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	Learning meaningful representations of protein sequences. Nature Communications, 2022, 13, 1914.	5.8	55
2	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
3	IDDomainSpotter: Compositional bias reveals domains in long disordered protein regionsâ€"Insights from transcription factors. Protein Science, 2020, 29, 169-183.	3.1	14
4	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
5	The PCNA interaction motifs revisited: thinking outside the PIP-box. Cellular and Molecular Life Sciences, 2019, 76, 4923-4943.	2.4	77
6	Barnaba: software for analysis of nucleic acid structures and trajectories. Rna, 2019, 25, 219-231.	1.6	50
7	Driving Structural Transitions in Molecular Simulations Using the Nonequilibrium Candidate Monte Carlo. Journal of Physical Chemistry B, 2018, 122, 1195-1204.	1.2	7
8	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
9	Bayesian inference of protein ensembles from SAXS data. Physical Chemistry Chemical Physics, 2016, 18, 5832-5838.	1.3	49
10	Combining Experiments and Simulations Using the Maximum Entropy Principle. PLoS Computational Biology, 2014, 10, e1003406.	1.5	167
11	Robust Estimation of Diffusion-Optimized Ensembles for Enhanced Sampling. Journal of Chemical Theory and Computation, 2014, 10, 543-553.	2.3	12
12	A Sticky Cage can Slow Down Folding. Biophysical Journal, 2013, 104, 964-965.	0.2	1
13	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
14	Protein Structure Validation and Refinement Using Amide Proton Chemical Shifts Derived from Quantum Mechanics. PLoS ONE, 2013, 8, e84123.	1.1	21
15	Inference of Structure Ensembles of Flexible Biomolecules from Sparse, Averaged Data. PLoS ONE, 2013, 8, e79439.	1.1	50
16	Fast large-scale clustering of protein structures using Gauss integrals. Bioinformatics, 2012, 28, 510-515.	1.8	29
17	Subtle Monte Carlo Updates in Dense Molecular Systems. Journal of Chemical Theory and Computation, 2012, 8, 695-702.	2.3	22
18	Generative probabilistic models extend the scope of inferential structure determination. Journal of Magnetic Resonance, 2011, 213, 182-186.	1.2	17

#	Article	IF	Citations
19	Beyond rotamers: a generative, probabilistic model of side chains in proteins. BMC Bioinformatics, 2010, 11, 306.	1.2	40
20	Potentials of Mean Force for Protein Structure Prediction Vindicated, Formalized and Generalized. PLoS ONE, 2010, 5, e13714.	1.1	64
21	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
22	Fast phylogenetic DNA barcoding. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 3997-4002.	1.8	64
23	Statistical Assignment of DNA Sequences Using Bayesian Phylogenetics. Systematic Biology, 2008, 57, 750-757.	2.7	170
24	Full cyclic coordinate descent: solving the protein loop closure problem in Calpha space. BMC Bioinformatics, 2005, 6, 159.	1.2	23