

# Leonid A Mirny

## List of Publications by Year in descending order

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135  
papers

34,981  
citations

13068

68  
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16127

124  
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183  
all docs

183  
docs citations

183  
times ranked

25300  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms of Chromosome Folding and Nuclear Organization: Their Interplay and Open Questions. Cold Spring Harbor Perspectives in Biology, 2022, 14, a040147.	2.3	68
2	Spatial organization of transcribed eukaryotic genes. Nature Cell Biology, 2022, 24, 327-339.	4.6	55
3	Promoter and enhancer RNAs regulate chromatin reorganization and activation of miR-10b/HOXD locus, and neoplastic transformation in glioma. Molecular Cell, 2022, 82, 1894-1908.e5.	4.5	15
4	Dynamics of CTCF- and cohesin-mediated chromatin looping revealed by live-cell imaging. Science, 2022, 376, 496-501.	6.0	190
5	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data. Nature Communications, 2022, 13, 2365.	5.8	49
6	MCM complexes are barriers that restrict cohesin-mediated loop extrusion. Nature, 2022, 606, 197-203.	13.7	58
7	Nucleome programming is required for the foundation of totipotency in mammalian germline development. EMBO Journal, 2022, 41, .	3.5	9
8	Cells use loop extrusion to weave and tie the genome. Nature, 2021, 590, 554-555.	13.7	8
9	DNA-loop-extruding SMC complexes can traverse one another in vivo. Nature Structural and Molecular Biology, 2021, 28, 642-651.	3.6	49
10	Systematic evaluation of chromosome conformation capture assays. Nature Methods, 2021, 18, 1046-1055.	9.0	108
11	Keeping chromatin in the loop(s). Nature Reviews Molecular Cell Biology, 2021, 22, 439-440.	16.1	26
12	Cooler: scalable storage for Hi-C data and other genomically labeled arrays. Bioinformatics, 2020, 36, 311-316.	1.8	754
13	Molecular basis of CTCF binding polarity in genome folding. Nature Communications, 2020, 11, 5612.	5.8	102
14	Intergenerationally Maintained Histone H4 Lysine 16 Acetylation Is Instructive for Future Gene Activation. Cell, 2020, 182, 127-144.e23.	13.5	57
15	Loop extrusion: theory meets single-molecule experiments. Current Opinion in Cell Biology, 2020, 64, 124-138.	2.6	116
16	Ultrastructural Details of Mammalian Chromosome Architecture. Molecular Cell, 2020, 78, 554-565.e7.	4.5	359
17	Viewing Nuclear Architecture through the Eyes of Nocturnal Mammals. Trends in Cell Biology, 2020, 30, 276-289.	3.6	30
18	Chromosome organization by one-sided and two-sided loop extrusion. ELife, 2020, 9, .	2.8	90

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19	The interplay between asymmetric and symmetric DNA loop extrusion. <i>ELife</i> , 2020, 9, .	2.8	16
20	Limits of Chromosome Compaction by Loop-Extruding Motors. <i>Physical Review X</i> , 2019, 9, .	2.8	8
21	The genome-wide multi-layered architecture of chromosome pairing in early <i>Drosophila</i> embryos. <i>Nature Communications</i> , 2019, 10, 4486.	5.8	38
22	Highly structured homolog pairing reflects functional organization of the <i>Drosophila</i> genome. <i>Nature Communications</i> , 2019, 10, 4485.	5.8	51
23	RNA polymerases as moving barriers to condensin loop extrusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20489-20499.	3.3	105
24	Two major mechanisms of chromosome organization. <i>Current Opinion in Cell Biology</i> , 2019, 58, 142-152.	2.6	167
25	Heterochromatin drives compartmentalization of inverted and conventional nuclei. <i>Nature</i> , 2019, 570, 395-399.	13.7	464
26	Extensive Heterogeneity and Intrinsic Variation in Spatial Genome Organization. <i>Cell</i> , 2019, 176, 1502-1515.e10.	13.5	348
27	RNAP as a Moving Barrier to Loop Extrusion. <i>Biophysical Journal</i> , 2019, 116, 22a.	0.2	0
28	Chromosome Organization by Loop Extrusion and Phase Separation. <i>Biophysical Journal</i> , 2019, 116, 171a.	0.2	0
29	Single Molecule Imaging of CTCF and Cohesin. Dissecting the Dynamic Interplay between Chromatin Loop Regulators. <i>Biophysical Journal</i> , 2019, 116, 22a.	0.2	0
30	Chromatin Organization by an Interplay of Loop Extrusion and Compartmental Segregation. <i>Biophysical Journal</i> , 2018, 114, 30a.	0.2	6
31	A pathway for mitotic chromosome formation. <i>Science</i> , 2018, 359, .	6.0	574
32	A Mechanism of Cohesin-Dependent Loop Extrusion Organizes Mammalian Chromatin Structure in the Developing Embryo. <i>Biophysical Journal</i> , 2018, 114, 255a.	0.2	4
33	Higher-Order Organization Principles of Pre-translational mRNPs. <i>Molecular Cell</i> , 2018, 72, 715-726.e3.	4.5	59
34	Chromatin organization by an interplay of loop extrusion and compartmental segregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6697-E6706.	3.3	510
35	HiGlass: web-based visual exploration and analysis of genome interaction maps. <i>Genome Biology</i> , 2018, 19, 125.	3.8	950
36	Polymer Models Integrate Inverted Nuclear Geometry with Conventional HI-C Compartmentalization. <i>Biophysical Journal</i> , 2017, 112, 373a.	0.2	0

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37	Targeted Degradation of CTCF Decouples Local Insulation of Chromosome Domains from Genomic Compartmentalization. <i>Cell</i> , 2017, 169, 930-944.e22.	13.5	1,374
38	The Damaging Effect of Passenger Mutations on Cancer Progression. <i>Cancer Research</i> , 2017, 77, 4763-4772.	0.4	78
39	Elucidating the Role of Transcription in Shaping the 3D Structure of the Bacterial Genome. <i>Biophysical Journal</i> , 2017, 112, 69a.	0.2	0
40	Compaction and Segregation of Sister Chromatids by Loop-Extruding Enzymes. <i>Biophysical Journal</i> , 2017, 112, 373a.	0.2	0
41	Single-nucleus Hi-C reveals unique chromatin reorganization at oocyte-to-zygote transition. <i>Nature</i> , 2017, 544, 110-114.	13.7	604
42	Isoform-Specific Expression and Feedback Regulation of E Protein TCF4 Control Dendritic Cell Lineage Specification. <i>Immunity</i> , 2017, 46, 65-77.	6.6	84
43	Diminished <i>PRRX1</i> Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	33
44	Two independent modes of chromatin organization revealed by cohesin removal. <i>Nature</i> , 2017, 551, 51-56.	13.7	935
45	SMC complexes differentially compact mitotic chromosomes according to genomic context. <i>Nature Cell Biology</i> , 2017, 19, 1071-1080.	4.6	123
46	The 4D nucleome project. <i>Nature</i> , 2017, 549, 219-226.	13.7	579
47	A mechanism of cohesin-dependent loop extrusion organizes zygotic genome architecture. <i>EMBO Journal</i> , 2017, 36, 3600-3618.	3.5	291
48	Emerging Evidence of Chromosome Folding by Loop Extrusion. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017, 82, 45-55.	2.0	227
49	Host proteostasis modulates influenza evolution. <i>ELife</i> , 2017, 6, .	2.8	34
50	History of chromosome rearrangements reflects the spatial organization of yeast chromosomes. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1641002.	0.3	5
51	Chromosome Compaction by Active Loop Extrusion. <i>Biophysical Journal</i> , 2016, 110, 2162-2168.	0.2	266
52	Formation of Chromosomal Domains by Loop Extrusion. <i>Cell Reports</i> , 2016, 15, 2038-2049.	2.9	1,570
53	Hematopoietic Stem Cells Are the Major Source of Multilineage Hematopoiesis in Adult Animals. <i>Immunity</i> , 2016, 45, 597-609.	6.6	317
54	Super-resolution imaging reveals distinct chromatin folding for different epigenetic states. <i>Nature</i> , 2016, 529, 418-422.	13.7	750

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55	Detecting Microbial Dysbiosis Associated with Pediatric Crohn Disease Despite the High Variability of the Gut Microbiota. <i>Cell Reports</i> , 2016, 14, 945-955.	2.9	49
56	The 3D Genome as Moderator of Chromosomal Communication. <i>Cell</i> , 2016, 164, 1110-1121.	13.5	793
57	Compaction and segregation of sister chromatids via active loop extrusion. <i>ELife</i> , 2016, 5, .	2.8	256
58	Effects of topological constraints on globular polymers. <i>Soft Matter</i> , 2015, 11, 665-671.	1.2	56
59	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. <i>Cell</i> , 2015, 163, 134-147.	13.5	399
60	Modeling chromosomes: Beyond pretty pictures. <i>FEBS Letters</i> , 2015, 589, 3031-3036.	1.3	80
61	Chromatin Loops as Allosteric Modulators of Enhancer-Promoter Interactions. <i>PLoS Computational Biology</i> , 2014, 10, e1003867.	1.5	102
62	ZFX Controls Propagation and Prevents Differentiation of Acute T-Lymphoblastic and Myeloid Leukemia. <i>Cell Reports</i> , 2014, 6, 528-540.	2.9	29
63	Cohesin-dependent globules and heterochromatin shape 3D genome architecture in <i>S. pombe</i> . <i>Nature</i> , 2014, 516, 432-435.	13.7	253
64	Tug-of-war between driver and passenger mutations in cancer and other adaptive processes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15138-15143.	3.3	138
65	Oncogene-triggered suppression of DNA repair leads to DNA instability in cancer. <i>Oncotarget</i> , 2014, 5, 8367-8378.	0.8	22
66	Abstract 18865: Identification of a Functional SNP Regulating PRRX1 at the 1q24 Locus for Atrial Fibrillation. <i>Circulation</i> , 2014, 130, .	1.6	1
67	Chromosomal architecture changes upon cell differentiation. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	0
68	Polymer models of yeast <i>S. cerevisiae</i> genome organization. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	0
69	<i>S. cerevisiae</i> genome as a confined equilibrium polymer brush. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	0
70	Organization of the Mitotic Chromosome. <i>Science</i> , 2013, 342, 948-953.	6.0	894
71	High-Resolution Mapping of the Spatial Organization of a Bacterial Chromosome. <i>Science</i> , 2013, 342, 731-734.	6.0	531
72	Chromosomes captured one by one. <i>Nature</i> , 2013, 502, 45-46.	13.7	16

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73	Impact of deleterious passenger mutations on cancer progression. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2910-2915.	3.3	274
74	Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data. Nature Reviews Genetics, 2013, 14, 390-403.	7.7	963
75	Sequence-dependent sliding kinetics of p53. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16552-16557.	3.3	87
76	Higher-order chromatin structure: bridging physics and biology. Current Opinion in Genetics and Development, 2012, 22, 115-124.	1.5	154
77	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. Nature Methods, 2012, 9, 999-1003.	9.0	1,187
78	Three-Dimensional Genome Architecture Influences Partner Selection for Chromosomal Translocations in Human Disease. PLoS ONE, 2012, 7, e44196.	1.1	109
79	High order chromatin architecture shapes the landscape of chromosomal alterations in cancer. Nature Biotechnology, 2011, 29, 1109-1113.	9.4	204
80	High-order chromatin architecture determines the landscape of chromosomal alterations in cancer. Nature Precedings, 2011, , .	0.1	1
81	The fractal globule as a model of chromatin architecture in the cell. Chromosome Research, 2011, 19, 37-51.	1.0	482
82	Dancing on DNA: Kinetic Aspects of Search Processes on DNA. ChemPhysChem, 2011, 12, 1481-1489.	1.0	118
83	GPU Based Molecular Dynamics Simulations of Polymer Rings in Concentrated Solution: Structure and Scaling. Progress of Theoretical Physics Supplement, 2011, 191, 135-145.	0.2	17
84	A single-molecule characterization of p53 search on DNA. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 563-568.	3.3	212
85	Bridging the Resolution Gap in Structural Modeling of 3D Genome Organization. PLoS Computational Biology, 2011, 7, e1002125.	1.5	76
86	Abstract 24: A genetic model of metastatic evolution: Driver and passenger mutations affect metastatic fitness. , 2011, , .		3
87	Hi-C: A Method to Study the Three-dimensional Architecture of Genomes.. Journal of Visualized Experiments, 2010, , .	0.2	318
88	Nucleosome-mediated cooperativity between transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22534-22539.	3.3	302
89	Fast Microtubule Dynamics in Meiotic Spindles Measured by Single Molecule Imaging: Evidence That the Spindle Environment Does Not Stabilize Microtubules. Molecular Biology of the Cell, 2010, 21, 323-333.	0.9	80
90	A Stevedore's Protein Knot. PLoS Computational Biology, 2010, 6, e1000731.	1.5	149

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91	Quantitative Characterization of Filament Dynamics by Single-Molecule Lifetime Measurements. <i>Methods in Cell Biology</i> , 2010, 95, 582-600.	0.5	11
92	Using Evolutionary Information to Find Specificity-Determining and Co-evolving Residues. <i>Methods in Molecular Biology</i> , 2009, 541, 421-448.	0.4	12
93	Using genome-wide measurements for computational prediction of SH2-peptide interactions. <i>Nucleic Acids Research</i> , 2009, 37, 4629-4641.	6.5	18
94	Different gene regulation strategies revealed by analysis of binding motifs. <i>Trends in Genetics</i> , 2009, 25, 434-440.	2.9	231
95	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. <i>Science</i> , 2009, 326, 289-293.	6.0	7,170
96	How a protein searches for its site on DNA: the mechanism of facilitated diffusion. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2009, 42, 434013.	0.7	304
97	Sequence-Dependent Kinetics of One-Dimensional Diffusion of p53 on DNA. <i>Biophysical Journal</i> , 2009, 96, 416a.	0.2	1
98	Cell commuters avoid delays. <i>Nature Physics</i> , 2008, 4, 93-95.	6.5	23
99	Tumor Suppressor p53 Slides on DNA with Low Friction and High Stability. <i>Biophysical Journal</i> , 2008, 95, L01-L03.	0.2	157
100	Spatial effects on the speed and reliability of protein-DNA search. <i>Nucleic Acids Research</i> , 2008, 36, 3570-3578.	6.5	99
101	Predicting transcription factor specificity with all-atom models. <i>Nucleic Acids Research</i> , 2008, 36, 6209-6217.	6.5	14
102	Fundamentally different strategies for transcriptional regulation are revealed by analysis of binding motifs. <i>Nature Precedings</i> , 2008, , .	0.1	0
103	Operating Regimes of Signaling Cycles: Statics, Dynamics, and Noise Filtering. <i>PLoS Computational Biology</i> , 2007, 3, e246.	1.5	101
104	Protein knot server: detection of knots in protein structures. <i>Nucleic Acids Research</i> , 2007, 35, W425-W428.	6.5	91
105	Zfx Controls the Self-Renewal of Embryonic and Hematopoietic Stem Cells. <i>Cell</i> , 2007, 129, 345-357.	13.5	219
106	How gene order is influenced by the biophysics of transcription regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13948-13953.	3.3	165
107	Intrinsic Fluctuations, Robustness, and Tunability in Signaling Cycles. <i>Biophysical Journal</i> , 2007, 92, 4473-4481.	0.2	48
108	Using the Topology of Metabolic Networks to Predict Viability of Mutant Strains. <i>Biophysical Journal</i> , 2006, 91, 2304-2311.	0.2	68

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109	A metabolic network in the evolutionary context: Multiscale structure and modularity. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8774-8779.	3.3	77
110	Intricate Knots in Proteins: Function and Evolution. PLoS Computational Biology, 2006, 2, e122.	1.5	286
111	CoC: a database of universally conserved residues in protein folds. Bioinformatics, 2005, 21, 2539-2540.	1.8	11
112	Diffusion in correlated random potentials, with applications to DNA. Physical Review E, 2004, 69, 061903.	0.8	98
113	Kinetics of Protein-DNA Interaction: Facilitated Target Location in Sequence-Dependent Potential. Biophysical Journal, 2004, 87, 4021-4035.	0.2	469
114	THE PROTEIN-FOLDING NUCLEUS: FROM SIMPLE MODELS TO REAL PROTEINS. , 2004, , .		0
115	Fold recognition with minimal gaps. Proteins: Structure, Function and Bioinformatics, 2003, 51, 531-543.	1.5	5
116	Protein complexes and functional modules in molecular networks. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12123-12128.	3.3	1,327
117	Virus shapes and buckling transitions in spherical shells. Physical Review E, 2003, 68, 051910.	0.8	365
118	Amino acids determining enzyme-substrate specificity in prokaryotic and eukaryotic protein kinases. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4463-4468.	3.3	84
119	Structural analysis of conserved base pairs in protein-DNA complexes. Nucleic Acids Research, 2002, 30, 1704-1711.	6.5	59
120	Using Orthologous and Paralogous Proteins to Identify Specificity-determining Residues in Bacterial Transcription Factors. Journal of Molecular Biology, 2002, 321, 7-20.	2.0	127
121	Understanding conserved amino acids in proteins. Physica A: Statistical Mechanics and Its Applications, 2002, 314, 600-606.	1.2	17
122	A ligand-based approach to understanding selectivity of nuclear hormone receptors PXR, CAR, FXR, LXRalpha, and LXRbeta. Pharmaceutical Research, 2002, 19, 1788-1800.	1.7	93
123	Protein Folding Theory: From Lattice to All-Atom Models. Annual Review of Biophysics and Biomolecular Structure, 2001, 30, 361-396.	18.3	326
124	Evolutionary conservation of the folding nucleus <sup>1</sup> Edited by A. R. Fersht. Journal of Molecular Biology, 2001, 308, 123-129.	2.0	116
125	Comparison of two optimization methods to derive energy parameters for protein folding: Perceptron and Z score. Proteins: Structure, Function and Bioinformatics, 2000, 41, 192-201.	1.5	34
126	Kinetics, thermodynamics and evolution of non-native interactions in a protein folding nucleus. Nature Structural Biology, 2000, 7, 336-342.	9.7	153

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127	Statistical significance of protein structure prediction by threading. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 9978-9983.	3.3	33
128	Universally conserved positions in protein folds: reading evolutionary signals about stability, folding kinetics and function. Journal of Molecular Biology, 1999, 291, 177-196.	2.0	382
129	Protein structure prediction by threading. why it works and why it does not 1 Edited by F. Cohen. Journal of Molecular Biology, 1998, 283, 507-526.	2.0	47
130	How evolution makes proteins fold quickly. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 4976-4981.	3.3	169
131	How to Derive a Protein Folding Potential? A New Approach to an Old Problem. Journal of Molecular Biology, 1996, 264, 1164-1179.	2.0	268
132	Universality and diversity of the protein folding scenarios:a comprehensive analysis with the aid of a lattice model. Folding & Design, 1996, 1, 103-116.	4.5	106
133	Protein fold recognition and dynamics in the space of contact maps. , 1996, 26, 391-410.		64
134	Monte Carlo modeling of epidemiological studies. Human and Ecological Risk Assessment (HERA), 1996, 2, 920-938.	1.7	8
135	Detection of $\beta$ -hydrolase fold in the cell surface esterases of Acinetobacter species using an analysis of 3D profiles. FEBS Letters, 1995, 371, 231-235.	1.3	8