Daniel Jost

List of Publications by Year
in descending order

42 papers	1,684 citations	361296 20 h-index	345118 36 g-index
52 all docs	52 docs citations	52 times ranked	1845 citing authors

#	Article	IF	Citations
1	Modeling epigenome folding: formation and dynamics of topologically associated chromatin domains. Nucleic Acids Research, 2014, 42, 9553-9561.	6.5	362
2	TADs are 3D structural units of higher-order chromosome organization in Drosophila. Science Advances, 2018, 4, eaar8082.	4.7	237
3	4D Genome Rewiring during Oncogene-Induced and Replicative Senescence. Molecular Cell, 2020, 78, 522-538.e9.	4.5	107
4	How epigenome drives chromatin folding and dynamics, insights from efficient coarse-grained models of chromosomes. PLoS Computational Biology, 2018, 14, e1006159.	1.5	72
5	Perspectives: using polymer modeling to understand the formation and function of nuclear compartments. Chromosome Research, 2017, 25, 35-50.	1.0	65
6	Epigenomics in 3D: importance of long-range spreading and specific interactions in epigenomic maintenance. Nucleic Acids Research, 2018, 46, 2252-2264.	6.5	65
7	IC-Finder: inferring robustly the hierarchical organization of chromatin folding. Nucleic Acids Research, 2017, 45, gkx036.	6.5	54
8	Rouse model with transient intramolecular contacts on a timescale of seconds recapitulates folding and fluctuation of yeast chromosomes. Nucleic Acids Research, 2019, 47, 6195-6207.	6.5	53
9	Differential spatial and structural organization of the X chromosome underlies dosage compensation in C. elegans. Genes and Development, 2014, 28, 2591-2596.	2.7	48
10	Chromosome dynamics during interphase: a biophysical perspective. Current Opinion in Genetics and Development, 2020, 61, 37-43.	1.5	48
11	Bifurcation in epigenetics: Implications in development, proliferation, and diseases. Physical Review E, 2014, 89, 010701.	0.8	40
12	Coupling 1D modifications and 3D nuclear organization: data, models and function. Current Opinion in Cell Biology, 2017, 44, 20-27.	2.6	37
13	A Unified Poland-Scheraga Model of Oligo- and Polynucleotide DNA Melting: Salt Effects and Predictive Power. Biophysical Journal, 2009, 96, 1056-1067.	0.2	36
14	Small RNA biology is systems biology. BMB Reports, 2011, 44, 11-21.	1.1	36
15	Temperature Dependence of the DNA Double Helix at the Nanoscale: Structure, Elasticity, and Fluctuations. Biophysical Journal, 2013, 105, 1904-1914.	0.2	34
16	Guidelines for cell-type heterogeneity quantification based on a comparative analysis of reference-free DNA methylation deconvolution software. BMC Bioinformatics, 2020, 21, 16.	1.2	34
17	4D nucleome modeling. Current Opinion in Genetics and Development, 2021, 67, 25-32.	1.5	34
18	Polymer modelling unveils the roles of heterochromatin and nucleolar organizing regions in shaping 3D genome organization inArabidopsis thaliana. Nucleic Acids Research, 2021, 49, 1840-1858.	6.5	34

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19	The folding landscape of the epigenome. Physical Biology, 2016, 13, 026001.	0.8	32
20	Global chromatin conformation differences in the Drosophila dosage compensated chromosome X. Nature Communications, 2019, 10, 5355.	5.8	28
21	Spatial organization of chromosomes leads to heterogeneous chromatin motion and drives the liquid- or gel-like dynamical behavior of chromatin. Genome Research, 2022, 32, 28-43.	2.4	27
22	Regulating the Many to Benefit the Few: Role of Weak Small RNA Targets. Biophysical Journal, 2013, 104, 1773-1782.	0.2	21
23	Live imaging and biophysical modeling support a button-based mechanism of somatic homolog pairing in Drosophila. ELife, 2021, 10, .	2.8	21
24	Effect of replication on epigenetic memory and consequences on gene transcription. Physical Biology, 2015, 12, 026007.	0.8	20
25	Bubble statistics and positioning in superhelically stressed DNA. Physical Review E, 2011, 84, 031912.	0.8	16
26	Prediction of RNA multiloop and pseudoknot conformations from a lattice-based, coarse-grain tertiary structure model. Journal of Chemical Physics, 2010, 132, 095101.	1.2	14
27	Genome wide application of DNA melting analysis. Journal of Physics Condensed Matter, 2009, 21, 034108.	0.7	13
28	Quantitative effect of target translation on small RNA efficacy reveals a novel mode of interaction. Nucleic Acids Research, 2014, 42, 12200-12211.	6.5	11
29	Exploiting Single-Cell Quantitative Data to Map Genetic Variants Having Probabilistic Effects. PLoS Genetics, 2016, 12, e1006213.	1.5	11
30	Genome organization via loop extrusion, insights from polymer physics models. Briefings in Functional Genomics, 2020, 19, 119-127.	1.3	11
31	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. PLoS Computational Biology, 2020, 16, e1007869.	1.5	10
32	3DGenBench: a web-server to benchmark computational models for 3D Genomics. Nucleic Acids Research, 2022, 50, W4-W12.	6.5	10
33	Twist-DNA: computing base-pair and bubble opening probabilities in genomic superhelical DNA. Bioinformatics, 2013, 29, 2479-2481.	1.8	8
34	A Polymer Physics View on Universal and Sequence-Specific Aspects of Chromosome Folding. , 2018, , 149-169.		7
35	Ground-state energy and Wigner crystallization in thick two-dimensional electron systems. Physical Review B, 2005, 72, .	1.1	6
36	Polymer Modeling of 3D Epigenome Folding: Application to Drosophila. Methods in Molecular Biology, 2022, 2301, 293-305.	0.4	5

#	Article	IF	Citations
37	Modeling the Functional Coupling between 3D Chromatin Organization and Epigenome. , 2019, , 21-56.		4
38	Assigning function to natural allelic variation via dynamic modeling of gene network induction. Molecular Systems Biology, 2018, 14, e7803.	3.2	1
39	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. , 2020, 16, e1007869.		0
40	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. , 2020, 16, e1007869.		0
41	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. , 2020, 16, e1007869.		0
42	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. , 2020, 16, e1007869.		0