Paolo De Los Rios

List of Publications by Year
in descending order

120	6,302	41	74
papers	citations	h-index	g-index
		71102	76900

131	131	131	6868
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Scale-Free Networks from Varying Vertex Intrinsic Fitness. Physical Review Letters, 2002, 89, 258702.	7.8	612
2	Understanding amyloid aggregation by statistical analysis of atomic force microscopy images. Nature Nanotechnology, 2010, 5, 423-428.	31.5	526
3	Hsp70 chaperones accelerate protein translocation and the unfolding of stable protein aggregates by entropic pulling. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6166-6171.	7.1	220
4	The kinetic parameters and energy cost of the Hsp70 chaperone as a polypeptide unfoldase. Nature Chemical Biology, 2010, 6, 914-920.	8.0	205
5	Kosmotropes and chaotropes: modelling preferential exclusion, binding and aggregate stability. Biophysical Chemistry, 2004, 112, 45-57.	2.8	167
6	Complex network analysis of free-energy landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1817-1822.	7.1	159
7	The mechanism of Hsp70 chaperones: (entropic) pulling the models together. Trends in Biochemical Sciences, 2007, 32, 372-380.	7.5	156
8	Molecular dissection of amyloid disaggregation by human HSP70. Nature, 2020, 587, 483-488.	27.8	153
9	Hydrophobic hydration of poly-N-isopropyl acrylamide: a matter of the mean energetic state of water. Scientific Reports, 2014, 4, 4377.	3.3	139
10	Scaling Exponents and Probability Distributions of DNA End-to-End Distance. Physical Review Letters, 2005, 95, 158105.	7.8	124
11	Functional Dynamics of PDZ Binding Domains: A Normal-Mode Analysis. Biophysical Journal, 2005, 89, 14-21.	0.5	124
12	Self-organization of <i>parS</i> centromeres by the ParB CTP hydrolase. Science, 2019, 366, 1129-1133.	12.6	110
13	Finding instabilities in the community structure of complex networks. Physical Review E, 2005, 72, 056135.	2.1	109
14	Fractal Dimension and Localization of DNA Knots. Physical Review Letters, 2007, 98, 058102.	7.8	109
15	Hsp70 chaperones are non-equilibrium machines that achieve ultra-affinity by energy consumption. ELife, 2014, 3, e02218.	6.0	98
16	Active Solubilization and Refolding of Stable Protein Aggregates By Cooperative Unfolding Action of Individual Hsp70 Chaperones. Journal of Biological Chemistry, 2004, 279, 37298-37303.	3.4	95
17	Spectral Coarse Graining of Complex Networks. Physical Review Letters, 2007, 99, 038701.	7.8	95
18	DNA-segment-capture model for loop extrusion by structural maintenance of chromosome (SMC) protein complexes. Nucleic Acids Research, 2019, 47, 6956-6972.	14.5	92

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19	Elastic Membrane Heterogeneity of Living Cells Revealed by Stiff Nanoscale Membrane Domains. Biophysical Journal, 2008, 94, 1521-1532.	0.5	83
20	Effective interactions between chaotropic agents and proteins. Proteins: Structure, Function and Bioinformatics, 2005, 61, 492-499.	2.6	81
21	Discrete Breathers in Nonlinear Network Models of Proteins. Physical Review Letters, 2007, 99, 238104.	7.8	80
22	Interactions between synaptic vesicle fusion proteins explored by atomic force microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8736-8741.	7.1	79
23	Chaperones convert the energy from ATP into the nonequilibrium stabilization of native proteins. Nature Chemical Biology, 2018, 14, 388-395.	8.0	78
24	GroEL and CCT are catalytic unfoldases mediating out-of-cage polypeptide refolding without ATP. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7199-7204.	7.1	75
25	Quantitative proteomics of heat-treated human cells show an across-the-board mild depletion of housekeeping proteins to massively accumulate few HSPs. Cell Stress and Chaperones, 2015, 20, 605-620.	2.9	69
26	Spectral Coarse Graining and Synchronization in Oscillator Networks. Physical Review Letters, 2008, 100, 174104.	7.8	68
27	Universal1/fNoise from Dissipative Self-Organized Criticality Models. Physical Review Letters, 1999, 82, 472-475.	7.8	66
28	Freezing immunoglobulins to see them move. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6466-6471.	7.1	66
29	Putting proteins back into water. Physical Review E, 2000, 62, 8449-8452.	2.1	61
30	Large-Scale Conformational Transitions and Dimerization Are Encoded in the Amino-Acid Sequences of Hsp70 Chaperones. PLoS Computational Biology, 2015, 11, e1004262.	3.2	61
31	Evolution of an intricate J-protein network driving protein disaggregation in eukaryotes. ELife, 2017, 6, .	6.0	60
32	Oscillation modes of microtubules. Biology of the Cell, 2004, 96, 697-700.	2.0	59
33	Exploration of scale-free networks. European Physical Journal B, 2004, 38, 201-204.	1.5	59
34	Cold Denaturation of Yeast Frataxin Offers the Clue to Understand the Effect of Alcohols on Protein Stability. Journal of the American Chemical Society, 2008, 130, 9963-9970.	13.7	59
35	Diffusion-Limited Reactions in Crowded Environments. Physical Review Letters, 2010, 105, 120601.	7.8	58
36	Physical realizability of small-world networks. Physical Review E, 2006, 73, 026114.	2.1	52

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37	Mechanisms of Quantum Dot Energy Engineering by Metalorganic Vapor Phase Epitaxy on Patterned Nonplanar Substrates. Nano Letters, 2007, 7, 1282-1285.	9.1	51
38	Role of clustering and gridlike ordering in epidemic spreading. Physical Review E, 2004, 69, 066116.	2.1	50
39	Simulation and Theory of Antibody Binding to Crowded Antigen-Covered Surfaces. PLoS Computational Biology, 2016, 12, e1004752.	3.2	49
40	Membraneless organelles: phasing out of equilibrium. Emerging Topics in Life Sciences, 2020, 4, 343-354.	2.6	48
41	Modeling Hsp70/Hsp40 interaction by multi-scale molecular simulations and coevolutionary sequence analysis. ELife, 2017, 6, .	6.0	48
42	Universal Behavior in the Mesoscale Properties of Amyloid Fibrils. Physical Review Letters, 2014, 113, 268103.	7.8	44
43	Cold and warm denaturation of proteins. Journal of Biological Physics, 2001, 27, 229-241.	1.5	40
44	The local minority game. Physica A: Statistical Mechanics and Its Applications, 2002, 303, 217-225.	2.6	40
45	Dynamics of antibodies from cryo-electron tomography. Biophysical Chemistry, 2005, 115, 235-240.	2.8	39
46	Hydrophobic Interaction Model for Upper and Lower Critical Solution Temperatures. Macromolecules, 2003, 36, 5845-5853.	4.8	37
47	Numerical Simulation of Gel Electrophoresis of DNA Knots in Weak and Strong Electric Fields. Biophysical Journal, 2006, 90, 3100-3105.	0.5	37
48	Relief of ParB autoinhibition by <i>parS</i> DNA catalysis and recycling of ParB by CTP hydrolysis promote bacterial centromere assembly. Science Advances, 2021, 7, eabj2854.	10.3	35
49	Dynamical Jahn-Teller effect and Berry phase in positively charged fullerenes: Basic considerations. Physical Review B, 1996, 54, 7157-7167.	3.2	34
50	Cold and warm swelling of hydrophobic polymers. Physical Review E, 2001, 63, 031802.	2.1	34
51	Cluster approximations for epidemic processes: a systematic description of correlations beyond the pair level. Journal of Theoretical Biology, 2004, 229, 1-11.	1.7	34
52	Hyperplectonemes: A Higher Order Compact and Dynamic DNA Self-Organization. Nano Letters, 2017, 17, 1938-1948.	9.1	34
53	Probing the different chaperone activities of the bacterial HSP70â€HSP40 system using a thermolabile luciferase substrate. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1991-1998.	2.6	33
54	First-order coil-globule transition driven by vibrational entropy. Nature Communications, 2012, 3, 1065.	12.8	32

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55	The effect of crowding and confinement: a comparison of Yfh1 stability in different environments. Physical Biology, 2013, 10, 045002.	1.8	32
56	High-Dimensional Bak-Sneppen Model. Physical Review Letters, 1998, 80, 5746-5749.	7.8	31
57	Statistical features of drainage basins in mars channel networks. European Physical Journal B, 2004, 38, 387-391.	1.5	31
58	Extended Navigability of Small World Networks: Exact Results and New Insights. Physical Review Letters, 2009, 102, 238703.	7.8	31
59	Hsp70 chaperones use ATP to remodel native protein oligomers and stable aggregates by entropic pulling. Nature Structural and Molecular Biology, 2016, 23, 766-769.	8.2	30
60	J-domain protein chaperone circuits in proteostasis and disease. Trends in Cell Biology, 2023, 33, 30-47.	7.9	30
61	Effective Interactions Cannot Replace Solvent Effects in a Lattice Model of Proteins. Physical Review Letters, 2003, 91, 258102.	7.8	29
62	Uncovering the topology of configuration space networks. Physical Review E, 2007, 76, 026113.	2.1	29
63	Power law size distribution of supercritical random trees. Europhysics Letters, 2001, 56, 898-903.	2.0	26
64	Real-Time Monitoring of Protein Conformational Changes Using a Nano-Mechanical Sensor. PLoS ONE, 2014, 9, e103674.	2.5	26
65	Efficient conversion of chemical energy into mechanical work by Hsp70 chaperones. ELife, 2019, 8, .	6.0	26
66	Berry phase and ground-state symmetry inHâŠ—hdynamical Jahn-Teller systems. Physical Review B, 2000, 62, 29-32.	3.2	25
67	Slow Energy Relaxation of Macromolecules and Nanoclusters in Solution. Physical Review Letters, 2005, 94, 145502.	7.8	25
68	Non-equilibrium conformational dynamics in the function of molecular chaperones. Current Opinion in Structural Biology, 2015, 30, 161-169.	5.7	25
69	Expansion Around the Mean-Field Solution of the Bak-Sneppen Model. Physical Review Letters, 1998, 80, 1457-1460.	7.8	24
70	Protein Structural Information and Evolutionary Landscape by In Vitro Evolution. Molecular Biology and Evolution, 2020, 37, 1179-1192.	8.9	24
71	Bottleneck Genes and Community Structure in the Cell Cycle Network of S. pombe. PLoS Computational Biology, 2007, 3, e103.	3.2	23
72	A dynamical study of antibodyâ€"antigen encounter reactions. Physical Biology, 2007, 4, 172-180.	1.8	20

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73	Chaperoning protein evolution. Nature Chemical Biology, 2012, 8, 226-228.	8.0	20
74	The cold denaturation of IscU highlights structureâ€"function dualism in marginally stable proteins. Communications Chemistry, 2018, 1, .	4.5	19
75	Dissipation-driven selection of states in non-equilibrium chemical networks. Communications Chemistry, 2021, 4, .	4.5	19
76	Ant behavioral maturation is mediated by a stochastic transition between two fundamental states. Current Biology, 2021, 31, 2253-2260.e3.	3.9	19
77	Anticooperativity in diffusion-controlled reactions with pairs of anisotropic domains: a model for the antigenâ€"antibody encounter. European Biophysics Journal, 2005, 34, 899-911.	2.2	18
78	Glasslike Structure of Globular Proteins and the Boson Peak. Physical Review Letters, 2006, 96, 198103.	7.8	18
79	Design of lattice proteins with explicit solvent. Physical Review E, 2002, 66, 061911.	2.1	17
80	Interfaces and the edge percolation map of random directed networks. Physical Review E, 2007, 76, 056121.	2.1	17
81	Interplay between cost and benefits triggers nontrivial vaccination uptake. Physical Review E, 2018, 97, 032308.	2.1	17
82	Equilibrium and non-equilibrium furanose selection in the ribose isomerisation network. Nature Communications, 2021, 12, 2749.	12.8	17
83	Repair or Degrade: the Thermodynamic Dilemma of Cellular Protein Quality-Control. Frontiers in Molecular Biosciences, 2021, 8, 768888.	3.5	17
84	The rÃ1e of the Berry phase in dynamical Jahn-Teller systems. Journal of Physics Condensed Matter, 1998, 10, 8485-8495.	1.8	15
85	Critical exponents of the anisotropic Bak-Sneppen model. Physical Review E, 1998, 58, 7141-7145.	2.1	15
86	Widespread occurrence of the inverse square distribution in social sciences and taxonomy. Physical Review E, 2004, 69, 035101.	2.1	15
87	Chaotropic effect and preferential binding in a hydrophobic interaction model. Journal of Chemical Physics, 2003, 119, 7988-8001.	3.0	13
88	Quantitative description and modeling of real networks. Physical Review E, 2003, 68, 047101.	2.1	12
89	Thermodynamic Bounds on the Ultra- and Infra-affinity of Hsp70 for Its Substrates. Biophysical Journal, 2017, 113, 362-370.	0.5	12
90	Simulations of electrophoretic collisions of DNA knots with gel obstacles. Journal of Physics Condensed Matter, 2006, 18, S161-S171.	1.8	11

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91	Model of correlated evolution. Physical Review E, 1996, 54, 6053-6057.	2.1	10
92	Self-organized criticality driven by deterministic rules. Physical Review E, 1997, 56, 4876-4879.	2.1	10
93	Discretized Diffusion Processes. Physical Review Letters, 2000, 85, 4848-4851.	7.8	10
94	Bethe approximation for self-interacting lattice trees. Europhysics Letters, 2001, 53, 176-182.	2.0	10
95	Preferential exchange: Strengthening connections in complex networks. Physical Review E, 2004, 70, 027102.	2.1	10
96	Diffusion-limited reactions in crowded environments: a local density approximation. Journal of Physics Condensed Matter, 2013, 25, 375104.	1.8	10
97	Directed Polymers on a Factorized Disorder Landscape. Physical Review Letters, 1998, 81, 1023-1026.	7.8	8
98	Shape of a Stretched Polymer. Physical Review Letters, 2017, 119, 037801.	7.8	8
99	Solvent-induced micelle formation in a hydrophobic interaction model. Physical Review E, 2004, 69, 061924.	2.1	7
100	Temperature Dependence of Normal Mode Reconstructions of Protein Dynamics. Physical Review Letters, 2009, 102, 218104.	7.8	7
101	New Techniques for Ancient Proteins: Direct Coupling Analysis Applied on Proteins Involved in Iron Sulfur Cluster Biogenesis. Frontiers in Molecular Biosciences, 2017, 4, 40.	3.5	7
102	Explaining the length threshold of polyglutamine aggregation. Journal of Physics Condensed Matter, 2012, 24, 244105.	1.8	6
103	Quantifying the role of chaperones in protein translocation by computational modeling. Frontiers in Molecular Biosciences, 2015, 2, 8.	3.5	6
104	Structural Efficiency of Percolated Landscapes in Flow Networks. PLoS ONE, 2008, 3, e3654.	2.5	6
105	Reentrant behaviour in a highly anisotropic system. Physica A: Statistical Mechanics and Its Applications, 1994, 203, 640-654.	2.6	5
106	Optimal path and directed percolation. Physical Review E, 1996, 53, R2029-R2032.	2.1	5
107	Universality and Crossover of Directed Polymers and Growing Surfaces. Physical Review Letters, 1999, 82, 4236-4239.	7.8	5
108	Levy-nearest-neighbors Bak-Sneppen model. Physical Review E, 1999, 60, R1111-R1114.	2.1	5

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109	Diffusion-Limited Unbinding of Small Peptides from PDZ Domains. Journal of Physical Chemistry B, 2007, 111, 11057-11063.	2.6	5
110	Vibrational entropy and the structural organization of proteins. European Physical Journal E, 2010, 33, 89-96.	1.6	5
111	Self-organized criticality in deterministic systems with disorder. Physical Review E, 1998, 57, 6451-6459.	2.1	4
112	Exploration Bias of Complex Networks. AIP Conference Proceedings, 2003, , .	0.4	4
113	EXISTENCE, COST AND ROBUSTNESS OF SPATIAL SMALL-WORLD NETWORKS. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 2007, 17, 2331-2342.	1.7	3
114	Stochastic fluctuations and the detectability limit of network communities. Physical Review E, 2013, 88, 060801.	2.1	3
115	Polymers with a bimodal disorder distribution and directed percolation. Journal of Physics A, 1997, 30, L617-L621.	1.6	2
116	Statistical analysis of genealogical trees for polygamic species. Physical Review E, 2000, 61, 5620-5623.	2.1	1
117	On the origin of the boson peak in globular proteins. Philosophical Magazine, 2007, 87, 631-641.	1.6	1
118	Dissipation-Driven Selection under Finite Diffusion: Hints from Equilibrium and Separation of Time Scales. Entropy, 2021, 23, 1068.	2.2	1
119	MONTE-CARLO SIMULATIONS OF GEL-ELECTROPHORESIS OF DNA KNOTS. Series on Knots and Everything, 2005, , 149-159.	0.0	1
120	How Complex Molecules Could Possibly be Stable at the Dawn of Life: Out of Equilibrium Dissipation Shapes Selection. Biophysical Journal, 2020, 118, 611a.	0.5	0