Wouter Boomsma

List of Publications by Year
in descending order

24	1,155	430754 18	610775 24
papers	citations	h-index	g-index

26	26	26	1595
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Statistical Assignment of DNA Sequences Using Bayesian Phylogenetics. Systematic Biology, 2008, 57, 750-757.	2.7	170
2	Combining Experiments and Simulations Using the Maximum Entropy Principle. PLoS Computational Biology, 2014, 10, e1003406.	1.5	167
3	A generative, probabilistic model of local protein structure. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8932-8937.	3.3	113
4	The PCNA interaction motifs revisited: thinking outside the PIP-box. Cellular and Molecular Life Sciences, 2019, 76, 4923-4943.	2.4	77
5	Fast phylogenetic DNA barcoding. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 3997-4002.	1.8	64
6	Potentials of Mean Force for Protein Structure Prediction Vindicated, Formalized and Generalized. PLoS ONE, 2010, 5, e13714.	1.1	64
7	Learning meaningful representations of protein sequences. Nature Communications, 2022, 13, 1914.	5.8	55
8	Barnaba: software for analysis of nucleic acid structures and trajectories. Rna, 2019, 25, 219-231.	1.6	50
9	Inference of Structure Ensembles of Flexible Biomolecules from Sparse, Averaged Data. PLoS ONE, 2013, 8, e79439.	1.1	50
10	Bayesian inference of protein ensembles from SAXS data. Physical Chemistry Chemical Physics, 2016, 18, 5832-5838.	1.3	49
11	Beyond rotamers: a generative, probabilistic model of side chains in proteins. BMC Bioinformatics, 2010, 11, 306.	1.2	40
12	PHAISTOS: A framework for Markov chain Monte Carlo simulation and inference of protein structure. Journal of Computational Chemistry, 2013, 34, 1697-1705.	1.5	35
13	Single-particle diffusional fingerprinting: A machine-learning framework for quantitative analysis of heterogeneous diffusion. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	35
14	Fast large-scale clustering of protein structures using Gauss integrals. Bioinformatics, 2012, 28, 510-515.	1.8	29
15	Random coil chemical shifts for serine, threonine and tyrosine phosphorylation over a broad pH range. Journal of Biomolecular NMR, 2019, 73, 713-725.	1.6	24
16	Full cyclic coordinate descent: solving the protein loop closure problem in Calpha space. BMC Bioinformatics, 2005, 6, 159.	1.2	23
17	Subtle Monte Carlo Updates in Dense Molecular Systems. Journal of Chemical Theory and Computation, 2012, 8, 695-702.	2.3	22
18	Protein Structure Validation and Refinement Using Amide Proton Chemical Shifts Derived from Quantum Mechanics. PLoS ONE, 2013, 8, e84123.	1.1	21

#	Article	IF	Citations
19	Generative probabilistic models extend the scope of inferential structure determination. Journal of Magnetic Resonance, 2011, 213, 182-186.	1.2	17
20	IDDomainSpotter: Compositional bias reveals domains in long disordered protein regionsâ€"Insights from transcription factors. Protein Science, 2020, 29, 169-183.	3.1	14
21	Robust Estimation of Diffusion-Optimized Ensembles for Enhanced Sampling. Journal of Chemical Theory and Computation, 2014, 10, 543-553.	2.3	12
22	Driving Structural Transitions in Molecular Simulations Using the Nonequilibrium Candidate Monte Carlo. Journal of Physical Chemistry B, 2018, 122, 1195-1204.	1.2	7
23	Monte Carlo Sampling of Protein Folding by Combining an All-Atom Physics-Based Model with a Native State Bias. Journal of Physical Chemistry B, 2018, 122, 11174-11185.	1.2	3
24	A Sticky Cage can Slow Down Folding. Biophysical Journal, 2013, 104, 964-965.	0.2	1