Antonio Rey

List of Publications by Year in descending order

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331259 414034 1,309 70 21 32 h-index citations g-index papers 70 70 70 714 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A method for predicting protein structure from sequence. Current Biology, 1993, 3, 414-423.	1.8	80
2	Comparison of lattice Monte Carlo dynamics and Brownian dynamics folding pathways of \hat{l}_{\pm} -helical hairpins. Chemical Physics, 1991, 158, 199-219.	0.9	71
3	Monte Carlo calculations for linear chains and star polymers with intermolecular interactions. 3. Dimensions and hydrodynamic properties in good solvent conditions. Macromolecules, 1987, 20, 342-346.	2.2	69
4	Monte Carlo calculations for linear and star polymers with intramolecular interactions. 1. Dimensions. Macromolecules, 1986, 19, 452-457.	2.2	60
5	Efficient algorithm for the reconstruction of a protein backbone from the ?-carbon coordinates. Journal of Computational Chemistry, 1992, 13, 443-456.	1.5	49
6	Monte Carlo calculations for linear and star polymers with intramolecular interactions. 2. Nonpreaveraged study of hydrodynamic properties at the \hat{l}_s state. Macromolecules, 1986, 19, 457-462.	2.2	44
7	Computer modeling and folding of four-helix bundles. Proteins: Structure, Function and Bioinformatics, 1993, 16, 8-28.	1.5	39
8	Effect of double bonds on the dynamics of hydrocarbon chains. Journal of Chemical Physics, 1992, 97, 1240-1249.	1.2	36
9	Dimensions and intrinsic viscosities of long linear and star chains in good- and $\hat{\Gamma}$ -solvent conditions. Macromolecules, 1991, 24, 6494-6499.	2.2	35
10	The shape of linear and star polymers with and without excluded volume. Journal of Chemical Physics, 1991, 94, 4009-4011.	1.2	35
11	Thermodynamics of Gŕtype models for protein folding. Journal of Chemical Physics, 2005, 123, 154903.	1.2	35
12	Experimental and theoretical study of the equation of state of trifluoromethane in the near-critical region. The Journal of Physical Chemistry, 1991, 95, 3351-3357.	2.9	30
13	Influence of the native topology on the folding barrier for small proteins. Journal of Chemical Physics, 2007, 127, 175101.	1.2	30
14	Steric confinement and enhanced local flexibility assist knotting in simple models of protein folding. Physical Chemistry Chemical Physics, 2016, 18, 26391-26403.	1.3	30
15	Investigation of the endâ€ŧoâ€end vector distribution function for linear polymers in different regimes. Journal of Chemical Physics, 1991, 95, 4589-4592.	1.2	28
16	Brownian dynamics simulation of flexible polymer chains with excluded volume and hydrodynamic interactions. A comparison with Monte Carlo and theoretical results. Polymer, 1992, 33, 3477-3481.	1.8	27
17	Monte Carlo calculations for linear chains and star polymers with intramolecular interactions. 4. Dimensions and hydrodynamic properties below the .THETA. state. Macromolecules, 1987, 20, 2385-2390.	2.2	25
18	A refined hydrogen bond potential for flexible protein models. Journal of Chemical Physics, 2010, 132, 235102.	1.2	25

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19	Radius of gyration and viscosity of linear and star polymers in different regimes. Macromolecules, 1992, 25, 1311-1315.	2.2	24
20	Why Do Protein Folding Rates Correlate with Metrics of Native Topology?. PLoS ONE, 2012, 7, e35599.	1.1	24
21	Numerical simulation of the cyclization dynamics for flexible chains with excluded volume. Macromolecules, 1991, 24, 4673-4678.	2.2	23
22	Brownian dynamics of a flexible polymer. Internal modes and quaiselastic scattering function. Journal of Chemical Physics, 1989, 90, 2035-2041.	1.2	21
23	Self-Consistent Mean Field Calculations of Polyelectrolyte-Surfactant Mixtures in Solution and upon Adsorption onto Negatively Charged Surfaces. Polymers, 2020, 12, 624.	2.0	21
24	Translational diffusion, relaxation times, and quasi-elastic scattering of flexible chains with excluded volume and fluctuating hydrodynamic interactions: a Brownian dynamics study. Macromolecules, 1991, 24, 4666-4672.	2.2	20
25	Intramolecular Reaction Rates of Flexible Polymers. 1. Simulation Results and the Classical Theory. Macromolecules, 1998, 31, 8356-8362.	2.2	19
26	A simple simulation model can reproduce the thermodynamic folding intermediate of apoflavodoxin. Proteins: Structure, Function and Bioinformatics, 2010, 78, 73-82.	1.5	18
27	Hydrophobic confinement modulates thermal stability and assists knotting in the folding of tangled proteins. Physical Chemistry Chemical Physics, 2019, 21, 11764-11775.	1.3	18
28	Lower bounds for the intrinsic viscosity of flexible polymers. Comparison with Brownian dynamics simulation results for different types of chains. Computer Physics Communications, 1990, 61, 297-303.	3.0	17
29	Improvement of Structure-Based Potentials for Protein Folding by Native and Nonnative Hydrogen Bonds. Biophysical Journal, 2011, 101, 1474-1482.	0.2	17
30	Simple model for the simulation of peptide folding and aggregation with different sequences. Journal of Chemical Physics, 2012, 136, 215103.	1.2	17
31	Brownian dynamics of nonlinear Gaussian chains with fluctuating hydrodynamic interactions. 1. Star chains. Macromolecules, 1990, 23, 3948-3953.	2.2	16
32	Computer simulation of the folding of coiled coils. Journal of Chemical Physics, 1994, 100, 2267-2276.	1.2	16
33	Topologyâ€based models and NMR structures in protein folding simulations. Journal of Computational Chemistry, 2009, 30, 1212-1219.	1.5	16
34	Cyclization dynamics of flexible polymers. Numerical results from Brownian trajectories. Macromolecules, 1990, 23, 2057-2061.	2.2	15
35	The shape of twoâ€dimensional linear and star polymers with and without excluded volume. Journal of Chemical Physics, 1991, 95, 608-611.	1.2	15
36	Monte Carlo simulation of the dynamics and quasielastic scattering in many-chain polymer systems. Macromolecules, 1992, 25, 3266-3272.	2.2	14

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37	Dynamicâ€mechanical and light scattering study of the glass transition of poly(vinylacetate) and a poly(vinylacetate) +poly(4â€hydroxystyrene) blend. Journal of Chemical Physics, 1994, 100, 3258-3267.	1.2	14
38	Intramolecular Reaction Rates of Flexible Polymers. 2. Comparison with the Renormalization Group Theory. Macromolecules, 1998, 31, 8363-8369.	2.2	14
39	The protein folding transition state: Insights from kinetics and thermodynamics. Journal of Chemical Physics, 2010, 133, 125102.	1.2	14
40	How determinant is N-terminal to C-terminal coupling for protein folding?. Physical Chemistry Chemical Physics, 2015, 17, 3512-3524.	1.3	14
41	Conformation of A2B and A3B Miktoarm Star Copolymers in Dilute Solutions. Macromolecules, 1996, 29, 5599-5604.	2.2	13
42	Influence of the chain stiffness on the thermodynamics of a GÅ-type model for protein folding. Journal of Chemical Physics, 2007, 126, 165103.	1,2	12
43	Simulating protein unfolding under pressure with a coarse-grained model. Journal of Chemical Physics, 2012, 137, 185102.	1.2	12
44	Conformational properties of flexible polymer chains in highly confined environments. Journal of Chemical Physics, 1997, 106, 5720-5730.	1.2	11
45	Evaluation of coarse grained models for hydrogen bonds in proteins. Journal of Computational Chemistry, 2007, 28, 1187-1199.	1.5	11
46	Simulations of the protein folding process using topology-based models depend on the experimental structure. Journal of Chemical Physics, 2008, 129, 115101.	1.2	8
47	Frequencyâ€dependent viscosity of linear, ring, and star Gaussian chains with fluctuating hydrodynamic interactions. Journal of Chemical Physics, 1990, 92, 6278-6282.	1.2	7
48	Energy minimizations with a combination of two knowledgeâ€based potentials for protein folding. Journal of Computational Chemistry, 2008, 29, 1684-1692.	1,5	7
49	Topology-based potentials and the study of the competition between protein folding and aggregation. Journal of Chemical Physics, 2009, 130, 115101.	1.2	7
50	Dynamic scattering function for diblock copolymer chains in dilute solutions. Journal of Chemical Physics, 1994, 101, 2455-2462.	1,2	6
51	Frequencyâ€dependent viscosity of linear polymer chains. Influence of nonâ€Gaussian effects. Journal of Chemical Physics, 1995, 102, 6900-6907.	1.2	6
52	Dynamics of chains in excluded volume conditions: Frequencyâ€dependent viscosity of regular star chains. Journal of Chemical Physics, 1996, 104, 758-766.	1,2	6
53	Numerical simulation of the scattering form factor of star polymers. Computational and Theoretical Polymer Science, 1997, 7, 243-252.	1.1	6
54	Relaxation of flexible chains in dilute and non-dilute systems. Dynamic Monte Carlo results for linear and star chains. Macromolecular Theory and Simulations, 1999, 8, 321-327.	0.6	6

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55	Evolutionary method for the assembly of rigid protein fragments. Journal of Computational Chemistry, 2005, 26, 131-141.	1.5	6
56	Design of a Rotamer Library for Coarse-Grained Models in Protein-Folding Simulations. Journal of Chemical Information and Modeling, 2014, 54, 302-313.	2.5	6
57	Behavior of Proteins under Pressure from Experimental Pressure-Dependent Structures. Journal of Physical Chemistry B, 2021, 125, 6179-6191.	1.2	6
58	Crosslinking of poly(allylamine) with esters of diimidic acids in aqueous media. Die Makromolekulare Chemie Rapid Communications, 1989, 10, 675-681.	1.1	5
59	Influence of the hydrophobic face width on the degree of association of coiled–coil proteins. Journal of Chemical Physics, 2002, 117, 10321-10328.	1.2	4
60	Assessment of protein folding potentials with an evolutionary method. Journal of Chemical Physics, 2006, 125, 014904.	1.2	4
61	Sketching protein aggregation with a physics-based toy model. Journal of Chemical Physics, 2013, 139, 115101.	1.2	4
62	Brownian dynamics of nonlinear Gaussian chains with fluctuating hydrodynamic interactions. 2. Rings. Macromolecules, 1990, 23, 3953-3957.	2.2	3
63	Simplified model for the analysis of interaction types in two-stranded coiled-coils. Journal of Chemical Physics, 1999, 111, 2311-2321.	1.2	3
64	Peptide length dependence of a simplified model for the folding of regular two-stranded coiled-coils. Macromolecular Theory and Simulations, 2000, 9, 534-542.	0.6	3
65	Evaluation of a mean field potential for protein folding with different interaction centers. Physica A: Statistical Mechanics and Its Applications, 2006, 371, 449-462.	1.2	3
66	On the use of the gaussian chain as a monte carlo simulation model for the equilibrium properties of polymer solutions. Macromolecular Theory and Simulations, 1997, 6, 271-286.	0.6	2
67	Thermodynamic aspects in a simplified model for the folding of two-stranded coiled-coils. Journal of Chemical Physics, 2000, 113, 11343-11354.	1.2	2
68	Intermediates in the folding equilibrium of repeat proteins from the TPR family. European Biophysics Journal, 2014, 43, 433-443.	1.2	2
69	Design of a structure-based model for protein folding from flexible conformations. Physical Chemistry Chemical Physics, 2019, 21, 6544-6552.	1.3	2
70	Influence of the Helical Backbone in the Behavior of a Simple Model for Dimeric Coiled-Coil Proteins. Macromolecular Theory and Simulations, 2003, 12, 669-678.	0.6	1