Ugo Bastolla

List of Publications by Year
in descending order

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89

papers

4,418

citations

126907

33

h-index

118850

62

g-index

99

all docs

99

docs citations

99

times ranked

4804

citing authors

#	ARTICLE	IF	CITATIONS
1	The architecture of mutualistic networks minimizes competition and increases biodiversity. Nature, 2009, 458, 1018-1020.	27.8	878
2	Reductive genome evolution in Buchnera aphidicola. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 581-586.	7.1	461
3	The Functional Topography of the <i>Arabidopsis</i> Genome Is Organized in a Reduced Number of Linear Motifs of Chromatin States Â. Plant Cell, 2014, 26, 2351-2366.	6.6	281
4	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188
5	How to guarantee optimal stability for most representative structures in the protein data bank. Proteins: Structure, Function and Bioinformatics, 2001, 44, 79-96.	2.6	109
6	Phase Transitions of Single Semistiff Polymer Chains. Journal of Statistical Physics, 1997, 89, 1061-1078.	1.2	100
7	Relevant elements, magnetization and dynamical properties in Kauffman networks: A numerical study. Physica D: Nonlinear Phenomena, 1998, 115, 203-218.	2.8	85
8	The modular structure of Kauffman networks. Physica D: Nonlinear Phenomena, 1998, 115, 219-233.	2.8	83
9	Neutral Evolution of Model Proteins: Diffusion in Sequence Space and Overdispersion. Journal of Theoretical Biology, 1999, 200, 49-64.	1.7	81
10	Torsional Network Model: Normal Modes in Torsion Angle Space Better Correlate with Conformation Changes in Proteins. Physical Review Letters, 2010, 104, 228103.	7.8	79
11	Testing a new Monte Carlo algorithm for protein folding. Proteins: Structure, Function and Bioinformatics, 1998, 32, 52-66.	2.6	78
12	Biodiversity in model ecosystems, I: coexistence conditions for competing species. Journal of Theoretical Biology, 2005, 235, 521-530.	1.7	77
13	New Monte Carlo Algorithm for Protein Folding. Physical Review Letters, 1998, 80, 3149-3152.	7.8	76
14	Principal eigenvector of contact matrices and hydrophobicity profiles in proteins. Proteins: Structure, Function and Bioinformatics, 2004, 58, 22-30.	2.6	71
15	Connectivity of Neutral Networks, Overdispersion, and Structural Conservation in Protein Evolution. Journal of Molecular Evolution, 2003, 56, 243-254.	1.8	65
16	Genomic Determinants of Protein Folding Thermodynamics in Prokaryotic Organisms. Journal of Molecular Biology, 2004, 343, 1451-1466.	4.2	59
17	Closing probabilities in the Kauffman model: An annealed computation. Physica D: Nonlinear Phenomena, 1996, 98, 1-25.	2.8	52
18	Cross-Over between Discrete and Continuous Protein Structure Space: Insights into Automatic Classification and Networks of Protein Structures. PLoS Computational Biology, 2009, 5, e1000331.	3.2	52

#	ARTICLE	IF	CITATIONS
19	High-resolution analysis of DNA synthesis start sites and nucleosome architecture at efficient mammalian replication origins. EMBO Journal, 2013, 32, 2631-2644.	7.8	52
20	A statistical mechanical method to optimize energy functions for protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 3977-3981.	7.1	51
21	Mutualism supports biodiversity when the direct competition is weak. Nature Communications, 2017, 8, 14326.	12.8	51
22	Stability constraints and protein evolution: the role of chain length, composition and disulfide bonds. Protein Engineering, Design and Selection, 2005, 18, 405-415.	2.1	50
23	Shape of Ecological Networks. Physical Review Letters, 2001, 86, 4418-4421.	7.8	49
24	A Numerical Study of the Critical Line of Kauffman Networks. Journal of Theoretical Biology, 1997, 187, 117-133.	1.7	48
25	Protein evolution along phylogenetic histories under structurally constrained substitution models. Bioinformatics, 2013, 29, 3020-3028.	4.1	48
26	Maximum-Likelihood Phylogenetic Inference with Selection on Protein Folding Stability. Molecular Biology and Evolution, 2015, 32, 2195-2207.	8.9	48
27	A protein evolution model with independent sites that reproduces site-specific amino acid distributions from the Protein Data Bank. BMC Evolutionary Biology, 2006, 6, 43.	3.2	46
28	Reconstruction of Protein Structures from a Vectorial Representation. Physical Review Letters, 2004, 92, 218101.	7.8	45
29	Statistical Properties of Neutral Evolution. Journal of Molecular Evolution, 2003, 57, S103-S119.	1.8	42
30	SABERTOOTH: protein structural alignment based on a vectorial structure representation. BMC Bioinformatics, 2007, 8, 425.	2.6	42
31	Mutation Bias Favors Protein Folding Stability in the Evolution of Small Populations. PLoS Computational Biology, 2010, 6, e1000767.	3.2	41
32	Testing similarity measures with continuous and discrete protein models. Proteins: Structure, Function and Bioinformatics, 2002, 50, 144-157.	2.6	40
33	What evolution tells us about protein physics, and protein physics tells us about evolution. Current Opinion in Structural Biology, 2017, 42, 59-66.	5.7	40
34	Prediction of Site-Specific Amino Acid Distributions and Limits of Divergent Evolutionary Changes in Protein Sequences. Molecular Biology and Evolution, 2005, 22, 630-638.	8.9	36
35	Quantifying the evolutionary divergence of protein structures: The role of function change and function conservation. Proteins: Structure, Function and Bioinformatics, 2010, 78, 181-196.	2.6	34
36	Computing protein dynamics from protein structure with elastic network models. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2014, 4, 488-503.	14.6	34

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37	Lack of Self-Averaging in Neutral Evolution of Proteins. Physical Review Letters, 2002, 89, 208101.	7.8	33
38	ProtASR: An Evolutionary Framework for Ancestral Protein Reconstruction with Selection on Folding Stability. Systematic Biology, 2017, 66, syw121.	5.6	29
39	Biodiversity in model ecosystems, II: species assembly and food web structure. Journal of Theoretical Biology, 2005, 235, 531-539.	1.7	28
40	Two-Dimensional Oriented Self-Avoiding Walks with Parallel Contacts. Journal of Statistical Physics, 1998, 90, 1311-1324.	1.2	27
41	Bacteria dialog with Santa Rosalia: Are aggregations of cosmopolitan bacteria mainly explained by habitat filtering or by ecological interactions?. BMC Microbiology, 2014, 14, 284.	3.3	27
42	An efficient conformational sampling method for homology modeling. Proteins: Structure, Function and Bioinformatics, 2008, 71, 175-188.	2.6	25
43	Structure and Non-Structure of Centrosomal Proteins. PLoS ONE, 2013, 8, e62633.	2.5	25
44	Is Covid-19 Severity Associated With ACE2 Degradation?. Frontiers in Drug Discovery, 2022, 1, .	2.8	25
45	Protein disorder in the centrosome correlates with complexity in cell types number. Molecular BioSystems, 2012, 8, 353-367.	2.9	24
46	Detecting selection for negative design in proteins through an improved model of the misfolded state. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1102-1112.	2.6	24
47	Substitution Rates Predicted by Stability-Constrained Models of Protein Evolution Are Not Consistent with Empirical Data. Molecular Biology and Evolution, 2018, 35, 743-755.	8.9	24
48	Effective connectivity profile: A structural representation that evidences the relationship between protein structures and sequences. Proteins: Structure, Function and Bioinformatics, 2008, 73, 872-888.	2.6	22
49	Differences in firing efficiency, chromatin, and transcription underlie the developmental plasticity of the <i>Arabidopsis</i> DNA replication origins. Genome Research, 2019, 29, 784-797.	5.5	20
50	Looking at structure, stability, and evolution of proteins through the principal eigenvector of contact matrices and hydrophobicity profiles. Gene, 2005, 347, 219-230.	2.2	19
51	Diversity Patterns from Ecological Models at Dynamical Equilibrium. Journal of Theoretical Biology, 2001, 212, 11-34.	1.7	18
52	High quality protein sequence alignment by combining structural profile prediction and profile alignment using SABER-TOOTH. BMC Bioinformatics, 2010, 11, 251.	2.6	18
53	Structural basis for allosteric transitions of a multidomain pentameric ligand-gated ion channel. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13437-13446.	7.1	18
54	Relaxation, closing probabilities and transition from oscillatory to chaotic attractors in asymmetric neural networks. Journal of Physics A, 1998, 31, 4583-4602.	1.6	17

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55	ProtASR2: Ancestral reconstruction of protein sequences accounting for folding stability. Methods in Ecology and Evolution, 2020, 11, 248-257.	5.2	17
56	ACE2 Serum Levels as Predictor of Infectability and Outcome in COVID-19. Frontiers in Immunology, 2022, 13, 836516.	4.8	16
57	Structurally constrained protein evolution: results from a lattice simulation. European Physical Journal B, 2000, 15, 385-397.	1.5	15
58	Detecting Selection on Protein Stability through Statistical Mechanical Models of Folding and Evolution. Biomolecules, 2014, 4, 291-314.	4.0	14
59	The Molecular Clock in the Evolution of Protein Structures. Systematic Biology, 2019, 68, 987-1002.	5.6	14
60	Attractors in fully asymmetric neural networks. Journal of Physics A, 1997, 30, 5613-5631.	1.6	13
61	The maximum penalty criterion for ridge regression: application to the calibration of the force constant in elastic network models. Integrative Biology (United Kingdom), 2017, 9, 627-641.	1.3	13
62	Molecular and Functional Bases of Selection against a Mutation Bias in an RNA Virus. Genome Biology and Evolution, 2017, 9, 1212-1228.	2.5	13
63	Predicted dynamical couplings of protein residues characterize catalysis, transport and allostery. Bioinformatics, 2019, 35, 4971-4978.	4.1	13
64	Mathematical Model of SARS-Cov-2 Propagation Versus ACE2 Fits COVID-19 Lethality Across Age and Sex and Predicts That of SARS. Frontiers in Molecular Biosciences, 2021, 8, 706122.	3.5	13
65	Influence of mutation bias and hydrophobicity on the substitution rates and sequence entropies of protein evolution. PeerJ, 2018, 6, e5549.	2.0	12
66	Phase diagram of random heteropolymers: Replica approach and application of a new Monte Carlo algorithm. Journal of Molecular Liquids, 2000, 84, 111-129.	4.9	11
67	Attraction basins in discretized maps. Journal of Physics A, 1997, 30, 3757-3769.	1.6	10
68	Exactness of the annealed and the replica symmetric approximations for random heteropolymers. Physical Review E, 2001, 63, 031901.	2.1	10
69	Sequence determinants of protein folding rates: Positive correlation between contact energy and contact range indicates selection for fast folding. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2287-2304.	2.6	10
70	Characterizing conformation changes in proteins through the torsional elastic response. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 836-846.	2.3	10
71	Emergence of structure through proteinâ€"protein interactions and pH changes in dually predicted coiled-coil and disordered regions of centrosomal proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1808-1819.	2.3	9
72	Can Conformational Changes of Proteins Be Represented in Torsion Angle Space? A Study with Rescaled Ridge Regression. Journal of Chemical Information and Modeling, 2019, 59, 4929-4941.	5.4	9

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73	The Influence of Protein Stability on Sequence Evolution: Applications to Phylogenetic Inference. Methods in Molecular Biology, 2019, 1851, 215-231.	0.9	9
74	Comparison of translation loads for standard and alternative genetic codes. BMC Evolutionary Biology, 2010, 10, 178.	3.2	8
75	Why are large conformational changes well described by harmonic normal modes?. Biophysical Journal, 2021, 120, 5343-5354.	0.5	7
76	Protein evolution in viral quasispecies under selective pressure: A thermodynamic and phylogenetic analysis. Gene, 2005, 347, 237-246.	2.2	6
77	Local interactions in protein folding determined through an inverse folding model. Proteins: Structure, Function and Bioinformatics, 2008, 71, 278-299.	2.6	5
78	The emerging dynamic view of proteins: Protein plasticity in allostery, evolution and self-assembly. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 817-819.	2.3	5
79	Replica-symmetry breaking in dynamical glasses. European Physical Journal B, 2001, 23, 497-508.	1.5	4
80	Computational proteomics on the grid. New Generation Computing, 2004, 22, 191-192.	3.3	4
81	A framework for protein structure prediction on the grid. New Generation Computing, 2005, 23, 277-290.	3.3	4
82	The Structurally Constrained Neutral Model of Protein Evolution. Biological and Medical Physics Series, 2007, , 75-112.	0.4	4
83	Effective competition determines the global stability of model ecosystems. Theoretical Ecology, 2017, 10, 195-205.	1.0	2
84	Learning structural bioinformatics and evolution with a snake puzzle. PeerJ Computer Science, 0, 2, e100.	4.5	2
85	Testing a new Monte Carlo algorithm for protein folding. Proteins: Structure, Function and Bioinformatics, 1998, 32, 52-66.	2.6	1
86	Overlap distribution in random and designed heteropolymers. European Physical Journal E, 2001, 4, 305-313.	1.6	0
87	In memoriam. Proteins: Structure, Function and Bioinformatics, 2010, 78, iii-viii.	2.6	0
88	Editorial overview: Proteins: bridging theory and experiment. Current Opinion in Structural Biology, 2017, 42, viii-x.	5.7	0
89	Modeling Structural and Genomic Constraints in the Evolution of Proteins. Biological and Medical Physics Series, 2012, , 327-345.	0.4	0