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	PASTA 2.0: an improved server for protein aggregation prediction. Nucleic Acids Research, 2014, 42, W301-W307.	6.5	349
2	Brownian yet Non-Gaussian Diffusion: From Superstatistics to Subordination of Diffusing Diffusivities. Physical Review X, 2017, 7, .	2.8	235
3	The PASTA server for protein aggregation prediction. Protein Engineering, Design and Selection, 2007, 20, 521-523.	1.0	217
4	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
5	Insight into the Structure of Amyloid Fibrils from the Analysis of Globular Proteins. PLoS Computational Biology, 2006, 2, e170.	1.5	180
6	Protein Structures and Optimal Folding from a Geometrical Variational Principle. Physical Review Letters, 1999, 82, 3372-3375.	2.9	124
7	A measure of data collapse for scaling. Journal of Physics A, 2001, 34, 6375-6380.	1.6	124
8	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
9	Optimal Protein Design Procedure. Physical Review Letters, 1996, 77, 1901-1904.	2.9	87
10	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
11	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
12	Exploring the Universe of Protein Structures beyond the Protein Data Bank. PLoS Computational Biology, 2010, 6, e1000957.	1.5	62
13	Unified perspective on proteins: A physics approach. Physical Review E, 2004, 70, 041905.	0.8	61
14	Consequences of relative cellular positioning on quorum sensing and bacterial cell-to-cell communication. FEMS Microbiology Letters, 2009, 292, 149-161.	0.7	59
15	REPETITA: detection and discrimination of the periodicity of protein solenoid repeats by discrete Fourier transform. Bioinformatics, 2009, 25, i289-i295.	1.8	57
16	Unexpected crossovers in correlated random-diffusivity processes. New Journal of Physics, 2020, 22, 083041.	1.2	53
17	Complete Phase Diagram of DNA Unzipping: Eye,YFork, and Triple Point. Physical Review Letters, 2004, 93, 248102.	2.9	52
18	Learning effective amino acid interactions through iterative stochastic techniques. Proteins: Structure, Function and Bioinformatics, 2001, 42, 422-431.	1.5	51

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19	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
20	A simple and efficient statistical potential for scoring ensembles of protein structures. Scientific Reports, 2012, 2, .	1.6	48
21	Mechanical denaturation of DNA: existence of a low-temperature denaturation. Journal of Physics A, 2001, 34, L751-L758.	1.6	45
22	Amyloidogenic Potential of Transthyretin Variants. Journal of Biological Chemistry, 2009, 284, 25832-25841.	1.6	44
23	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
24	Protein Design in a Lattice Model of Hydrophobic and Polar Amino Acids. Physical Review Letters, 1998, 80, 2237-2240.	2.9	41
25	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
26	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
27	Variational Approach to Protein Design and Extraction of Interaction Potentials. Physical Review Letters, 1998, 81, 2172-2175.	2.9	35
28	Interaction potentials for protein folding. , 1998, 30, 244-248.		34
29	Maximum Entropy Approach for Deducing Amino Acid Interactions in Proteins. Physical Review Letters, 2008, 100, 078102.	2.9	34
30	Linking in domain-swapped protein dimers. Scientific Reports, 2016, 6, 33872.	1.6	33
31	Design of proteins with hydrophobic and polar amino acids. Proteins: Structure, Function and Bioinformatics, 1998, 32, 80-87.	1.5	32
32	Universal spectral features of different classes of random-diffusivity processes. New Journal of Physics, 2020, 22, 063056.	1.2	32
33	Sequence and structural patterns detected in entangled proteins reveal the importance of co-translational folding. Scientific Reports, 2019, 9, 8426.	1.6	30
34	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
35	Optical tweezers in single-molecule experiments. European Physical Journal Plus, 2020, 135, 1.	1.2	28
36	Polymerization Induces Non-Gaussian Diffusion. Frontiers in Physics, 2019, 7, .	1.0	27

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37	Steric Constraints in Model Proteins. Physical Review Letters, 1998, 80, 5683-5686.	2.9	25
38	Phase diagram of branched polymer collapse. Physical Review E, 1996, 53, 3662-3672.	0.8	21
39	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
40	Modeling quorum sensing trade-offs between bacterial cell density and system extension from open boundaries. Scientific Reports, 2016, 6, 39142.	1.6	20
41	A Self-Consistent Knowledge-Based Approach to Protein Design. Biophysical Journal, 2001, 80, 480-490.	0.2	19
42	Simulations of deposition growth models in various dimensions: The possible importance of overhangs. Physical Review E, 1994, 50, R1741-R1744.	0.8	18
43	Adsorptionlike Collapse of Diblock Copolymers. Physical Review Letters, 2000, 84, 294-297.	2.9	17
44	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
45	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
46	When a DNA triple helix melts: an analogue of the Efimov state. New Journal of Physics, 2010, 12, 083057.	1.2	16
47	Geometry of proteins: Hydrogen bonding, sterics, and marginally compact tubes. Physical Review E, 2006, 73, 031921.	0.8	14
48	An Efficient Algorithm to Perform Local Concerted Movements of a Chain Molecule. PLoS ONE, 2015, 10, e0118342.	1.1	14
49	Assembly of protein tertiary structures from secondary structures using optimized potentials. Proteins: Structure, Function and Bioinformatics, 2003, 52, 155-165.	1.5	13
50	Helicase on DNA: a phase coexistence based mechanism. Journal of Physics A, 2003, 36, L181-L187.	1.6	13
51	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
52	Phase diagrams for DNA denaturation under stretching forces. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, L04001.	0.9	11
53	Self-avoiding walks in the presence of strongly correlated, annealed vacancies. Physical Review Letters, 1990, 65, 2897-2900.	2.9	10
54	Boundary critical behavior ofd=2 self-avoiding walks on correlated and uncorrelated vacancies. Journal of Statistical Physics, 1993, 73, 21-46.	0.5	9

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55	Simple model to study insertion of a protein into a membrane. Physical Review E, 1999, 60, 7290-7298.	0.8	9
56	Anisotropic effective interactions in a coarse-grained tube picture of proteins. Proteins: Structure, Function and Bioinformatics, 2002, 49, 246-254.	1.5	9
57	Bacterial bioluminescence onset and quenching: a dynamical model for aquorum sensing-mediated property. Royal Society Open Science, 2017, 4, 171586.	1.1	9
58	Exact first-passage time distributions for three random diffusivity models. Journal of Physics A: Mathematical and Theoretical, 2021, 54, 04LT01.	0.7	9
59	Brownian non-Gaussian polymer diffusion and queuing theory in the mean-field limit. New Journal of Physics, 2022, 24, 023003.	1.2	9
60	Polymers critical point originates Brownian non-Gaussian diffusion. Physical Review E, 2021, 104, L062501.	0.8	9
61	Structure-based design of model proteins. , 1998, 31, 10-20.		8
62	Strategies for protein folding and design. Annals of Combinatorics, 1999, 3, 431-450.	0.3	8
63	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
64	Melting behavior and different bound states in three-stranded DNA models. Physical Review E, 2014, 89, 012121.	0.8	8
65	Exact distributions of the maximum and range of random diffusivity processes. New Journal of Physics, 2021, 23, 023014.	1.2	8
66	Geometrical model for the native-state folds of proteins. Biophysical Chemistry, 2005, 115, 289-294.	1.5	7
67	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
68	Marginal compactness of protein native structures. Journal of Physics Condensed Matter, 2006, 18, S297-S306.	0.7	6
69	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
70	Folding Rate Optimization Promotes Frustrated Interactions in Entangled Protein Structures. International Journal of Molecular Sciences, 2020, 21, 213.	1.8	6
71	What determines the structures of native folds of proteins?. Journal of Physics Condensed Matter, 2005, 17, S1515-S1522.	0.7	5
72	Aggregation of natively folded proteins: a theoretical approach. Journal of Physics Condensed Matter, 2007, 19, 285221.	0.7	5

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73	Deposition growth modes from numerical simulations. Physical Review B, 1994, 50, 17583-17586.	1.1	4
74	Minireview: The compact phase in polymers and proteins. Physica A: Statistical Mechanics and Its Applications, 2007, 384, 122-127.	1.2	4
75	Inference of the solvation energy parameters of amino acids using maximum entropy approach. Journal of Chemical Physics, 2008, 129, 035102.	1.2	4
76	Protein Sequence and Structure: Is One More Fundamental than the Other?. Journal of Statistical Physics, 2012, 148, 637-646.	0.5	4
77	Polymers with a bimodal disorder distribution and directed percolation. Journal of Physics A, 1997, 30, L617-L621.	1.6	2
78	Sequence repeats and protein structure. Physical Review E, 2012, 86, 050901.	0.8	2
79	New trends in modern statistical physics. Open Physics, 2012, 10, .	0.8	1
80	Efimov-Like Behaviour in Low-Dimensional Polymer Models. Journal of Low Temperature Physics, 2016, 185, 102-121.	0.6	1
81	Learning Effective Amino-Acid Interactions. Lecture Notes in Computer Science, 2003, , 139-145.	1.0	1
82	Statistical potentials from the Gaussian scaling behaviour of chain fragments buried within protein globules. PLoS ONE, 2022, 17, e0254969.	1.1	0