Martin Weigt

List of Publications by Year
in descending order

98 papers	7,976 citations	94433 37 h-index	62596 80 g-index
119 all docs	119 docs citations	119 times ranked	4811 citing authors

#	Article	IF	Citations
1	Direct-coupling analysis of residue coevolution captures native contacts across many protein families. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1293-301.	7.1	1,231
2	Identification of direct residue contacts in protein–protein interaction by message passing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 67-72.	7.1	902
3	On the properties of small-world network models. European Physical Journal B, 2000, 13, 547-560.	1.5	686
4	Improved contact prediction in proteins: Using pseudolikelihoods to infer Potts models. Physical Review E, 2013, 87, 012707.	2.1	545
5	Coevolutionary Landscape Inference and the Context-Dependence of Mutations in Beta-Lactamase TEM-1. Molecular Biology and Evolution, 2016, 33, 268-280.	8.9	233
6	Genomics-aided structure prediction. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10340-10345.	7.1	210
7	An evolution-based model for designing chorismate mutase enzymes. Science, 2020, 369, 440-445.	12.6	195
8	Inverse statistical physics of protein sequences: a key issues review. Reports on Progress in Physics, 2018, 81, 032601.	20.1	178
9	High-resolution protein complexes from integrating genomic information with molecular simulation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22124-22129.	7.1	174
10	Coloring Random Graphs. Physical Review Letters, 2002, 89, 268701.	7.8	166
11	Number of Guards Needed by a Museum: A Phase Transition in Vertex Covering of Random Graphs. Physical Review Letters, 2000, 84, 6118-6121.	7.8	156
12	Structural basis of histidine kinase autophosphorylation deduced by integrating genomics, molecular dynamics, and mutagenesis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1733-42.	7.1	140
13	Perturbation Biology: Inferring Signaling Networks in Cellular Systems. PLoS Computational Biology, 2013, 9, e1003290.	3.2	128
14	Fast and Accurate Multivariate Gaussian Modeling of Protein Families: Predicting Residue Contacts and Protein-Interaction Partners. PLoS ONE, 2014, 9, e92721.	2.5	127
15	Simultaneous identification of specifically interacting paralogs and interprotein contacts by direct coupling analysis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12186-12191.	7.1	116
16	Simplest randomK-satisfiability problem. Physical Review E, 2001, 63, 026702.	2.1	114
17	From Principal Component to Direct Coupling Analysis of Coevolution in Proteins: Low-Eigenvalue Modes are Needed for Structure Prediction. PLoS Computational Biology, 2013, 9, e1003176.	3.2	113
18	A ferromagnet with a glass transition. Europhysics Letters, 2001, 55, 465-471.	2.0	108

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19	Clustering by soft-constraint affinity propagation: applications to gene-expression data. Bioinformatics, 2007, 23, 2708-2715.	4.1	106
20	A variational description of the ground state structure in random satisfiability problems. European Physical Journal B, 2000, 14, 551-568.	1.5	99
21	Structures of a dimodular nonribosomal peptide synthetase reveal conformational flexibility. Science, 2019, 366, .	12.6	99
22	Direct-Coupling Analysis of nucleotide coevolution facilitates RNA secondary and tertiary structure prediction. Nucleic Acids Research, 2015, 43, gkv932.	14.5	93
23	Large-scale identification of coevolution signals across homo-oligomeric protein interfaces by direct coupling analysis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2662-E2671.	7.1	93
24	How Pairwise Coevolutionary Models Capture the Collective Residue Variability in Proteins?. Molecular Biology and Evolution, 2018, 35, 1018-1027.	8.9	92
25	Dissecting the Specificity of Protein-Protein Interaction in Bacterial Two-Component Signaling: Orphans and Crosstalks. PLoS ONE, 2011, 6, e19729.	2.5	91
26	Polynomial iterative algorithms for coloring and analyzing random graphs. Physical Review E, 2003, 68, 036702.	2.1	89
27	Mutator genomes decay, despite sustained fitness gains, in a long-term experiment with bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9026-E9035.	7.1	87
28	Inter-residue, inter-protein and inter-family coevolution: bridging the scales. Current Opinion in Structural Biology, 2018, 50, 26-32.	5.7	70
29	Hiding Solutions in Random Satisfiability Problems: A Statistical Mechanics Approach. Physical Review Letters, 2002, 88, 188701.	7.8	65
30	Minimal vertex covers on finite-connectivity random graphs: A hard-sphere lattice-gas picture. Physical Review E, 2001, 63, 056127.	2.1	58
31	Inter-Protein Sequence Co-Evolution Predicts Known Physical Interactions in Bacterial Ribosomes and the Trp Operon. PLoS ONE, 2016, 11, e0149166.	2.5	58
32	Epistatic models predict mutable sites in SARS-CoV-2 proteins and epitopes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	54
33	Threshold values, stability analysis, and high-q asymptotics for the coloring problem on random graphs. Physical Review E, 2004, 70, 046705.	2.1	52
34	Direct Coupling Analysis for Protein Contact Prediction. Methods in Molecular Biology, 2014, 1137, 55-70.	0.9	52
35	Efficient generative modeling of protein sequences using simple autoregressive models. Nature Communications, 2021, 12, 5800.	12.8	51
36	Computational complexity arising from degree correlations in networks. Physical Review E, 2003, 67, 027101.	2.1	50

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37	Message passing for vertex covers. Physical Review E, 2006, 74, 046110.	2.1	45
38	Typical Solution Time for a Vertex-Covering Algorithm on Finite-Connectivity Random Graphs. Physical Review Letters, 2001, 86, 1658-1661.	7.8	42
39	Inference of Direct Residue Contacts in Two-Component Signaling. Methods in Enzymology, 2010, 471, 17-41.	1.0	40
40	Solving satisfiability problems by fluctuations: The dynamics of stochastic local search algorithms. Physical Review E, 2003, 67, 066104.	2.1	38
41	Inference of sparse combinatorial-control networks from gene-expression data: a message passing approach. BMC Bioinformatics, 2010, 11, 355.	2.6	35
42	Glassy behavior induced by geometrical frustration in a hard-core lattice-gas model. Europhysics Letters, 2003, 62, 533-539.	2.0	31
43	Statistical mechanics of the vertex-cover problem. Journal of Physics A, 2003, 36, 11069-11093.	1.6	27
44	Aligning graphs and finding substructures by a cavity approach. Europhysics Letters, 2010, 89, 37009.	2.0	27
45	Approximation schemes for the dynamics of diluted spin models: the Ising ferromagnet on a Bethe lattice. Journal of Physics A, 2004, 37, 5525-5546.	1.6	26
46	Phylogenetic correlations can suffice to infer protein partners from sequences. PLoS Computational Biology, 2019, 15, e1007179.	3.2	25
47	A multi-scale coevolutionary approach to predict interactions between protein domains. PLoS Computational Biology, 2019, 15, e1006891.	3.2	25
48	Modeling Sequence-Space Exploration and Emergence of Epistatic Signals in Protein Evolution. Molecular Biology and Evolution, 2022, 39, .	8.9	25
49	Core Percolation and Onset of Complexity in Boolean Networks. Physical Review Letters, 2006, 96, 018101.	7.8	24
50	Statistical mechanics perspective on the phase transition in vertex covering of finite-connectivity random graphs. Theoretical Computer Science, 2001, 265, 199-225.	0.9	23
51	Unsupervised and semi-supervised clustering by message passing: soft-constraint affinity propagation. European Physical Journal B, 2008, 66, 125-135.	1.5	23
52	Direct coevolutionary couplings reflect biophysical residue interactions in proteins. Journal of Chemical Physics, 2016, 145, 174102.	3.0	22
53	Selection of sequence motifs and generative Hopfield-Potts models for protein families. Physical Review E, 2019, 100, 032128.	2.1	22
54	Inference algorithms for gene networks: a statistical mechanics analysis. Journal of Statistical Mechanics: Theory and Experiment, 2008, 2008, P12001.	2.3	21

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55	Replica structure of one-dimensional disordered Ising models. Europhysics Letters, 1996, 36, 209-214.	2.0	20
56	Entropy and typical properties of Nash equilibria in two-player games. Europhysics Letters, 1999, 48, 129-135.	2.0	19
57	The evolution of the temporal program of genome replication. Nature Communications, 2018, 9, 2199.	12.8	19
58	Computational Modeling of Phosphotransfer Complexes in Two-Component Signaling. Methods in Enzymology, 2010, 471, 43-58.	1.0	18
59	Toward Inferring Potts Models for Phylogenetically Correlated Sequence Data. Entropy, 2019, 21, 1090.	2.2	18
60	Dynamics of heuristic optimization algorithms on random graphs. European Physical Journal B, 2002, 28, 369-381.	1.5	17
61	Finitely coordinated models for low-temperature phases of amorphous systems. Journal of Physics A: Mathematical and Theoretical, 2007, 40, 9227-9252.	2.1	16
62	On the effect of phylogenetic correlations in coevolution-based contact prediction in proteins. PLoS Computational Biology, 2021, 17, e1008957.	3.2	15
63	Sparse generative modeling via parameter reduction of Boltzmann machines: Application to protein-sequence families. Physical Review E, 2021, 104, 024407.	2.1	15
64	Multifractal analysis of the coupling space of feedforward neural networks. Physical Review E, 1996, 53, R2064-R2067.	2.1	14
65	Improving landscape inference by integrating heterogeneous data in the inverse Ising problem. Scientific Reports, 2016, 6, 37812.	3.3	14
66	Sudden emergence of q-regular subgraphs in random graphs. Europhysics Letters, 2006, 75, 8-14.	2.0	13
67	Towards finite-dimensional gelation. European Physical Journal B, 2002, 29, 441-455.	1.5	12
68	The computational core and fixed point organization in Boolean networks. Journal of Statistical Mechanics: Theory and Experiment, 2006, 2006, P03002-P03002.	2.3	12
69	Aligning biological sequences by exploiting residue conservation and coevolution. Physical Review E, 2020, 102, 062409.	2.1	12
70	adabmDCA: adaptive Boltzmann machine learning for biological sequences. BMC Bioinformatics, 2021, 22, 528.	2.6	11
71	Gene-network inference by message passing. Journal of Physics: Conference Series, 2008, 95, 012016.	0.4	10
72	A hard-sphere model on generalized Bethe lattices: statics. Journal of Statistical Mechanics: Theory and Experiment, 2005, 2005, P04006.	2.3	8

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73	Statistical physics of interacting proteins: Impact of dataset size and quality assessed in synthetic sequences. Physical Review E, 2020, 101, 032413.	2.1	8
74	FilterDCA: Interpretable supervised contact prediction using inter-domain coevolution. PLoS Computational Biology, 2020, 16, e1007621.	3.2	8
75	Statistical mechanics of sparse generalization and graphical model selection. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, P10009.	2.3	7
76	Statistical Mechanics of Combinatorial Auctions. Physical Review Letters, 2006, 97, 128701.	7.8	6
77	An efficient biological pathway layout algorithm combining grid-layout and spring embedder for complicated cellular location information. BMC Bioinformatics, 2010, 11, 335.	2.6	6
78	Deciphering polymorphism in 61,157 Escherichia coli genomes via epistatic sequence landscapes. Nature Communications, 2022, 13, .	12.8	6
79	Phase transition and finite-size scaling in the vertex-cover problem. Computer Physics Communications, 2005, 169, 234-237.	7.5	5
80	Classification and sparse-signature extraction from gene-expression data. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, P05001.	2.3	5
81	Multifractality and percolation in the coupling space of perceptrons. Physical Review E, 1997, 55, 4552-4561.	2.1	4
82	Meet-U: Educating through research immersion. PLoS Computational Biology, 2018, 14, e1005992.	3.2	4
83	A replica approach to products of random matrices. Journal of Physics A, 1998, 31, 951-961.	1.6	3
84	A hard-sphere model on generalized Bethe lattices: dynamics. Journal of Statistical Mechanics: Theory and Experiment, 2005, 2005, P08001-P08001.	2.3	3
85	Propagation of external regulation and asynchronous dynamics in random Boolean networks. Chaos, 2007, 17, 026109.	2.5	3
86	Estimation of Residue-Residue Coevolution using Direct Coupling Analysis Identifies Many Native Contacts Across a Large Number of Domain Families. Biophysical Journal, 2012, 102, 250a.	0.5	3
87	Global multivariate model learning from hierarchically correlated data. Journal of Statistical Mechanics: Theory and Experiment, 2021, 2021, 073501.	2.3	3
88	Cavity Approach to the Random Solid State. Physical Review Letters, 2005, 95, 148302.	7.8	2
89	A thermodynamic model for the agglomeration of DNA-looping proteins. Journal of Statistical Mechanics: Theory and Experiment, 2008, 2008, P11005.	2.3	2
90	RNA Secondary and Tertiary Structure Prediction by Tracing Nucleotide Co-Evolution with Direct Coupling Analysis. Biophysical Journal, 2016, 110, 364a.	0.5	2

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91	Storage capacity of the truncated projection rule. Journal of Physics A, 1991, 24, 3707-3709.	1.6	1
92	Inference of Hopfield-Potts patterns from covariation in protein families: calculation and statistical error bars. Journal of Physics: Conference Series, 2013, 473, 012010.	0.4	1
93	Protein and RNA Structure Prediction by Integration of Co-Evolutionary Information into Molecular Simulation. Biophysical Journal, 2015, 108, 13a-14a.	0.5	1
94	Predicting Interacting Protein Pairs by Coevolutionary Paralog Matching. Methods in Molecular Biology, 2020, 2074, 57-65.	0.9	1
95	Multifractal analysis of perceptron learning with errors. Physical Review E, 1998, 57, 955-963.	2.1	0
96	The importance of dilution in the inference of biological networks. , 2009, , .		0
97	Integrating Genomic Information with Molecular Simulation to Understand Protein Complex- and Active Conformation Formation in Two-Component Signal Transduction. Biophysical Journal, 2012, 102, 45a.	0.5	0
98	Integrating Genomic Information with Molecular Simulation for Protein Dynamics. Biophysical Journal, 2013, 104, 212a-213a.	0.5	0