

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	Is Covid-19 Severity Associated With ACE2 Degradation?. <i>Frontiers in Drug Discovery</i> , 2022, 1, .	2.8	25
2	ACE2 Serum Levels as Predictor of Infectability and Outcome in COVID-19. <i>Frontiers in Immunology</i> , 2022, 13, 836516.	4.8	16
3	Mathematical Model of SARS-Cov-2 Propagation Versus ACE2 Fits COVID-19 Lethality Across Age and Sex and Predicts That of SARS. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 706122.	3.5	13
4	Why are large conformational changes well described by harmonic normal modes?. <i>Biophysical Journal</i> , 2021, 120, 5343-5354.	0.5	7
5	ProtASR2: Ancestral reconstruction of protein sequences accounting for folding stability. <i>Methods in Ecology and Evolution</i> , 2020, 11, 248-257.	5.2	17
6	Structural basis for allosteric transitions of a multidomain pentameric ligand-gated ion channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13437-13446.	7.1	18
7	Can Conformational Changes of Proteins Be Represented in Torsion Angle Space? A Study with Rescaled Ridge Regression. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4929-4941.	5.4	9
8	Predicted dynamical couplings of protein residues characterize catalysis, transport and allostery. <i>Bioinformatics</i> , 2019, 35, 4971-4978.	4.1	13
9	The Molecular Clock in the Evolution of Protein Structures. <i>Systematic Biology</i> , 2019, 68, 987-1002.	5.6	14
10	Differences in firing efficiency, chromatin, and transcription underlie the developmental plasticity of the <i>Arabidopsis</i> DNA replication origins. <i>Genome Research</i> , 2019, 29, 784-797.	5.5	20
11	The Influence of Protein Stability on Sequence Evolution: Applications to Phylogenetic Inference. <i>Methods in Molecular Biology</i> , 2019, 1851, 215-231.	0.9	9
12	Substitution Rates Predicted by Stability-Constrained Models of Protein Evolution Are Not Consistent with Empirical Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 743-755.	8.9	24
13	Influence of mutation bias and hydrophobicity on the substitution rates and sequence entropies of protein evolution. <i>PeerJ</i> , 2018, 6, e5549.	2.0	12
14	ProtASR: An Evolutionary Framework for Ancestral Protein Reconstruction with Selection on Folding Stability. <i>Systematic Biology</i> , 2017, 66, syw121.	5.6	29
15	Editorial overview: Proteins: bridging theory and experiment. <i>Current Opinion in Structural Biology</i> , 2017, 42, viii-x.	5.7	0
16	Mutualism supports biodiversity when the direct competition is weak. <i>Nature Communications</i> , 2017, 8, 14326.	12.8	51
17	Effective competition determines the global stability of model ecosystems. <i>Theoretical Ecology</i> , 2017, 10, 195-205.	1.0	2
18	The maximum penalty criterion for ridge regression: application to the calibration of the force constant in elastic network models. <i>Integrative Biology (United Kingdom)</i> , 2017, 9, 627-641.	1.3	13

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19	Molecular and Functional Bases of Selection against a Mutation Bias in an RNA Virus. <i>Genome Biology and Evolution</i> , 2017, 9, 1212-1228.	2.5	13
20	What evolution tells us about protein physics, and protein physics tells us about evolution. <i>Current Opinion in Structural Biology</i> , 2017, 42, 59-66.	5.7	40
21	Maximum-Likelihood Phylogenetic Inference with Selection on Protein Folding Stability. <i>Molecular Biology and Evolution</i> , 2015, 32, 2195-2207.	8.9	48
22	Bacteria dialog with Santa Rosalia: Are aggregations of cosmopolitan bacteria mainly explained by habitat filtering or by ecological interactions?. <i>BMC Microbiology</i> , 2014, 14, 284.	3.3	27
23	Detecting Selection on Protein Stability through Statistical Mechanical Models of Folding and Evolution. <i>Biomolecules</i> , 2014, 4, 291-314.	4.0	14
24	Computing protein dynamics from protein structure with elastic network models. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2014, 4, 488-503.	14.6	34
25	The Functional Topography of the <i>Arabidopsis</i> Genome Is Organized in a Reduced Number of Linear Motifs of Chromatin States. <i>Plant Cell</i> , 2014, 26, 2351-2366.	6.6	281
26	Emergence of structure through protein-protein interactions and pH changes in dually predicted coiled-coil and disordered regions of centrosomal proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1808-1819.	2.3	9
27	High-resolution analysis of DNA synthesis start sites and nucleosome architecture at efficient mammalian replication origins. <i>EMBO Journal</i> , 2013, 32, 2631-2644.	7.8	52
28	Protein evolution along phylogenetic histories under structurally constrained substitution models. <i>Bioinformatics</i> , 2013, 29, 3020-3028.	4.1	48
29	Characterizing conformation changes in proteins through the torsional elastic response. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 836-846.	2.3	10
30	The emerging dynamic view of proteins: Protein plasticity in allostery, evolution and self-assembly. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 817-819.	2.3	5
31	Detecting selection for negative design in proteins through an improved model of the misfolded state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1102-1112.	2.6	24
32	Structure and Non-Structure of Centrosomal Proteins. <i>PLoS ONE</i> , 2013, 8, e62633.	2.5	25
33	Protein disorder in the centrosome correlates with complexity in cell types number. <i>Molecular BioSystems</i> , 2012, 8, 353-367.	2.9	24
34	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	7.6	188
35	Sequence determinants of protein folding rates: Positive correlation between contact energy and contact range indicates selection for fast folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2287-2304.	2.6	10
36	Modeling Structural and Genomic Constraints in the Evolution of Proteins. <i>Biological and Medical Physics Series</i> , 2012, , 327-345.	0.4	0

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37	High quality protein sequence alignment by combining structural profile prediction and profile alignment using SABER-TOOTH. <i>BMC Bioinformatics</i> , 2010, 11, 251.	2.6	18
38	Comparison of translation loads for standard and alternative genetic codes. <i>BMC Evolutionary Biology</i> , 2010, 10, 178.	3.2	8
39	Quantifying the evolutionary divergence of protein structures: The role of function change and function conservation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 181-196.	2.6	34
40	In memoriam. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, iii-viii.	2.6	0
41	Torsional Network Model: Normal Modes in Torsion Angle Space Better Correlate with Conformation Changes in Proteins. <i>Physical Review Letters</i> , 2010, 104, 228103.	7.8	79
42	Mutation Bias Favors Protein Folding Stability in the Evolution of Small Populations. <i>PLoS Computational Biology</i> , 2010, 6, e1000767.	3.2	41
43	Cross-Over between Discrete and Continuous Protein Structure Space: Insights into Automatic Classification and Networks of Protein Structures. <i>PLoS Computational Biology</i> , 2009, 5, e1000331.	3.2	52
44	The architecture of mutualistic networks minimizes competition and increases biodiversity. <i>Nature</i> , 2009, 458, 1018-1020.	27.8	878
45	An efficient conformational sampling method for homology modeling. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 175-188.	2.6	25
46	Local interactions in protein folding determined through an inverse folding model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 278-299.	2.6	5
47	Effective connectivity profile: A structural representation that evidences the relationship between protein structures and sequences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 872-888.	2.6	22
48	The Structurally Constrained Neutral Model of Protein Evolution. <i>Biological and Medical Physics Series</i> , 2007, , 75-112.	0.4	4
49	SABERTOOTH: protein structural alignment based on a vectorial structure representation. <i>BMC Bioinformatics</i> , 2007, 8, 425.	2.6	42
50	A protein evolution model with independent sites that reproduces site-specific amino acid distributions from the Protein Data Bank. <i>BMC Evolutionary Biology</i> , 2006, 6, 43.	3.2	46
51	Biodiversity in model ecosystems, I: coexistence conditions for competing species. <i>Journal of Theoretical Biology</i> , 2005, 235, 521-530.	1.7	77
52	Biodiversity in model ecosystems, II: species assembly and food web structure. <i>Journal of Theoretical Biology</i> , 2005, 235, 531-539.	1.7	28
53	A framework for protein structure prediction on the grid. <i>New Generation Computing</i> , 2005, 23, 277-290.	3.3	4
54	Prediction of Site-Specific Amino Acid Distributions and Limits of Divergent Evolutionary Changes in Protein Sequences. <i>Molecular Biology and Evolution</i> , 2005, 22, 630-638.	8.9	36

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55	Stability constraints and protein evolution: the role of chain length, composition and disulfide bonds. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 405-415.	2.1	50
56	Looking at structure, stability, and evolution of proteins through the principal eigenvector of contact matrices and hydrophobicity profiles. <i>Gene</i> , 2005, 347, 219-230.	2.2	19
57	Protein evolution in viral quasispecies under selective pressure: A thermodynamic and phylogenetic analysis. <i>Gene</i> , 2005, 347, 237-246.	2.2	6
58	Reconstruction of Protein Structures from a Vectorial Representation. <i>Physical Review Letters</i> , 2004, 92, 218101.	7.8	45
59	Computational proteomics on the grid. <i>New Generation Computing</i> , 2004, 22, 191-192.	3.3	4
60	Principal eigenvector of contact matrices and hydrophobicity profiles in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 22-30.	2.6	71
61	Genomic Determinants of Protein Folding Thermodynamics in Prokaryotic Organisms. <i>Journal of Molecular Biology</i> , 2004, 343, 1451-1466.	4.2	59
62	Connectivity of Neutral Networks, Overdispersion, and Structural Conservation in Protein Evolution. <i>Journal of Molecular Evolution</i> , 2003, 56, 243-254.	1.8	65
63	Statistical Properties of Neutral Evolution. <i>Journal of Molecular Evolution</i> , 2003, 57, S103-S119.	1.8	42
64	Reductive genome evolution in <i>Buchnera aphidicola</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 581-586.	7.1	461
65	Lack of Self-Averaging in Neutral Evolution of Proteins. <i>Physical Review Letters</i> , 2002, 89, 208101.	7.8	33
66	Testing similarity measures with continuous and discrete protein models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 50, 144-157.	2.6	40
67	Replica-symmetry breaking in dynamical glasses. <i>European Physical Journal B</i> , 2001, 23, 497-508.	1.5	4
68	Overlap distribution in random and designed heteropolymers. <i>European Physical Journal E</i> , 2001, 4, 305-313.	1.6	0
69	How to guarantee optimal stability for most representative structures in the protein data bank. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 44, 79-96.	2.6	109
70	Diversity Patterns from Ecological Models at Dynamical Equilibrium. <i>Journal of Theoretical Biology</i> , 2001, 212, 11-34.	1.7	18
71	Shape of Ecological Networks. <i>Physical Review Letters</i> , 2001, 86, 4418-4421.	7.8	49
72	Exactness of the annealed and the replica symmetric approximations for random heteropolymers. <i>Physical Review E</i> , 2001, 63, 031901.	2.1	10

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73	Phase diagram of random heteropolymers: Replica approach and application of a new Monte Carlo algorithm. <i>Journal of Molecular Liquids</i> , 2000, 84, 111-129.	4.9	11
74	Structurally constrained protein evolution: results from a lattice simulation. <i>European Physical Journal B</i> , 2000, 15, 385-397.	1.5	15
75	A statistical mechanical method to optimize energy functions for protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 3977-3981.	7.1	51
76	Neutral Evolution of Model Proteins: Diffusion in Sequence Space and Overdispersion. <i>Journal of Theoretical Biology</i> , 1999, 200, 49-64.	1.7	81
77	Two-Dimensional Oriented Self-Avoiding Walks with Parallel Contacts. <i>Journal of Statistical Physics</i> , 1998, 90, 1311-1324.	1.2	27
78	Testing a new Monte Carlo algorithm for protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 32, 52-66.	2.6	78
79	The modular structure of Kauffman networks. <i>Physica D: Nonlinear Phenomena</i> , 1998, 115, 219-233.	2.8	83
80	Relevant elements, magnetization and dynamical properties in Kauffman networks: A numerical study. <i>Physica D: Nonlinear Phenomena</i> , 1998, 115, 203-218.	2.8	85
81	Relaxation, closing probabilities and transition from oscillatory to chaotic attractors in asymmetric neural networks. <i>Journal of Physics A</i> , 1998, 31, 4583-4602.	1.6	17
82	New Monte Carlo Algorithm for Protein Folding. <i>Physical Review Letters</i> , 1998, 80, 3149-3152.	7.8	76
83	Testing a new Monte Carlo algorithm for protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 32, 52-66.	2.6	1
84	Attractors in fully asymmetric neural networks. <i>Journal of Physics A</i> , 1997, 30, 5613-5631.	1.6	13
85	Attraction basins in discretized maps. <i>Journal of Physics A</i> , 1997, 30, 3757-3769.	1.6	10
86	Phase Transitions of Single Semistiff Polymer Chains. <i>Journal of Statistical Physics</i> , 1997, 89, 1061-1078.	1.2	100
87	A Numerical Study of the Critical Line of Kauffman Networks. <i>Journal of Theoretical Biology</i> , 1997, 187, 117-133.	1.7	48
88	Closing probabilities in the Kauffman model: An annealed computation. <i>Physica D: Nonlinear Phenomena</i> , 1996, 98, 1-25.	2.8	52
89	Learning structural bioinformatics and evolution with a snake puzzle. <i>PeerJ Computer Science</i> , 0, 2, e100.	4.5	2