3	Reliably quantifying the evolving worldwide dynamic state of the COVID-19 outbreak from death records, clinical parametrization, and demographic data. Scientific Reports, 2021, 11, 19952.	3.3	6
4	Cellâ€toâ€cell and typeâ€toâ€type heterogeneity of signaling networks: insights from the crowd. Molecular Systems Biology, 2021, 17, e10402.	7.2	9
5	Ascertaining the initiation of epidemic resurgences: an application to the COVID-19 second surges in Europe and the Northeast United States. Royal Society Open Science, 2021, 8, 210773.	2.4	6
6	Clearly Detectable, Kinetically Restricted Solidâ€“Solid Phase Transition in cis-Ceramide Monolayers. Langmuir, 2018, 34, 11749-11758.	3.5	6
7	Predicting human olfactory perception from chemical features of odor molecules. Science, 2017, 355, 820-826.	12.6	194
8	Computing at the Front-End by Receptor Networks. Cell Systems, 2017, 5, 316-318.	6.2	1
9	Insights into Signaling and the Functional Complexity of Biological Membranes. Journal of Membrane Biology, 2017, 250, 335-336.	2.1	2
10	Three-dimensional modeling of single stranded DNA hairpins for aptamer-based biosensors. Scientific Reports, 2017, 7, 1178.	3.3	113
11	Suppression and enhancement of transcriptional noise by DNA looping. Physical Review E, 2014, 89, 062703.	2.1	11
12	Literature-Based Automated Reconstruction, Expansion, and Refinement of the TGF-Î² Superfamily Ligand-Receptor Network. Journal of Membrane Biology, 2014, 247, 381-386.	2.1	5
13	In silico identification of potential therapeutic targets in the TGF-Î² signal transduction pathway. Molecular BioSystems, 2014, 10, 537.	2.9	6
14	Determinants of proteinâ€“ligand complex formation in the thyroid hormone receptor Î±: A molecular dynamics simulation study. Computational and Theoretical Chemistry, 2014, 1038, 57-66.	2.5	4
15	Reliable Prediction of Complex Phenotypes from a Modular Design in Free Energy Space: An Extensive Exploration of thelacOperon. ACS Synthetic Biology, 2013, 2, 576-586.	3.8	31
16	Systems Biophysics of Gene Expression. Biophysical Journal, 2013, 104, 2574-2585.	0.5	26
17	Computational modelling of Smad-mediated negative feedback and crosstalk in the TGF-Î² superfamily network. Journal of the Royal Society Interface, 2013, 10, 20130363.	3.4	26
18	Characterization of Negative Feedback Network Motifs in the TGF-Î² Signaling Pathway. PLoS ONE, 2013, 8, e83531.	2.5	15

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19	The physics of proteinâ€“DNA interaction networks in the control of gene expression. Journal of Physics Condensed Matter, 2012, 24, 193102.	1.8	20
20	Computational Analysis of the TGF-Beta and BMP Signal Transduction Pathways. Biophysical Journal, 2011, 100, 164a.	0.5	3
21	Trafficking Coordinate Description of Intracellular Transport Control of Signaling Networks. Biophysical Journal, 2011, 101, 2315-2323.	0.5	13
22	Control of gene expression by modulated self-assembly. Nucleic Acids Research, 2011, 39, 6854-6863.	14.5	15
23	CplexA: a Mathematica package to study macromolecular-assembly control of gene expression. Bioinformatics, 2010, 26, 2060-2061.	4.1	37
24	Proteinâ€“protein/DNA interaction networks: versatile macromolecular structures for the control of gene expression. IET Systems Biology, 2008, 2, 247-255.	1.5	12
25	Ab initio thermodynamic modeling of distal multisite transcription regulation. Nucleic Acids Research, 2007, 36, 726-731.	14.5	38
26	Multilevel Deconstruction of the In Vivo Behavior of Looped DNA-Protein Complexes. PLoS ONE, 2007, 2, e355.	2.5	27
27	Partitioning of Anesthetics into a Lipid Bilayer and their Interaction with Membrane-Bound Peptide Bundles. Biophysical Journal, 2006, 91, 2815-2825.	0.5	67
28	DNA looping: the consequences and its control. Current Opinion in Structural Biology, 2006, 16, 344-350.	5.7	79
29	Stochastic dynamics of macromolecularâ€assembly networks. Molecular Systems Biology, 2006, 2, 2006.0024.	7.2	47
30	Multiprotein DNA Looping. Physical Review Letters, 2006, 96, 238103.	7.8	26
31	Inferring the in vivo looping properties of DNA. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17642-17645.	7.1	54
32	DNA looping in gene regulation: from the assembly of macromolecular complexes to the control of transcriptional noise. Current Opinion in Genetics and Development, 2005, 15, 136-144.	3.3	129
33	Concentration Effects of Volatile Anesthetics on the Properties of Model Membranes: A Coarse-Grain Approach. Biophysical Journal, 2005, 88, 1524-1534.	0.5	65
34	The Transmembrane Domain of the Acetylcholine Receptor: Insights from Simulations on Synthetic Peptide Models. Biophysical Journal, 2005, 88, 959-970.	0.5	23
35	Effect of the Pore Region of a Transmembrane Ion Channel on the Physical Properties of a Simple Membrane. Journal of Physical Chemistry B, 2004, 108, 2608-2613.	2.6	21
36	Influence of Anesthetic and Nonimmobilizer Molecules on the Physical Properties of a Polyunsaturated Lipid Bilayer. Journal of Physical Chemistry B, 2003, 107, 14500-14508.	2.6	41

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37	Electrostatic interactions in a neutral model phospholipid bilayer by molecular dynamics simulations. Journal of Chemical Physics, 2002, 116, 3052-3057.	3.0	88
38	Computer Simulation Studies of Model Biological Membranes. Accounts of Chemical Research, 2002, 35, 482-489.	15.6	181
39	Dynamics in hydrogen bonded liquids: water and alcohols. Journal of Molecular Liquids, 2002, 96-97, 3-17.	4.9	99
40	Towards an Understanding of Complex Biological Membranes from Atomistic Molecular Dynamics Simulations. Bioscience Reports, 2002, 22, 151-173.	2.4	83
41	Structure of liquid ethylene glycol: A molecular dynamics simulation study with different force fields. Journal of Chemical Physics, 2001, 114, 3187-3199.	3.0	89
42	Structural Properties of a Highly Polyunsaturated Lipid Bilayer from Molecular Dynamics Simulations. Biophysical Journal, 2001, 81, 204-216.	0.5	136
43	Influence of Highly Polyunsaturated Lipid Acyl Chains of Biomembranes on the NMR Order Parameters. Journal of the American Chemical Society, 2001, 123, 7381-7387.	13.7	34
44	Field-induced force-suppression in ferromagnetic colloids. Physica A: Statistical Mechanics and Its Applications, 2001, 293, 51-58.	2.6	1
45	Dielectric properties of liquid ethanol. A computer simulation study. Journal of Chemical Physics, 2000, 113, 2814-2822.	3.0	76
46	Dynamics and hydrogen bonding in liquid ethanol. Molecular Physics, 1999, 97, 897-905.	1.7	47
47	Structure and Dynamics of Liquid Ethanol. Journal of Physical Chemistry B, 1997, 101, 78-86.	2.6	194
48	Hydrogen bonding in liquid alcohols: a computer simulation study. Journal of Molecular Structure, 1997, 416, 243-248.	3.6	211