Michael Habeck

List of Publications by Year in Descending Order

68 papers	3,593 citations	27 h-index	59 g-index
73 ext. papers	4,071 ext. citations	7.2 avg, IF	5.11 L-index

#	Paper	IF	Citations
68	Bayesian Random Tomography of Particle Systems. *Frontiers in Molecular Biosciences*, **2021**, 8, 658269	5.6	
67	A graph-based algorithm for detecting rigid domains in protein structures. *BMC Bioinformatics*, **2021**, 22, 66	3.6	
66	Non-negative blind deconvolution for signal processing in a CRISPR-edited iPSC-cardiomyocyte model of dilated cardiomyopathy. *FEBS Letters*, **2021**, 595, 2544-2557	3.8	0
65	Bayesian inference of chromatin structure ensembles from population-averaged contact data. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 7824-7830	11.5	5
64	Architecture of the flexible tail tube of bacteriophage SPP1. *Nature Communications*, **2020**, 11, 5759	17.4	14
63	Auto-regulation of Rab5 GEF activity in Rabex5 by allosteric structural changes, catalytic core dynamics and ubiquitin binding. *ELife*, **2019**, 8,	8.9	8
62	A probabilistic network model for structural transitions in biomolecules. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86, 634-643	4.2	1
61	An evolutionarily conserved glycine-tyrosine motif forms a folding core in outer membrane proteins. *PLoS ONE*, **2017**, 12, e0182016	3.7	15
60	Data-driven coarse graining of large biomolecular structures. *PLoS ONE*, **2017**, 12, e0183057	3.7	6
59	Bayesian Modeling of Biomolecular Assemblies with Cryo-EM Maps. *Frontiers in Molecular Biosciences*, **2017**, 4, 15	5.6	12
58	The adaptor protein CIN85 assembles intracellular signaling clusters for B cell activation. *Science Signaling*, **2016**, 9, ra66	8.8	11
57	Cooperative binding: a multiple personality. *Journal of Mathematical Biology*, **2016**, 72, 1747-74	2	11
56	Inferential Structure Determination of Chromosomes from Single-Cell Hi-C Data. *PLoS Computational Biology*, **2016**, 12, e1005292	5	36
55	Comparison of the kinetics of different Markov models for ligand binding under varying conditions. *Journal of Chemical Physics*, **2015**, 142, 094104	3.9	4
54	Bayesian inference of initial models in cryo-electron microscopy using pseudo-atoms. *Biophysical Journal*, **2015**, 108, 1165-75	2.9	12
53	Bayesian evidence and model selection **2015**, 47, 50-67		41
52	Solid-state NMR Study of the YadA Membrane-Anchor Domain in the Bacterial Outer Membrane. *Angewandte Chemie - International Edition*, **2015**, 54, 12602-6	16.4	12

51	Hybrid Structure of the Type 1 Pilus of Uropathogenic Escherichia coli. *Angewandte Chemie - International Edition*, **2015**, 54, 11691-5	16.4	27
50	Hybrid Structure of the Type 1 Pilus of Uropathogenic Escherichia coli. *Angewandte Chemie*, **2015**, 127, 11857-11861	3.6	3
49	Festkörper-NMR-Studien an der Membrananker-Domäne von YadA in der bakteriellen Außenmembran. *Angewandte Chemie*, **2015**, 127, 12792-12797	3.6	2
48	Structure and evolution of N-domains in AAA metalloproteases. *Journal of Molecular Biology*, **2015**, 427, 910-923	6.5	18
47	Bayesian approach to inverse statistical mechanics. *Physical Review E*, **2014**, 89, 052113	2.4	13
46	Kinetics or equilibrium? A commentary on a recent simulation study of semiochemical dose-response curves of insect olfactory sensing. *Journal of Chemical Ecology*, **2014**, 40, 1163-4	2.7	2
45	A derivation of the Grand Canonical Partition Function for systems with a finite number of binding sites using a Markov chain model for the dynamics of single molecules. *Journal of Mathematical Chemistry*, **2014**, 52, 665-674	2.1	4
44	Bayesian weighting of statistical potentials in NMR structure calculation. *PLoS ONE*, **2014**, 9, e100197	3.7	4
43	Structures of the human and Drosophila 80S ribosome. *Nature*, **2013**, 497, 80-5	50.4	358
42	Estimation of Interaction Potentials through the Configurational Temperature Formalism. *Journal of Chemical Theory and Computation*, **2013**, 9, 5685-92	6.4	9
41	A probabilistic model for secondary structure prediction from protein chemical shifts. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 984-93	4.2	11
40	Confidence-guided local structure prediction with HHfrag. *PLoS ONE*, **2013**, 8, e76512	3.7	1
39	Inferential NMR/X-ray-based structure determination of a dibenzo[a,d]cycloheptenone inhibitor-p38α MAP kinase complex in solution. *Angewandte Chemie - International Edition*, **2012**, 51, 2359-62	16.4	6
38	CSB: a Python framework for structural bioinformatics. *Bioinformatics*, **2012**, 28, 2996-7	7.2	10
37	Membrane-protein structure determination by solid-state NMR spectroscopy of microcrystals. *Nature Methods*, **2012**, 9, 1212-7	21.6	128
36	Structure-activity analysis of the dermcidin-derived peptide DCD-1L, an anionic antimicrobial peptide present in human sweat. *Journal of Biological Chemistry*, **2012**, 287, 8434-43	5.4	72
35	Is the C-terminal insertional signal in Gram-negative bacterial outer membrane proteins species-specific or not?. *BMC Genomics*, **2012**, 13, 510	4.5	37
34	Inferential NMR/X-ray-Based Structure Determination of a Dibenzo[a,d]cycloheptenone Inhibitor–p38α MAP Kinase Complex in Solution. *Angewandte Chemie*, **2012**, 124, 2409-2412	3.6	2

33	Calibration of Boltzmann distribution priors in Bayesian data analysis. *Physical Review E*, **2012**, 86, 066705	2.4	3
32	Bayesian estimation of free energies from equilibrium simulations. *Physical Review Letters*, **2012**, 109, 100601	7.4	28
31	Statistical mechanics analysis of sparse data. *Journal of Structural Biology*, **2011**, 173, 541-8	3.4	14
30	A blind deconvolution approach for improving the resolution of cryo-EM density maps. *Journal of Computational Biology*, **2011**, 18, 335-46	1.7	9
29	HHfrag: HMM-based fragment detection using HHpred. *Bioinformatics*, **2011**, 27, 3110-6	7.2	23
28	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-A resolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 19748-53	11.5	158
27	Localization of eukaryote-specific ribosomal proteins in a 5.5-Å cryo-EM map of the 80S eukaryotic ribosome. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 19754-9	11.5	112
26	Generation of three-dimensional random rotations in fitting and matching problems. *Computational Statistics*, **2009**, 24, 719-731	1	6
25	Influence of different assignment conditions on the determination of symmetric homodimeric structures with ARIA. *Proteins: Structure, Function and Bioinformatics*, **2009**, 75, 569-85	4.2	29
24	The GD box: a widespread noncontiguous supersecondary structural element. *Protein Science*, **2009**, 18, 1961-6	6.3	10
23	Structure and activity of the N-terminal substrate recognition domains in proteasomal ATPases. *Molecular Cell*, **2009**, 34, 580-90	17.6	106
22	Accurate NMR structures through minimization of an extended hybrid energy. *Structure*, **2008**, 16, 1305-12	5.2	43
21	Comparative analysis of structural and dynamic properties of the loaded and unloaded hemophore HasA: functional implications. *Journal of Molecular Biology*, **2008**, 376, 517-25	6.5	47
20	Mixture models for protein structure ensembles. *Bioinformatics*, **2008**, 24, 2184-92	7.2	8
19	Structure of the human voltage-dependent anion channel. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 15370-5	11.5	434
18	ISD: a software package for Bayesian NMR structure calculation. *Bioinformatics*, **2008**, 24, 1104-5	7.2	28
17	A unifying probabilistic framework for analyzing residual dipolar couplings. *Journal of Biomolecular NMR*, **2008**, 40, 135-44	3	16
16	Graphical analysis of NMR structural quality and interactive contact map of NOE assignments in ARIA. *BMC Structural Biology*, **2008**, 8, 30	2.7	4

15	Probabilistic structure calculation. *Comptes Rendus Chimie*, **2008**, 11, 356-369	2.7	3
14	Bayesian reconstruction of the density of states. *Physical Review Letters*, **2007**, 98, 200601	7.4	14
13	ARIA2: automated NOE assignment and data integration in NMR structure calculation. *Bioinformatics*, **2007**, 23, 381-2	7.2	404
12	Weighting of experimental evidence in macromolecular structure determination. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 1756-61	11.5	66
11	Error distribution derived NOE distance restraints. *Proteins: Structure, Function and Bioinformatics*, **2006**, 64, 652-64	4.2	11
10	Structure validation of the Josephin domain of ataxin-3: conclusive evidence for an open conformation. *Journal of Biomolecular NMR*, **2006**, 36, 267-77	3	37
9	Modeling errors in NOE data with a log-normal distribution improves the quality of NMR structures. *Journal of the American Chemical Society*, **2005**, 127, 16026-7	16.4	34
8	Bayesian estimation of Karplus parameters and torsion angles from three-bond scalar couplings constants. *Journal of Magnetic Resonance*, **2005**, 177, 160-5	3	21
7	Inferential structure determination. *Science*, **2005**, 309, 303-6	33.3	268
6	Replica-exchange Monte Carlo scheme for bayesian data analysis. *Physical Review Letters*, **2005**, 94, 018105	7.4	56
5	Bayesian inference applied to macromolecular structure determination. *Physical Review E*, **2005**, 72, 031912	2.4	27
4	Correction of spin diffusion during iterative automated NOE assignment. *Journal of Magnetic Resonance*, **2004**, 167, 334-42	3	51
3	NOE assignment with ARIA 2.0: the nuts and bolts. *Methods in Molecular Biology*, **2004**, 278, 379-402	1.4	50
2	ARIA: automated NOE assignment and NMR structure calculation. *Bioinformatics*, **2003**, 19, 315-6	7.2	397
1	Structural and functional studies of titin's Fn3 modules reveal conserved surface patterns and binding to myosin S1--a possible role in the Frank-Starling mechanism of the heart. *Journal of Molecular Biology*, **2001**, 313, 431-47	6.5	82