

# Daniel Jost

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Polymer Modeling of 3D Epigenome Folding: Application to Drosophila. <i>Methods in Molecular Biology</i> , 2022, 2301, 293-305.	0.4	5
2	Spatial organization of chromosomes leads to heterogeneous chromatin motion and drives the liquid- or gel-like dynamical behavior of chromatin. <i>Genome Research</i> , 2022, 32, 28-43.	2.4	27
3	3DGenBench: a web-server to benchmark computational models for 3D Genomics. <i>Nucleic Acids Research</i> , 2022, 50, W4-W12.	6.5	10
4	4D nucleome modeling. <i>Current Opinion in Genetics and Development</i> , 2021, 67, 25-32.	1.5	34
5	Live imaging and biophysical modeling support a button-based mechanism of somatic homolog pairing in Drosophila. <i>ELife</i> , 2021, 10, .	2.8	21
6	Polymer modelling unveils the roles of heterochromatin and nucleolar organizing regions in shaping 3D genome organization in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2021, 49, 1840-1858.	6.5	34
7	Genome organization via loop extrusion, insights from polymer physics models. <i>Briefings in Functional Genomics</i> , 2020, 19, 119-127.	1.3	11
8	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. <i>PLoS Computational Biology</i> , 2020, 16, e1007869.	1.5	10
9	4D Genome Rewiring during Oncogene-Induced and Replicative Senescence. <i>Molecular Cell</i> , 2020, 78, 522-538.e9.	4.5	107
10	Guidelines for cell-type heterogeneity quantification based on a comparative analysis of reference-free DNA methylation deconvolution software. <i>BMC Bioinformatics</i> , 2020, 21, 16.	1.2	34
11	Chromosome dynamics during interphase: a biophysical perspective. <i>Current Opinion in Genetics and Development</i> , 2020, 61, 37-43.	1.5	48
12	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. , 2020, 16, e1007869.		0
13	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. , 2020, 16, e1007869.		0
14	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. , 2020, 16, e1007869.		0
15	PenDA, a rank-based method for personalized differential analysis: Application to lung cancer. , 2020, 16, e1007869.		0
16	Rouse model with transient intramolecular contacts on a timescale of seconds recapitulates folding and fluctuation of yeast chromosomes. <i>Nucleic Acids Research</i> , 2019, 47, 6195-6207.	6.5	53
17	Global chromatin conformation differences in the Drosophila dosage compensated chromosome X. <i>Nature Communications</i> , 2019, 10, 5355.	5.8	28
18	Modeling the Functional Coupling between 3D Chromatin Organization and Epigenome. , 2019, , 21-56.		4

#	ARTICLE	IF	CITATIONS
19	TADs are 3D structural units of higher-order chromosome organization in <i>Drosophila</i> . <i>Science Advances</i> , 2018, 4, eaar8082.	4.7	237
20	Epigenomics in 3D: importance of long-range spreading and specific interactions in epigenomic maintenance. <i>Nucleic Acids Research</i> , 2018, 46, 2252-2264.	6.5	65
21	Assigning function to natural allelic variation via dynamic modeling of gene network induction. <i>Molecular Systems Biology</i> , 2018, 14, e7803.	3.2	1
22	A Polymer Physics View on Universal and Sequence-Specific Aspects of Chromosome Folding. , 2018, , 149-169.		7
23	How epigenome drives chromatin folding and dynamics, insights from efficient coarse-grained models of chromosomes. <i>PLoS Computational Biology</i> , 2018, 14, e1006159.	1.5	72
24	Perspectives: using polymer modeling to understand the formation and function of nuclear compartments. <i>Chromosome Research</i> , 2017, 25, 35-50.	1.0	65
25	IC-Finder: inferring robustly the hierarchical organization of chromatin folding. <i>Nucleic Acids Research</i> , 2017, 45, gkx036.	6.5	54
26	Coupling 1D modifications and 3D nuclear organization: data, models and function. <i>Current Opinion in Cell Biology</i> , 2017, 44, 20-27.	2.6	37
27	Exploiting Single-Cell Quantitative Data to Map Genetic Variants Having Probabilistic Effects. <i>PLoS Genetics</i> , 2016, 12, e1006213.	1.5	11
28	The folding landscape of the epigenome. <i>Physical Biology</i> , 2016, 13, 026001.	0.8	32
29	Effect of replication on epigenetic memory and consequences on gene transcription. <i>Physical Biology</i> , 2015, 12, 026007.	0.8	20
30	Differential spatial and structural organization of the X chromosome underlies dosage compensation in <i>C. elegans</i> . <i>Genes and Development</i> , 2014, 28, 2591-2596.	2.7	48
31	Bifurcation in epigenetics: Implications in development, proliferation, and diseases. <i>Physical Review E</i> , 2014, 89, 010701.	0.8	40
32	Quantitative effect of target translation on small RNA efficacy reveals a novel mode of interaction. <i>Nucleic Acids Research</i> , 2014, 42, 12200-12211.	6.5	11
33	Modeling epigenome folding: formation and dynamics of topologically associated chromatin domains. <i>Nucleic Acids Research</i> , 2014, 42, 9553-9561.	6.5	362
34	Temperature Dependence of the DNA Double Helix at the Nanoscale: Structure, Elasticity, and Fluctuations. <i>Biophysical Journal</i> , 2013, 105, 1904-1914.	0.2	34
35	Regulating the Many to Benefit the Few: Role of Weak Small RNA Targets. <i>Biophysical Journal</i> , 2013, 104, 1773-1782.	0.2	21
36	Twist-DNA: computing base-pair and bubble opening probabilities in genomic superhelical DNA. <i>Bioinformatics</i> , 2013, 29, 2479-2481.	1.8	8

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37	Bubble statistics and positioning in superhelically stressed DNA. <i>Physical Review E</i> , 2011, 84, 031912.	0.8	16
38	Small RNA biology is systems biology. <i>BMB Reports</i> , 2011, 44, 11-21.	1.1	36
39	Prediction of RNA multiloop and pseudoknot conformations from a lattice-based, coarse-grain tertiary structure model. <i>Journal of Chemical Physics</i> , 2010, 132, 095101.	1.2	14
40	Genome wide application of DNA melting analysis. <i>Journal of Physics Condensed Matter</i> , 2009, 21, 034108.	0.7	13
41	A Unified Poland-Scheraga Model of Oligo- and Polynucleotide DNA Melting: Salt Effects and Predictive Power. <i>Biophysical Journal</i> , 2009, 96, 1056-1067.	0.2	36
42	Ground-state energy and Wigner crystallization in thick two-dimensional electron systems. <i>Physical Review B</i> , 2005, 72, .	1.1	6