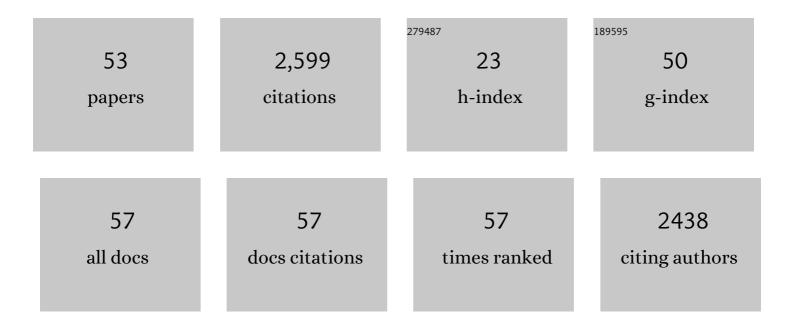
Dieter W Heermann

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Monte Carlo Simulation in Statistical Physics. Springer Series in Solid-state Sciences, 1988, , .	0.3	546
2	Monte Carlo Simulation in Statistical Physics. Graduate Texts in Physics, 2010, , .	0.1	315
3	Monte Carlo Simulation in Statistical Physics. Springer Series in Solid-state Sciences, 2002, , .	0.3	240
4	Spatially confined folding of chromatin in the interphase nucleus. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3812-3817.	3.3	233
5	Diffusion-Driven Looping Provides a Consistent Framework for Chromatin Organization. PLoS ONE, 2010, 5, e12218.	1.1	158
6	Chromatin folding – from biology to polymer models and back. Journal of Cell Science, 2011, 124, 839-845.	1.2	94
7	Random loop model for long polymers. Physical Review E, 2007, 76, 051805.	0.8	92
8	A model for Escherichia coli chromosome packaging supports transcription factor-induced DNA domain formation. Nucleic Acids Research, 2012, 40, 972-980.	6.5	84
9	Localization Microscopy Reveals Expression-Dependent Parameters ofÂChromatin Nanostructure. Biophysical Journal, 2010, 99, 1358-1367.	0.2	73
10	Topological interactions between ring polymers: Implications for chromatin loops. Journal of Chemical Physics, 2010, 132, 044904.	1.2	63
11	Depletion of the Chromatin Looping Proteins CTCF and Cohesin Causes Chromatin Compaction: Insight into Chromatin Folding by Polymer Modelling. PLoS Computational Biology, 2014, 10, e1003877.	1.5	57
12	Radiation Induced Chromatin Conformation Changes Analysed by Fluorescent Localization Microscopy, Statistical Physics, and Graph Theory. PLoS ONE, 2015, 10, e0128555.	1.1	42
13	A Three-Pronged Attack To Investigate the Electronic Structure of a Family of Ferromagnetic Fe ₄ Ln ₂ Cyclic Coordination Clusters: A Combined Magnetic Susceptibility, High-Field/High-Frequency Electron Paramagnetic Resonance, and ⁵⁷ Fe MA¶ssbauer Study. Inorganic Chemistry, 2017, 56, 4796-4806.	1.9	41
14	Histone Depletion Facilitates Chromatin Loops on the Kilobasepair Scale. Biophysical Journal, 2010, 99, 2995-3001.	0.2	39
15	Repulsive Forces Between Looping Chromosomes Induce Entropy-Driven Segregation. PLoS ONE, 2011, 6, e14428.	1.1	35
16	Physical nuclear organization: loops and entropy. Current Opinion in Cell Biology, 2011, 23, 332-337.	2.6	35
17	Depletion Effects Massively Change Chromatin Properties and Influence Genome Folding. Biophysical Journal, 2009, 97, 2146-2153.	0.2	34
18	The role of loops on the order of eukaryotes and prokaryotes. FEBS Letters, 2015, 589, 2958-2965.	1.3	31

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19	Using Persistent Homology as a New Approach for Super-Resolution Localization Microscopy Data Analysis and Classification of γH2AX Foci/Clusters. International Journal of Molecular Sciences, 2018, 19, 2263.	1.8	31
20	On the Influence of Topological Catenation and Bonding Constraints on Ring Polymers. Macromolecules, 2010, 43, 2564-2573.	2.2	30
21	Confinement driven spatial organization of semiflexible ring polymers: Implications for biopolymer packaging. Soft Matter, 2011, 7, 6906.	1.2	28
22	Robust detection and segmentation of cell nuclei in biomedical images based on a computational topology framework. Medical Image Analysis, 2017, 38, 90-103.	7.0	28
23	Loops Determine the Mechanical Properties of Mitotic Chromosomes. PLoS ONE, 2011, 6, e29225.	1.1	26
24	Expression-Dependent Folding of Interphase Chromatin. PLoS ONE, 2012, 7, e37525.	1.1	26
25	How Chromatin Looping and Nuclear Envelope Attachment Affect Genome Organization in Eukaryotic Cell Nuclei. International Review of Cell and Molecular Biology, 2014, 307, 351-381.	1.6	24
26	Superdiffusion in a Model for Diffusion in a Molecularly Crowded Environment. Journal of Biological Physics, 2007, 33, 305-312.	0.7	21
27	A topological similarity measure for proteins. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 1180-1190.	1.4	21
28	A chromosomal loop anchor mediates bacterial genome organization. Nature Genetics, 2022, 54, 194-201.	9.4	17
29	A model for the 3D chromatin architecture of pro and eukaryotes. Methods, 2012, 58, 307-314.	1.9	16
30	Conformational properties of compact polymers. Journal of Chemical Physics, 2009, 130, 174901.	1.2	15
31	Elucidation of the Clustered Nano-Architecture of Radiation-Induced DNA Damage Sites and Surrounding Chromatin in Cancer Cells: A Single Molecule Localization Microscopy Approach. International Journal of Molecular Sciences, 2021, 22, 3636.	1.8	15
32	Single Molecule Localization Microscopy Analyses of DNA-Repair Foci and Clusters Detected Along Particle Damage Tracks. Frontiers in Physics, 2020, 8, .	1.0	11
33	Topological Analysis of Î ³ H2AX and MRE11 Clusters Detected by Localization Microscopy during X-ray-Induced DNA Double-Strand Break Repair. Cancers, 2021, 13, 5561.	1.7	10
34	Zinc Finger Proteins and the 3D Organization of Chromosomes. Advances in Protein Chemistry and Structural Biology, 2013, 90, 67-117.	1.0	9
35	Transcriptional regulatory network shapes the genome structure of <i>Saccharomyces cerevisiae</i> . Nucleus, 2013, 4, 216-228.	0.6	9
36	The interaction of DNA with multi-Cys2His2 zinc finger proteins. Journal of Physics Condensed Matter, 2015, 27, 064107.	0.7	9

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#	Article	IF	CITATIONS
37	Conformational and Dynamical Properties of the Isolated, Threeâ€Dimensional Single―and Doubleâ€Tethered Polymer Chain on an Infinite Surface. Macromolecular Theory and Simulations, 2010, 19, 440-448.	0.6	6
38	Telomerase subunit Est2 marks internal sites that are prone to accumulate DNA damage. BMC Biology, 2021, 19, 247.	1.7	4
39	Diffusion of gas molecules in the polystyrene matrix. Macromolecular Theory and Simulations, 2000, 9, 687-697.	0.6	3
40	A multiscale approach to simulating the conformational properties of unbound multiâ€ <scp>C</scp> ₂ <scp>H</scp> ₂ zinc finger proteins. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1604-1615.	1.5	3
41	The Electronic Behavior of Zinc-Finger Protein Binding Sites in the Context of the DNA Extended Ladder Model. Frontiers in Physics, 2016, 4, .	1.0	3
42	Superstructure Detection in Nucleosome Distribution Shows Common Pattern within a Chromosome and within the Genome. Life, 2022, 12, 541.	1.1	3
43	Mitotic chromosome structure. Experimental Cell Research, 2012, 318, 1381-1385.	1.2	2
44	Persistence intervals of fractals. Physica A: Statistical Mechanics and Its Applications, 2014, 405, 252-259.	1.2	2
45	Deciphering 3D Organization of Chromosomes Using Hi-C Data. Methods in Molecular Biology, 2018, 1837, 389-401.	0.4	2
46	The Effect of Bending Rigidity on Polymers. Macromolecular Theory and Simulations, 2019, 28, 1800071.	0.6	2
47	Prediction and comparative analysis of CTCF binding sites based on a first principle approach. Physical Biology, 2022, 19, 036005.	0.8	2
48	Statistical analysis of protein ensembles. Frontiers in Physics, 2014, 2, .	1.0	1
49	Space and Time in the Universe of the Cell Nucleus after Ionizing Radiation Attacks: A Comparison of Cancer and Non-Cancer Cell Response. , 2021, 3, .		1
50	Inter-nucleosomal potentials from nucleosomal positioning data. European Physical Journal E, 2022, 45, 33.	0.7	1
51	A generalized Potts model for confocal microscopy images. International Journal of Modern Physics B, 2015, 29, 1550048.	1.0	0
52	Phase transition and winding properties of a flexible polymer adsorbed to a rigid perioidic copolymer. Physical Review E, 2015, 91, 032601.	0.8	0
53	Processing and Analysis of Hi-C Data on Bacteria. Methods in Molecular Biology, 2018, 1837, 19-31.	0.4	0