

# Martin Weigt

## List of Publications by Year in descending order

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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	Modeling Sequence-Space Exploration and Emergence of Epistatic Signals in Protein Evolution. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	25
2	Epistatic models predict mutable sites in SARS-CoV-2 proteins and epitopes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	54
3	Deciphering polymorphism in 61,157 <i>Escherichia coli</i> genomes via epistatic sequence landscapes. <i>Nature Communications</i> , 2022, 13, .	12.8	6
4	On the effect of phylogenetic correlations in coevolution-based contact prediction in proteins. <i>PLoS Computational Biology</i> , 2021, 17, e1008957.	3.2	15
5	Global multivariate model learning from hierarchically correlated data. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2021, 2021, 073501.	2.3	3
6	Sparse generative modeling via parameter reduction of Boltzmann machines: Application to protein-sequence families. <i>Physical Review E</i> , 2021, 104, 024407.	2.1	15
7	Efficient generative modeling of protein sequences using simple autoregressive models. <i>Nature Communications</i> , 2021, 12, 5800.	12.8	51
8	adabmDCA: adaptive Boltzmann machine learning for biological sequences. <i>BMC Bioinformatics</i> , 2021, 22, 528.	2.6	11
9	An evolution-based model for designing chorismate mutase enzymes. <i>Science</i> , 2020, 369, 440-445.	12.6	195
10	Statistical physics of interacting proteins: Impact of dataset size and quality assessed in synthetic sequences. <i>Physical Review E</i> , 2020, 101, 032413.	2.1	8
11	Aligning biological sequences by exploiting residue conservation and coevolution. <i>Physical Review E</i> , 2020, 102, 062409.	2.1	12
12	FilterDCA: Interpretable supervised contact prediction using inter-domain coevolution. <i>PLoS Computational Biology</i> , 2020, 16, e1007621.	3.2	8
13	Predicting Interacting Protein Pairs by Coevolutionary Paralog Matching. <i>Methods in Molecular Biology</i> , 2020, 2074, 57-65.	0.9	1
14	Selection of sequence motifs and generative Hopfield-Potts models for protein families. <i>Physical Review E</i> , 2019, 100, 032128.	2.1	22
15	Phylogenetic correlations can suffice to infer protein partners from sequences. <i>PLoS Computational Biology</i> , 2019, 15, e1007179.	3.2	25
16	A multi-scale coevolutionary approach to predict interactions between protein domains. <i>PLoS Computational Biology</i> , 2019, 15, e1006891.	3.2	25
17	Structures of a dimodular nonribosomal peptide synthetase reveal conformational flexibility. <i>Science</i> , 2019, 366, .	12.6	99
18	Toward Inferring Potts Models for Phylogenetically Correlated Sequence Data. <i>Entropy</i> , 2019, 21, 1090.	2.2	18

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19	How Pairwise Coevolutionary Models Capture the Collective Residue Variability in Proteins?. <i>Molecular Biology and Evolution</i> , 2018, 35, 1018-1027.	8.9	92
20	Inverse statistical physics of protein sequences: a key issues review. <i>Reports on Progress in Physics</i> , 2018, 81, 032601.	20.1	178
21	Inter-residue, inter-protein and inter-family coevolution: bridging the scales. <i>Current Opinion in Structural Biology</i> , 2018, 50, 26-32.	5.7	70
22	The evolution of the temporal program of genome replication. <i>Nature Communications</i> , 2018, 9, 2199.	12.8	19
23	Meet-U: Educating through research immersion. <i>PLoS Computational Biology</i> , 2018, 14, e1005992.	3.2	4
24	Large-scale identification of coevolution signals across homo-oligomeric protein interfaces by direct coupling analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2662-E2671.	7.1	93
25	Mutator genomes decay, despite sustained fitness gains, in a long-term experiment with bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9026-E9035.	7.1	87
26	Direct coevolutionary couplings reflect biophysical residue interactions in proteins. <i>Journal of Chemical Physics</i> , 2016, 145, 174102.	3.0	22
27	Simultaneous identification of specifically interacting paralogs and interprotein contacts by direct coupling analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12186-12191.	7.1	116
28	Improving landscape inference by integrating heterogeneous data in the inverse Ising problem. <i>Scientific Reports</i> , 2016, 6, 37812.	3.3	14
29	RNA Secondary and Tertiary Structure Prediction by Tracing Nucleotide Co-Evolution with Direct Coupling Analysis. <i>Biophysical Journal</i> , 2016, 110, 364a.	0.5	2
30	Coevolutionary Landscape Inference and the Context-Dependence of Mutations in Beta-Lactamase TEM-1. <i>Molecular Biology and Evolution</i> , 2016, 33, 268-280.	8.9	233
31	Inter-Protein Sequence Co-Evolution Predicts Known Physical Interactions in Bacterial Ribosomes and the Trp Operon. <i>PLoS ONE</i> , 2016, 11, e0149166.	2.5	58
32	Direct-Coupling Analysis of nucleotide coevolution facilitates RNA secondary and tertiary structure prediction. <i>Nucleic Acids Research</i> , 2015, 43, gkv932.	14.5	93
33	Protein and RNA Structure Prediction by Integration of Co-Evolutionary Information into Molecular Simulation. <i>Biophysical Journal</i> , 2015, 108, 13a-14a.	0.5	1
34	Direct Coupling Analysis for Protein Contact Prediction. <i>Methods in Molecular Biology</i> , 2014, 1137, 55-70.	0.9	52
35	Fast and Accurate Multivariate Gaussian Modeling of Protein Families: Predicting Residue Contacts and Protein-Interaction Partners. <i>PLoS ONE</i> , 2014, 9, e92721.	2.5	127
36	Integrating Genomic Information with Molecular Simulation for Protein Dynamics. <i>Biophysical Journal</i> , 2013, 104, 212a-213a.	0.5	0

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37	From Principal Component to Direct Coupling Analysis of Coevolution in Proteins: Low-Eigenvalue Modes are Needed for Structure Prediction. <i>PLoS Computational Biology</i> , 2013, 9, e1003176.	3.2	113
38	Perturbation Biology: Inferring Signaling Networks in Cellular Systems. <i>PLoS Computational Biology</i> , 2013, 9, e1003290.	3.2	128
39	Improved contact prediction in proteins: Using pseudolikelihoods to infer Potts models. <i>Physical Review E</i> , 2013, 87, 012707.	2.1	545
40	Inference of Hopfield-Potts patterns from covariation in protein families: calculation and statistical error bars. <i>Journal of Physics: Conference Series</i> , 2013, 473, 012010.	0.4	1
41	Genomics-aided structure prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10340-10345.	7.1	210
42	Estimation of Residue-Residue Coevolution using Direct Coupling Analysis Identifies Many Native Contacts Across a Large Number of Domain Families. <i>Biophysical Journal</i> , 2012, 102, 250a.	0.5	3
43	Integrating Genomic Information with Molecular Simulation to Understand Protein Complex- and Active Conformation Formation in Two-Component Signal Transduction. <i>Biophysical Journal</i> , 2012, 102, 45a.	0.5	0
44	Structural basis of histidine kinase autophosphorylation deduced by integrating genomics, molecular dynamics, and mutagenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1733-42.	7.1	140
45	Direct-coupling analysis of residue coevolution captures native contacts across many protein families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E1293-301.	7.1	1,231
46	Dissecting the Specificity of Protein-Protein Interaction in Bacterial Two-Component Signaling: Orphans and Crosstalks. <i>PLoS ONE</i> , 2011, 6, e19729.	2.5	91
47	An efficient biological pathway layout algorithm combining grid-layout and spring embedder for complicated cellular location information. <i>BMC Bioinformatics</i> , 2010, 11, 335.	2.6	6
48	Inference of sparse combinatorial-control networks from gene-expression data: a message passing approach. <i>BMC Bioinformatics</i> , 2010, 11, 355.	2.6	35
49	Computational Modeling of Phosphotransfer Complexes in Two-Component Signaling. <i>Methods in Enzymology</i> , 2010, 471, 43-58.	1.0	18
50	Inference of Direct Residue Contacts in Two-Component Signaling. <i>Methods in Enzymology</i> , 2010, 471, 17-41.	1.0	40
51	Aligning graphs and finding substructures by a cavity approach. <i>Europhysics Letters</i> , 2010, 89, 37009.	2.0	27
52	The importance of dilution in the inference of biological networks. , 2009, , .		0
53	High-resolution protein complexes from integrating genomic information with molecular simulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 22124-22129.	7.1	174
54	Statistical mechanics of sparse generalization and graphical model selection. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009, 2009, P10009.	2.3	7

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55	Classification and sparse-signature extraction from gene-expression data. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, P05001.	2.3	5
56	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
57	Unsupervised and semi-supervised clustering by message passing: soft-constraint affinity propagation. European Physical Journal B, 2008, 66, 125-135.	1.5	23
58	A thermodynamic model for the agglomeration of DNA-looping proteins. Journal of Statistical Mechanics: Theory and Experiment, 2008, 2008, P11005.	2.3	2
59	Inference algorithms for gene networks: a statistical mechanics analysis. Journal of Statistical Mechanics: Theory and Experiment, 2008, 2008, P12001.	2.3	21
60	Gene-network inference by message passing. Journal of Physics: Conference Series, 2008, 95, 012016.	0.4	10
61	Clustering by soft-constraint affinity propagation: applications to gene-expression data. Bioinformatics, 2007, 23, 2708-2715.	4.1	106
62	Finitely coordinated models for low-temperature phases of amorphous systems. Journal of Physics A: Mathematical and Theoretical, 2007, 40, 9227-9252.	2.1	16
63	Propagation of external regulation and asynchronous dynamics in random Boolean networks. Chaos, 2007, 17, 026109.	2.5	3
64	The computational core and fixed point organization in Boolean networks. Journal of Statistical Mechanics: Theory and Experiment, 2006, 2006, P03002-P03002.	2.3	12
65	Sudden emergence of $q$ -regular subgraphs in random graphs. Europhysics Letters, 2006, 75, 8-14.	2.0	13
66	Core Percolation and Onset of Complexity in Boolean Networks. Physical Review Letters, 2006, 96, 018101.	7.8	24
67	Statistical Mechanics of Combinatorial Auctions. Physical Review Letters, 2006, 97, 128701.	7.8	6
68	Message passing for vertex covers. Physical Review E, 2006, 74, 046110.	2.1	45
69	Phase transition and finite-size scaling in the vertex-cover problem. Computer Physics Communications, 2005, 169, 234-237.	7.5	5
70	Cavity Approach to the Random Solid State. Physical Review Letters, 2005, 95, 148302.	7.8	2
71	A hard-sphere model on generalized Bethe lattices: dynamics. Journal of Statistical Mechanics: Theory and Experiment, 2005, 2005, P08001-P08001.	2.3	3
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	Approximation schemes for the dynamics of diluted spin models: the Ising ferromagnet on a Bethe lattice. <i>Journal of Physics A</i> , 2004, 37, 5525-5546.	1.6	26
74	Threshold values, stability analysis, and high-qasymptotics for the coloring problem on random graphs. <i>Physical Review E</i> , 2004, 70, 046705.	2.1	52
75	Computational complexity arising from degree correlations in networks. <i>Physical Review E</i> , 2003, 67, 027101.	2.1	50
76	Solving satisfiability problems by fluctuations: The dynamics of stochastic local search algorithms. <i>Physical Review E</i> , 2003, 67, 066104.	2.1	38
77	Polynomial iterative algorithms for coloring and analyzing random graphs. <i>Physical Review E</i> , 2003, 68, 036702.	2.1	89
78	Statistical mechanics of the vertex-cover problem. <i>Journal of Physics A</i> , 2003, 36, 11069-11093.	1.6	27
79	Glassy behavior induced by geometrical frustration in a hard-core lattice-gas model. <i>Europhysics Letters</i> , 2003, 62, 533-539.	2.0	31
80	Coloring Random Graphs. <i>Physical Review Letters</i> , 2002, 89, 268701.	7.8	166
81	Hiding Solutions in Random Satisfiability Problems: A Statistical Mechanics Approach. <i>Physical Review Letters</i> , 2002, 88, 188701.	7.8	65
82	Dynamics of heuristic optimization algorithms on random graphs. <i>European Physical Journal B</i> , 2002, 28, 369-381.	1.5	17
83	Towards finite-dimensional gelation. <i>European Physical Journal B</i> , 2002, 29, 441-455.	1.5	12
84	Statistical mechanics perspective on the phase transition in vertex covering of finite-connectivity random graphs. <i>Theoretical Computer Science</i> , 2001, 265, 199-225.	0.9	23
85	A ferromagnet with a glass transition. <i>Europhysics Letters</i> , 2001, 55, 465-471.	2.0	108
86	Typical Solution Time for a Vertex-Covering Algorithm on Finite-Connectivity Random Graphs. <i>Physical Review Letters</i> , 2001, 86, 1658-1661.	7.8	42
87	Simplest randomK-satisfiability problem. <i>Physical Review E</i> , 2001, 63, 026702.	2.1	114
88	Minimal vertex covers on finite-connectivity random graphs: A hard-sphere lattice-gas picture. <i>Physical Review E</i> , 2001, 63, 056127.	2.1	58
89	On the properties of small-world network models. <i>European Physical Journal B</i> , 2000, 13, 547-560.	1.5	686
90	Number of Guards Needed by a Museum: A Phase Transition in Vertex Covering of Random Graphs. <i>Physical Review Letters</i> , 2000, 84, 6118-6121.	7.8	156

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91	A variational description of the ground state structure in random satisfiability problems. European Physical Journal B, 2000, 14, 551-568.	1.5	99
92	Entropy and typical properties of Nash equilibria in two-player games. Europhysics Letters, 1999, 48, 129-135.	2.0	19
93	A replica approach to products of random matrices. Journal of Physics A, 1998, 31, 951-961.	1.6	3
94	Multifractal analysis of perceptron learning with errors. Physical Review E, 1998, 57, 955-963.	2.1	0
95	Multifractality and percolation in the coupling space of perceptrons. Physical Review E, 1997, 55, 4552-4561.	2.1	4
96	Multifractal analysis of the coupling space of feedforward neural networks. Physical Review E, 1996, 53, R2064-R2067.	2.1	14
97	Replica structure of one-dimensional disordered Ising models. Europhysics Letters, 1996, 36, 209-214.	2.0	20
98	Storage capacity of the truncated projection rule. Journal of Physics A, 1991, 24, 3707-3709.	1.6	1