

# Antonio Trovato

## List of Publications by Year in descending order

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62  
papers

2,483  
citations

304368

22  
h-index

205818

48  
g-index

65  
all docs

65  
docs citations

65  
times ranked

2801  
citing authors

#	ARTICLE	IF	CITATIONS
1	PASTA 2.0: an improved server for protein aggregation prediction. <i>Nucleic Acids Research</i> , 2014, 42, W301-W307.	6.5	349
2	Optimal shapes of compact strings. <i>Nature</i> , 2000, 406, 287-290.	13.7	270
3	The PASTA server for protein aggregation prediction. <i>Protein Engineering, Design and Selection</i> , 2007, 20, 521-523.	1.0	217
4	Geometry and symmetry presculpt the free-energy landscape of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7960-7964.	3.3	203
5	Insight into the Structure of Amyloid Fibrils from the Analysis of Globular Proteins. <i>PLoS Computational Biology</i> , 2006, 2, e170.	1.5	180
6	Phase diagram of force-induced DNA unzipping in exactly solvable models. <i>Physical Review E</i> , 2001, 64, 031901.	0.8	92
7	A Condensation-Ordering Mechanism in Nanoparticle-Catalyzed Peptide Aggregation. <i>PLoS Computational Biology</i> , 2009, 5, e1000458.	1.5	90
8	Geometry and physics of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 315-322.	1.5	69
9	Exploring the Universe of Protein Structures beyond the Protein Data Bank. <i>PLoS Computational Biology</i> , 2010, 6, e1000957.	1.5	62
10	Unified perspective on proteins: A physics approach. <i>Physical Review E</i> , 2004, 70, 041905.	0.8	61
11	Consequences of relative cellular positioning on quorum sensing and bacterial cell-to-cell communication. <i>FEMS Microbiology Letters</i> , 2009, 292, 149-161.	0.7	59
12	REPETITA: detection and discrimination of the periodicity of protein solenoid repeats by discrete Fourier transform. <i>Bioinformatics</i> , 2009, 25, i289-i295.	1.8	57
13	Common attributes of native-state structures of proteins, disordered proteins, and amyloid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6883-6888.	3.3	48
14	A simple and efficient statistical potential for scoring ensembles of protein structures. <i>Scientific Reports</i> , 2012, 2, .	1.6	48
15	Amyloidogenic Potential of Transthyretin Variants. <i>Journal of Biological Chemistry</i> , 2009, 284, 25832-25841.	1.6	44
16	Exploring the correlation between the folding rates of proteins and the entanglement of their native states. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2017, 50, 504001.	0.7	44
17	Quorum vs. diffusion sensing: a quantitative analysis of the relevance of absorbing or reflecting boundaries. <i>FEMS Microbiology Letters</i> , 2014, 352, 198-203.	0.7	39
18	Maximum Entropy Approach for Deducing Amino Acid Interactions in Proteins. <i>Physical Review Letters</i> , 2008, 100, 078102.	2.9	34

#	ARTICLE	IF	CITATIONS
19	Linking in domain-swapped protein dimers. <i>Scientific Reports</i> , 2016, 6, 33872.	1.6	33
20	Structural motifs of biomolecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17283-17286.	3.3	31
21	Sequence and structural patterns detected in entangled proteins reveal the importance of co-translational folding. <i>Scientific Reports</i> , 2019, 9, 8426.	1.6	30
22	Geometry of Compact Tubes and Protein Structures. <i>Complexus</i> , 2003, 1, 4-13.	0.7	22
23	Physics of thick polymers. <i>Journal of Polymer Science, Part B: Polymer Physics</i> , 2005, 43, 650-679.	2.4	21
24	Heteropolymers in a solvent at an interface. <i>Journal of Physics A</i> , 1999, 32, L275-L280.	1.6	20
25	BACHSCORE. A tool for evaluating efficiently and reliably the quality of large sets of protein structures. <i>Computer Physics Communications</i> , 2013, 184, 2860-2865.	3.0	20
26	Modeling quorum sensing trade-offs between bacterial cell density and system extension from open boundaries. <i>Scientific Reports</i> , 2016, 6, 39142.	1.6	20
27	A variational approach to the localization transition of heteropolymers at interfaces. <i>Europhysics Letters</i> , 1999, 46, 301-306.	0.7	19
28	Native fold and docking pose discrimination by the same residue-based scoring function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 621-630.	1.5	17
29	A new perspective on analysis of helix-helix packing preferences in globular proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 1014-1022.	1.5	16
30	Continuum model for polymers with finite thickness. <i>Journal of Physics A</i> , 2005, 38, L277-L283.	1.6	16
31	When a DNA triple helix melts: an analogue of the Efimov state. <i>New Journal of Physics</i> , 2010, 12, 083057.	1.2	16
32	Simplified Exactly Solvable Model for $\langle r^2 \rangle$ -Amyloid Aggregation. <i>Physical Review Letters</i> , 2010, 105, 108102.	2.9	15
33	Universality for interacting oriented self-avoiding walk: A transfer matrix calculation. <i>Physical Review E</i> , 1997, 56, 131-143.	0.8	14
34	Geometry of proteins: Hydrogen bonding, sterics, and marginally compact tubes. <i>Physical Review E</i> , 2006, 73, 031921.	0.8	14
35	Symmetry, shape, and order. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19187-19192.	3.3	14
36	Different pulling modes in DNA overstretching: A theoretical analysis. <i>Physical Review E</i> , 2010, 81, 051926.	0.8	14

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37	An Efficient Algorithm to Perform Local Concerted Movements of a Chain Molecule. PLoS ONE, 2015, 10, e0118342.	1.1	14
38	Swollen-collapsed transition in random hetero-polymers. European Physical Journal B, 1998, 6, 63-73.	0.6	13
39	Emergence of secondary motifs in tubelike polymers in a solvent. Physical Review E, 2008, 77, 061804.	0.8	11
40	Phase diagrams for DNA denaturation under stretching forces. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, L04001.	0.9	11
41	Bacterial bioluminescence onset and quenching: a dynamical model for a quorum sensing-mediated property. Royal Society Open Science, 2017, 4, 171586.	1.1	9
42	Compact phases of polymers with hydrogen bonding. Physical Review E, 2003, 67, 021805.	0.8	8
43	Tubes near the edge of compactness and folded protein structures *. Journal of Physics Condensed Matter, 2003, 15, S1787-S1796.	0.7	8
44	Fibril elongation mechanisms of HET-s prion-forming domain: Topological evidence for growth polarity. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3067-3081.	1.5	8
45	Melting behavior and different bound states in three-stranded DNA models. Physical Review E, 2014, 89, 012121.	0.8	8
46	Signature of Pareto optimization in the Escherichia coli proteome. Scientific Reports, 2018, 8, 9141.	1.6	8
47	Geometrical model for the native-state folds of proteins. Biophysical Chemistry, 2005, 115, 289-294.	1.5	7
48	Vibrational entropy estimation can improve binding affinity prediction for non-obligatory protein complexes. Proteins: Structure, Function and Bioinformatics, 2018, 86, 393-404.	1.5	7
49	Marginal compactness of protein native structures. Journal of Physics Condensed Matter, 2006, 18, S297-S306.	0.7	6
50	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
51	Folding Rate Optimization Promotes Frustrated Interactions in Entangled Protein Structures. International Journal of Molecular Sciences, 2020, 21, 213.	1.8	6
52	What determines the structures of native folds of proteins?. Journal of Physics Condensed Matter, 2005, 17, S1515-S1522.	0.7	5
53	Aggregation of natively folded proteins: a theoretical approach. Journal of Physics Condensed Matter, 2007, 19, 285221.	0.7	5
54	Design of amino acid sequences to fold into C $\beta$ -model proteins. Journal of Chemical Physics, 2005, 123, 054904.	1.2	4

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55	Minireview: The compact phase in polymers and proteins. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 384, 122-127.	1.2	4
56	Simple solvation potential for coarse-grained models of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 285-292.	1.5	4
57	Inference of the solvation energy parameters of amino acids using maximum entropy approach. <i>Journal of Chemical Physics</i> , 2008, 129, 035102.	1.2	4
58	Protein Sequence and Structure: Is One More Fundamental than the Other?. <i>Journal of Statistical Physics</i> , 2012, 148, 637-646.	0.5	4
59	Sequence repeats and protein structure. <i>Physical Review E</i> , 2012, 86, 050901.	0.8	2
60	Efimov-Like Behaviour in Low-Dimensional Polymer Models. <i>Journal of Low Temperature Physics</i> , 2016, 185, 102-121.	0.6	1
61	Exploring by Enhanced Sampling Techniques: The Protein's Conformational Space Beyond the PDB. <i>Biophysical Journal</i> , 2011, 100, 209a.	0.2	0
62	Statistical potentials from the Gaussian scaling behaviour of chain fragments buried within protein globules. <i>PLoS ONE</i> , 2022, 17, e0254969.	1.1	0