

Dieter W Heermann

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

2,599
citations

279487

23
h-index

189595

50
g-index

57
all docs

57
docs citations

57
times ranked

2438
citing authors

#	ARTICLE	IF	CITATIONS
1	A chromosomal loop anchor mediates bacterial genome organization. <i>Nature Genetics</i> , 2022, 54, 194-201.	9.4	17
2	Superstructure Detection in Nucleosome Distribution Shows Common Pattern within a Chromosome and within the Genome. <i>Life</i> , 2022, 12, 541.	1.1	3
3	Prediction and comparative analysis of CTCF binding sites based on a first principle approach. <i>Physical Biology</i> , 2022, 19, 036005.	0.8	2
4	Inter-nucleosomal potentials from nucleosomal positioning data. <i>European Physical Journal E</i> , 2022, 45, 33.	0.7	1
5	Elucidation of the Clustered Nano-Architecture of Radiation-Induced DNA Damage Sites and Surrounding Chromatin in Cancer Cells: A Single Molecule Localization Microscopy Approach. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3636.	1.8	15
6	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
7	Topological Analysis of γ -H2AX and MRE11 Clusters Detected by Localization Microscopy during X-ray-Induced DNA Double-Strand Break Repair. <i>Cancers</i> , 2021, 13, 5561.	1.7	10
8	Telomerase subunit Est2 marks internal sites that are prone to accumulate DNA damage. <i>BMC Biology</i> , 2021, 19, 247.	1.7	4
9	Single Molecule Localization Microscopy Analyses of DNA-Repair Foci and Clusters Detected Along Particle Damage Tracks. <i>Frontiers in Physics</i> , 2020, 8, .	1.0	11
10	The Effect of Bending Rigidity on Polymers. <i>Macromolecular Theory and Simulations</i> , 2019, 28, 1800071.	0.6	2
11	Using Persistent Homology as a New Approach for Super-Resolution Localization Microscopy Data Analysis and Classification of γ -H2AX Foci/Clusters. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2263.	1.8	31
12	Processing and Analysis of Hi-C Data on Bacteria. <i>Methods in Molecular Biology</i> , 2018, 1837, 19-31.	0.4	0
13	Deciphering 3D Organization of Chromosomes Using Hi-C Data. <i>Methods in Molecular Biology</i> , 2018, 1837, 389-401.	0.4	2
14	Robust detection and segmentation of cell nuclei in biomedical images based on a computational topology framework. <i>Medical Image Analysis</i> , 2017, 38, 90-103.	7.0	28
15	A Three-Pronged Attack To Investigate the Electronic Structure of a Family of Ferromagnetic Fe_4Ln_2 Cyclic Coordination Clusters: A Combined Magnetic Susceptibility, High-Field/High-Frequency Electron Paramagnetic Resonance, and ^{57}Fe Mössbauer Study. <i>Inorganic Chemistry</i> , 2017, 56, 4796-4806.	1.9	41
16	The Electronic Behavior of Zinc-Finger Protein Binding Sites in the Context of the DNA Extended Ladder Model. <i>Frontiers in Physics</i> , 2016, 4, .	1.0	3
17	A multiscale approach to simulating the conformational properties of unbound multi- C_2H_2 zinc finger proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1604-1615.	1.5	3
18	Radiation Induced Chromatin Conformation Changes Analysed by Fluorescent Localization Microscopy, Statistical Physics, and Graph Theory. <i>PLoS ONE</i> , 2015, 10, e0128555.	1.1	42

#	ARTICLE	IF	CITATIONS
19	The interaction of DNA with multi-Cys2His2 zinc finger proteins. <i>Journal of Physics Condensed Matter</i> , 2015, 27, 064107.	0.7	9
20	A generalized Potts model for confocal microscopy images. <i>International Journal of Modern Physics B</i> , 2015, 29, 1550048.	1.0	0
21	Phase transition and winding properties of a flexible polymer adsorbed to a rigid periodic copolymer. <i>Physical Review E</i> , 2015, 91, 032601.	0.8	0
22	The role of loops on the order of eukaryotes and prokaryotes. <i>FEBS Letters</i> , 2015, 589, 2958-2965.	1.3	31
23	Statistical analysis of protein ensembles. <i>Frontiers in Physics</i> , 2014, 2, .	1.0	1
24	Depletion of the Chromatin Looping Proteins CTCF and Cohesin Causes Chromatin Compaction: Insight into Chromatin Folding by Polymer Modelling. <i>PLoS Computational Biology</i> , 2014, 10, e1003877.	1.5	57
25	How Chromatin Looping and Nuclear Envelope Attachment Affect Genome Organization in Eukaryotic Cell Nuclei. <i>International Review of Cell and Molecular Biology</i> , 2014, 307, 351-381.	1.6	24
26	Persistence intervals of fractals. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2014, 405, 252-259.	1.2	2
27	A topological similarity measure for proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 1180-1190.	1.4	21
28	Zinc Finger Proteins and the 3D Organization of Chromosomes. <i>Advances in Protein Chemistry and Structural Biology</i> , 2013, 90, 67-117.	1.0	9
29	Transcriptional regulatory network shapes the genome structure of <i>Saccharomyces cerevisiae</i> . <i>Nucleus</i> , 2013, 4, 216-228.	0.6	9
30	A model for Escherichia coli chromosome packaging supports transcription factor-induced DNA domain formation. <i>Nucleic Acids Research</i> , 2012, 40, 972-980.	6.5	84
31	A model for the 3D chromatin architecture of pro and eukaryotes. <i>Methods</i> , 2012, 58, 307-314.	1.9	16
32	Expression-Dependent Folding of Interphase Chromatin. <i>PLoS ONE</i> , 2012, 7, e37525.	1.1	26
33	Mitotic chromosome structure. <i>Experimental Cell Research</i> , 2012, 318, 1381-1385.	1.2	2
34	Loops Determine the Mechanical Properties of Mitotic Chromosomes. <i>PLoS ONE</i> , 2011, 6, e29225.	1.1	26
35	Confinement driven spatial organization of semiflexible ring polymers: Implications for biopolymer packaging. <i>Soft Matter</i> , 2011, 7, 6906.	1.2	28
36	Repulsive Forces Between Looping Chromosomes Induce Entropy-Driven Segregation. <i>PLoS ONE</i> , 2011, 6, e14428.	1.1	35

#	ARTICLE	IF	CITATIONS
37	Physical nuclear organization: loops and entropy. <i>Current Opinion in Cell Biology</i> , 2011, 23, 332-337.	2.6	35
38	Chromatin folding “ from biology to polymer models and back. <i>Journal of Cell Science</i> , 2011, 124, 839-845.	1.2	94
39	Conformational and Dynamical Properties of the Isolated, Three-dimensional Single- and Double-stranded Polymer Chain on an Infinite Surface. <i>Macromolecular Theory and Simulations</i> , 2010, 19, 440-448.	0.6	6
40	Diffusion-Driven Looping Provides a Consistent Framework for Chromatin Organization. <i>PLoS ONE</i> , 2010, 5, e12218.	1.1	158
41	Topological interactions between ring polymers: Implications for chromatin loops. <i>Journal of Chemical Physics</i> , 2010, 132, 044904.	1.2	63
42	Localization Microscopy Reveals Expression-Dependent Parameters of Chromatin Nanostructure. <i>Biophysical Journal</i> , 2010, 99, 1358-1367.	0.2	73
43	Histone Depletion Facilitates Chromatin Loops on the Kilobasepair Scale. <i>Biophysical Journal</i> , 2010, 99, 2995-3001.	0.2	39
44	On the Influence of Topological Catenation and Bonding Constraints on Ring Polymers. <i>Macromolecules</i> , 2010, 43, 2564-2573.	2.2	30
45	Monte Carlo Simulation in Statistical Physics. <i>Graduate Texts in Physics</i> , 2010, , .	0.1	315
46	Conformational properties of compact polymers. <i>Journal of Chemical Physics</i> , 2009, 130, 174901.	1.2	15
47	Spatially confined folding of chromatin in the interphase nucleus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3812-3817.	3.3	233
48	Depletion Effects Massively Change Chromatin Properties and Influence Genome Folding. <i>Biophysical Journal</i> , 2009, 97, 2146-2153.	0.2	34
49	Random loop model for long polymers. <i>Physical Review E</i> , 2007, 76, 051805.	0.8	92
50	Superdiffusion in a Model for Diffusion in a Molecularly Crowded Environment. <i>Journal of Biological Physics</i> , 2007, 33, 305-312.	0.7	21
51	Monte Carlo Simulation in Statistical Physics. <i>Springer Series in Solid-state Sciences</i> , 2002, , .	0.3	240
52	Diffusion of gas molecules in the polystyrene matrix. <i>Macromolecular Theory and Simulations</i> , 2000, 9, 687-697.	0.6	3
53	Monte Carlo Simulation in Statistical Physics. <i>Springer Series in Solid-state Sciences</i> , 1988, , .	0.3	546