Flavio Seno

List of Publications by Year
in descending order

82 papers	3,266 citations	147566 31 h-index	161609 54 g-index
84 all docs	84 docs citations	84 times ranked	3179 citing authors

#	Article	IF	Citations
1	Statistical potentials from the Gaussian scaling behaviour of chain fragments buried within protein globules. PLoS ONE, 2022, 17, e0254969.	1.1	0
2	Brownian non-Gaussian polymer diffusion and queuing theory in the mean-field limit. New Journal of Physics, 2022, 24, 023003.	1.2	9
3	Exact first-passage time distributions for three random diffusivity models. Journal of Physics A: Mathematical and Theoretical, 2021, 54, 04LT01.	0.7	9
4	Exact distributions of the maximum and range of random diffusivity processes. New Journal of Physics, 2021, 23, 023014.	1.2	8
5	Polymers critical point originates Brownian non-Gaussian diffusion. Physical Review E, 2021, 104, L062501.	0.8	9
6	Optical tweezers in single-molecule experiments. European Physical Journal Plus, 2020, 135, 1.	1.2	28
7	Fractional Brownian motion with random diffusivity: emerging residual nonergodicity below the correlation time. Journal of Physics A: Mathematical and Theoretical, 2020, 53, 474001.	0.7	64
8	Universal spectral features of different classes of random-diffusivity processes. New Journal of Physics, 2020, 22, 063056.	1.2	32
9	Unexpected crossovers in correlated random-diffusivity processes. New Journal of Physics, 2020, 22, 083041.	1.2	53
10	Folding Rate Optimization Promotes Frustrated Interactions in Entangled Protein Structures. International Journal of Molecular Sciences, 2020, 21, 213.	1.8	6
11	Polymerization Induces Non-Gaussian Diffusion. Frontiers in Physics, 2019, 7, .	1.0	27
12	Sequence and structural patterns detected in entangled proteins reveal the importance of co-translational folding. Scientific Reports, 2019, 9, 8426.	1.6	30
13	Vibrational entropy estimation can improve binding affinity prediction for nonâ€obligatory protein complexes. Proteins: Structure, Function and Bioinformatics, 2018, 86, 393-404.	1.5	7
14	Random diffusivity from stochastic equations: comparison of two models for Brownian yet non-Gaussian diffusion. New Journal of Physics, 2018, 20, 043044.	1.2	111
15	Bubble-bound state of triple-stranded DNA: Efimov physics in DNA with repulsion. Journal of Statistical Mechanics: Theory and Experiment, 2017, 2017, 073203.	0.9	6
16	Brownian yet Non-Gaussian Diffusion: From Superstatistics to Subordination of Diffusing Diffusivities. Physical Review X, 2017, 7, .	2.8	235
17	Exploring the correlation between the folding rates of proteins and the entanglement of their native states. Journal of Physics A: Mathematical and Theoretical, 2017, 50, 504001.	0.7	44
18	Bacterial bioluminescence onset and quenching: a dynamical model for aquorum sensing-mediated property. Royal Society Open Science, 2017, 4, 171586.	1.1	9

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19	Linking in domain-swapped protein dimers. Scientific Reports, 2016, 6, 33872.	1.6	33
20	Modeling quorum sensing trade-offs between bacterial cell density and system extension from open boundaries. Scientific Reports, 2016, 6, 39142.	1.6	20
21	Efimov-Like Behaviour in Low-Dimensional Polymer Models. Journal of Low Temperature Physics, 2016, 185, 102-121.	0.6	1
22	An Efficient Algorithm to Perform Local Concerted Movements of a Chain Molecule. PLoS ONE, 2015, 10, e0118342.	1.1	14
23	Native fold and docking pose discrimination by the same residueâ€based scoring function. Proteins: Structure, Function and Bioinformatics, 2015, 83, 621-630.	1.5	17
24	Quorum vs. diffusion sensing: a quantitative analysis of the relevance of absorbing or reflecting boundaries. FEMS Microbiology Letters, 2014, 352, 198-203.	0.7	39
25	Melting behavior and different bound states in three-stranded DNA models. Physical Review E, 2014, 89, 012121.	0.8	8
26	PASTA 2.0: an improved server for protein aggregation prediction. Nucleic Acids Research, 2014, 42, W301-W307.	6.5	349
27	BACHSCORE. A tool for evaluating efficiently and reliably the quality of large sets of protein structures. Computer Physics Communications, 2013, 184, 2860-2865.	3.0	20
28	A simple and efficient statistical potential for scoring ensembles of protein structures. Scientific Reports, 2012, 2, .	1.6	48
29	Sequence repeats and protein structure. Physical Review E, 2012, 86, 050901.	0.8	2
30	Protein Sequence and Structure: Is One More Fundamental than the Other?. Journal of Statistical Physics, 2012, 148, 637-646.	0.5	4
31	New trends in modern statistical physics. Open Physics, 2012, 10, .	0.8	1
32	Fibril elongation mechanisms of HETâ€s prionâ€forming domain: Topological evidence for growth polarity. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3067-3081.	1.5	8
33	Exploring the Universe of Protein Structures beyond the Protein Data Bank. PLoS Computational Biology, 2010, 6, e1000957.	1.5	62
34	When a DNA triple helix melts: an analogue of the Efimov state. New Journal of Physics, 2010, 12, 083057.	1.2	16
35	Amyloidogenic Potential of Transthyretin Variants. Journal of Biological Chemistry, 2009, 284, 25832-25841.	1.6	44
36	REPETITA: detection and discrimination of the periodicity of protein solenoid repeats by discrete Fourier transform. Bioinformatics, 2009, 25, i289-i295.	1.8	57

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37	Consequences of relative cellular positioning on quorum sensing and bacterial cell-to-cell communication. FEMS Microbiology Letters, 2009, 292, 149-161.	0.7	59
38	Phase diagrams for DNA denaturation under stretching forces. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, L04001.	0.9	11
39	Inference of the solvation energy parameters of amino acids using maximum entropy approach. Journal of Chemical Physics, 2008, 129, 035102.	1.2	4
40	Maximum Entropy Approach for Deducing Amino Acid Interactions in Proteins. Physical Review Letters, 2008, 100, 078102.	2.9	34
41	Aggregation of natively folded proteins: a theoretical approach. Journal of Physics Condensed Matter, 2007, 19, 285221.	0.7	5
42	The PASTA server for protein aggregation prediction. Protein Engineering, Design and Selection, 2007, 20, 521-523.	1.0	217
43	Minireview: The compact phase in polymers and proteins. Physica A: Statistical Mechanics and Its Applications, 2007, 384, 122-127.	1.2	4
44	Marginal compactness of protein native structures. Journal of Physics Condensed Matter, 2006, 18, S297-S306.	0.7	6
45	Insight into the Structure of Amyloid Fibrils from the Analysis of Globular Proteins. PLoS Computational Biology, 2006, 2, e170.	1.5	180
46	Geometry of proteins: Hydrogen bonding, sterics, and marginally compact tubes. Physical Review E, 2006, 73, 031921.	0.8	14
47	Common attributes of native-state structures of proteins, disordered proteins, and amyloid. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6883-6888.	3.3	48
48	Geometrical model for the native-state folds of proteins. Biophysical Chemistry, 2005, 115, 289-294.	1.5	7
49	What determines the structures of native folds of proteins?. Journal of Physics Condensed Matter, 2005, 17, S1515-S1522.	0.7	5
50	Complete Phase Diagram of DNA Unzipping: Eye,YFork, and Triple Point. Physical Review Letters, 2004, 93, 248102.	2.9	52
51	Unified perspective on proteins: A physics approach. Physical Review E, 2004, 70, 041905.	0.8	61
52	Geometry and symmetry presculpt the free-energy landscape of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7960-7964.	3.3	203
53	A new perspective on analysis of helix-helix packing preferences in globular proteins. Proteins: Structure, Function and Bioinformatics, 2004, 55, 1014-1022.	1.5	16
54	Unraveling the Schneeberg garnet puzzle: a numerical model of multiple nucleation and coalescence. Contributions To Mineralogy and Petrology, 2003, 146, 1-9.	1.2	38

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55	Assembly of protein tertiary structures from secondary structures using optimized potentials. Proteins: Structure, Function and Bioinformatics, 2003, 52, 155-165.	1.5	13
56	Helicase on DNA: a phase coexistence based mechanism. Journal of Physics A, 2003, 36, L181-L187.	1.6	13
57	Learning Effective Amino-Acid Interactions. Lecture Notes in Computer Science, 2003, , 139-145.	1.0	1
58	Anisotropic effective interactions in a coarse-grained tube picture of proteins. Proteins: Structure, Function and Bioinformatics, 2002, 49, 246-254.	1.5	9
59	A Self-Consistent Knowledge-Based Approach to Protein Design. Biophysical Journal, 2001, 80, 480-490.	0.2	19
60	Learning effective amino acid interactions through iterative stochastic techniques. Proteins: Structure, Function and Bioinformatics, 2001, 42, 422-431.	1.5	51
61	A measure of data collapse for scaling. Journal of Physics A, 2001, 34, 6375-6380.	1.6	124
62	Mechanical denaturation of DNA: existence of a low-temperature denaturation. Journal of Physics A, 2001, 34, L751-L758.	1.6	45
63	Recurrent oligomers in proteins: An optimal scheme reconciling accurate and concise backbone representations in automated folding and design studies. Proteins: Structure, Function and Bioinformatics, 2000, 40, 662-674.	1.5	72
64	Deciphering the folding kinetics of transmembrane helical proteins. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 14229-14234.	3.3	12
65	Adsorptionlike Collapse of Diblock Copolymers. Physical Review Letters, 2000, 84, 294-297.	2.9	17
66	Simple model to study insertion of a protein into a membrane. Physical Review E, 1999, 60, 7290-7298.	0.8	9
67	Protein Structures and Optimal Folding from a Geometrical Variational Principle. Physical Review Letters, 1999, 82, 3372-3375.	2.9	124
68	Strategies for protein folding and design. Annals of Combinatorics, 1999, 3, 431-450.	0.3	8
69	Determination of interaction potentials of amino acids from native protein structures: Tests on simple lattice models. Journal of Chemical Physics, 1999, 110, 10123-10133.	1.2	29
70	Interaction potentials for protein folding. , 1998, 30, 244-248.		34
71	Structure-based design of model proteins. , 1998, 31, 10-20.		8
72	Design of proteins with hydrophobic and polar amino acids. Proteins: Structure, Function and Bioinformatics, 1998, 32, 80-87.	1.5	32

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73	Variational Approach to Protein Design and Extraction of Interaction Potentials. Physical Review Letters, 1998, 81, 2172-2175.	2.9	35
74	Steric Constraints in Model Proteins. Physical Review Letters, 1998, 80, 5683-5686.	2.9	25
75	Protein Design in a Lattice Model of Hydrophobic and Polar Amino Acids. Physical Review Letters, 1998, 80, 2237-2240.	2.9	41
76	Polymers with a bimodal disorder distribution and directed percolation. Journal of Physics A, 1997, 30, L617-L621.	1.6	2
77	Optimal Protein Design Procedure. Physical Review Letters, 1996, 77, 1901-1904.	2.9	87
78	Phase diagram of branched polymer collapse. Physical Review E, 1996, 53, 3662-3672.	0.8	21
79	Simulations of deposition growth models in various dimensions: The possible importance of overhangs. Physical Review E, 1994, 50, R1741-R1744.	0.8	18
80	Deposition growth modes from numerical simulations. Physical Review B, 1994, 50, 17583-17586.	1.1	4
81	Boundary critical behavior ofd=2 self-avoiding walks on correlated and uncorrelated vacancies. Journal of Statistical Physics, 1993, 73, 21-46.	0.5	9
82	Self-avoiding walks in the presence of strongly correlated, annealed vacancies. Physical Review Letters, 1990, 65, 2897-2900.	2.9	10