

Leonid A Mirny

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2770870/publications.pdf>

Version: 2024-02-01

135
papers

34,981
citations

13068

68
h-index

16127

124
g-index

183
all docs

183
docs citations

183
times ranked

25300
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. <i>Science</i> , 2009, 326, 289-293.	6.0	7,170
2	Formation of Chromosomal Domains by Loop Extrusion. <i>Cell Reports</i> , 2016, 15, 2038-2049.	2.9	1,570
3	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
4	Protein complexes and functional modules in molecular networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12123-12128.	3.3	1,327
5	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <i>Nature Methods</i> , 2012, 9, 999-1003.	9.0	1,187
6	Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data. <i>Nature Reviews Genetics</i> , 2013, 14, 390-403.	7.7	963
7	HiGlass: web-based visual exploration and analysis of genome interaction maps. <i>Genome Biology</i> , 2018, 19, 125.	3.8	950
8	Two independent modes of chromatin organization revealed by cohesin removal. <i>Nature</i> , 2017, 551, 51-56.	13.7	935
9	Organization of the Mitotic Chromosome. <i>Science</i> , 2013, 342, 948-953.	6.0	894
10	The 3D Genome as Moderator of Chromosomal Communication. <i>Cell</i> , 2016, 164, 1110-1121.	13.5	793
11	Cooler: scalable storage for Hi-C data and other genomically labeled arrays. <i>Bioinformatics</i> , 2020, 36, 311-316.	1.8	754
12	Super-resolution imaging reveals distinct chromatin folding for different epigenetic states. <i>Nature</i> , 2016, 529, 418-422.	13.7	750
13	Single-nucleus Hi-C reveals unique chromatin reorganization at oocyte-to-zygote transition. <i>Nature</i> , 2017, 544, 110-114.	13.7	604
14	The 4D nucleome project. <i>Nature</i> , 2017, 549, 219-226.	13.7	579
15	A pathway for mitotic chromosome formation. <i>Science</i> , 2018, 359, .	6.0	574
16	High-Resolution Mapping of the Spatial Organization of a Bacterial Chromosome. <i>Science</i> , 2013, 342, 731-734.	6.0	531
17	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
18	The fractal globule as a model of chromatin architecture in the cell. <i>Chromosome Research</i> , 2011, 19, 37-51.	1.0	482

#	ARTICLE	IF	CITATIONS
19	Kinetics of Protein-DNA Interaction: Facilitated Target Location in Sequence-Dependent Potential. <i>Biophysical Journal</i> , 2004, 87, 4021-4035.	0.2	469
20	Heterochromatin drives compartmentalization of inverted and conventional nuclei. <i>Nature</i> , 2019, 570, 395-399.	13.7	464
21	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. <i>Cell</i> , 2015, 163, 134-147.	13.5	399
22	Universally conserved positions in protein folds: reading evolutionary signals about stability, folding kinetics and function. <i>Journal of Molecular Biology</i> , 1999, 291, 177-196.	2.0	382
23	Virus shapes and buckling transitions in spherical shells. <i>Physical Review E</i> , 2003, 68, 051910.	0.8	365
24	Ultrastructural Details of Mammalian Chromosome Architecture. <i>Molecular Cell</i> , 2020, 78, 554-565.e7.	4.5	359
25	Extensive Heterogeneity and Intrinsic Variation in Spatial Genome Organization. <i>Cell</i> , 2019, 176, 1502-1515.e10.	13.5	348
26	Protein Folding Theory: From Lattice to All-Atom Models. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2001, 30, 361-396.	18.3	326
27	Hi-C: A Method to Study the Three-dimensional Architecture of Genomes.. <i>Journal of Visualized Experiments</i> , 2010, , .	0.2	318
28	Hematopoietic Stem Cells Are the Major Source of Multilineage Hematopoiesis in Adult Animals. <i>Immunity</i> , 2016, 45, 597-609.	6.6	317
29	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
30	Nucleosome-mediated cooperativity between transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22534-22539.	3.3	302
31	A mechanism of cohesin-dependent loop extrusion organizes zygotic genome architecture. <i>EMBO Journal</i> , 2017, 36, 3600-3618.	3.5	291
32	Intricate Knots in Proteins: Function and Evolution. <i>PLoS Computational Biology</i> , 2006, 2, e122.	1.5	286
33	Impact of deleterious passenger mutations on cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2910-2915.	3.3	274
34	How to Derive a Protein Folding Potential? A New Approach to an Old Problem. <i>Journal of Molecular Biology</i> , 1996, 264, 1164-1179.	2.0	268
35	Chromosome Compaction by Active Loop Extrusion. <i>Biophysical Journal</i> , 2016, 110, 2162-2168.	0.2	266
36	Compaction and segregation of sister chromatids via active loop extrusion. <i>ELife</i> , 2016, 5, .	2.8	256

#	ARTICLE	IF	CITATIONS
37	Cohesin-dependent globules and heterochromatin shape 3D genome architecture in <i>S. pombe</i> . <i>Nature</i> , 2014, 516, 432-435.	13.7	253
38	Different gene regulation strategies revealed by analysis of binding motifs. <i>Trends in Genetics</i> , 2009, 25, 434-440.	2.9	231
39	Emerging Evidence of Chromosome Folding by Loop Extrusion. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017, 82, 45-55.	2.0	227
40	Zfx Controls the Self-Renewal of Embryonic and Hematopoietic Stem Cells. <i>Cell</i> , 2007, 129, 345-357.	13.5	219
41	A single-molecule characterization of p53 search on DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 563-568.	3.3	212
42	High order chromatin architecture shapes the landscape of chromosomal alterations in cancer. <i>Nature Biotechnology</i> , 2011, 29, 1109-1113.	9.4	204
43	Dynamics of CTCF- and cohesin-mediated chromatin looping revealed by live-cell imaging. <i>Science</i> , 2022, 376, 496-501.	6.0	190
44	How evolution makes proteins fold quickly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 4976-4981.	3.3	169
45	Two major mechanisms of chromosome organization. <i>Current Opinion in Cell Biology</i> , 2019, 58, 142-152.	2.6	167
46	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
47	Tumor Suppressor p53 Slides on DNA with Low Friction and High Stability. <i>Biophysical Journal</i> , 2008, 95, L01-L03.	0.2	157
48	Higher-order chromatin structure: bridging physics and biology. <i>Current Opinion in Genetics and Development</i> , 2012, 22, 115-124.	1.5	154
49	Kinetics, thermodynamics and evolution of non-native interactions in a protein folding nucleus. <i>Nature Structural Biology</i> , 2000, 7, 336-342.	9.7	153
50	A Stevedore's Protein Knot. <i>PLoS Computational Biology</i> , 2010, 6, e1000731.	1.5	149
51	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
52	Using Orthologous and Paralogous Proteins to Identify Specificity-determining Residues in Bacterial Transcription Factors. <i>Journal of Molecular Biology</i> , 2002, 321, 7-20.	2.0	127
53	SMC complexes differentially compact mitotic chromosomes according to genomic context. <i>Nature Cell Biology</i> , 2017, 19, 1071-1080.	4.6	123
54	Dancing on DNA: Kinetic Aspects of Search Processes on DNA. <i>ChemPhysChem</i> , 2011, 12, 1481-1489.	1.0	118

#	ARTICLE	IF	CITATIONS
55	Evolutionary conservation of the folding nucleus ¹ Edited by A. R. Fersht. Journal of Molecular Biology, 2001, 308, 123-129.	2.0	116
56	Loop extrusion: theory meets single-molecule experiments. Current Opinion in Cell Biology, 2020, 64, 124-138.	2.6	116
57	Three-Dimensional Genome Architecture Influences Partner Selection for Chromosomal Translocations in Human Disease. PLoS ONE, 2012, 7, e44196.	1.1	109
58	Systematic evaluation of chromosome conformation capture assays. Nature Methods, 2021, 18, 1046-1055.	9.0	108
59	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
60	RNA polymerases as moving barriers to condensin loop extrusion. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20489-20499.	3.3	105
61	Chromatin Loops as Allosteric Modulators of Enhancer-Promoter Interactions. PLoS Computational Biology, 2014, 10, e1003867.	1.5	102
62	Molecular basis of CTCF binding polarity in genome folding. Nature Communications, 2020, 11, 5612.	5.8	102
63	Operating Regimes of Signaling Cycles: Statics, Dynamics, and Noise Filtering. PLoS Computational Biology, 2007, 3, e246.	1.5	101
64	Spatial effects on the speed and reliability of protein-DNA search. Nucleic Acids Research, 2008, 36, 3570-3578.	6.5	99
65	Diffusion in correlated random potentials, with applications to DNA. Physical Review E, 2004, 69, 061903.	0.8	98
66	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
67	Protein knot server: detection of knots in protein structures. Nucleic Acids Research, 2007, 35, W425-W428.	6.5	91
68	Chromosome organization by one-sided and two-sided loop extrusion. ELife, 2020, 9, .	2.8	90
69	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
70	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
71	Isoform-Specific Expression and Feedback Regulation of E Protein TCF4 Control Dendritic Cell Lineage Specification. Immunity, 2017, 46, 65-77.	6.6	84
72	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

#	ARTICLE	IF	CITATIONS
73	Modeling chromosomes: Beyond pretty pictures. FEBS Letters, 2015, 589, 3031-3036.	1.3	80
74	The Damaging Effect of Passenger Mutations on Cancer Progression. Cancer Research, 2017, 77, 4763-4772.	0.4	78
75	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
76	Bridging the Resolution Gap in Structural Modeling of 3D Genome Organization. PLoS Computational Biology, 2011, 7, e1002125.	1.5	76
77	Using the Topology of Metabolic Networks to Predict Viability of Mutant Strains. Biophysical Journal, 2006, 91, 2304-2311.	0.2	68
78	Mechanisms of Chromosome Folding and Nuclear Organization: Their Interplay and Open Questions. Cold Spring Harbor Perspectives in Biology, 2022, 14, a040147.	2.3	68
79	Protein fold recognition and dynamics in the space of contact maps. , 1996, 26, 391-410.		64
80	Structural analysis of conserved base pairs in protein-DNA complexes. Nucleic Acids Research, 2002, 30, 1704-1711.	6.5	59
81	Higher-Order Organization Principles of Pre-translational mRNPs. Molecular Cell, 2018, 72, 715-726.e3.	4.5	59
82	MCM complexes are barriers that restrict cohesin-mediated loop extrusion. Nature, 2022, 606, 197-203.	13.7	58
83	Intergenerationally Maintained Histone H4 Lysine 16 Acetylation Is Instructive for Future Gene Activation. Cell, 2020, 182, 127-144.e23.	13.5	57
84	Effects of topological constraints on globular polymers. Soft Matter, 2015, 11, 665-671.	1.2	56
85	Spatial organization of transcribed eukaryotic genes. Nature Cell Biology, 2022, 24, 327-339.	4.6	55
86	Highly structured homolog pairing reflects functional organization of the Drosophila genome. Nature Communications, 2019, 10, 4485.	5.8	51
87	Detecting Microbial Dysbiosis Associated with Pediatric Crohn Disease Despite the High Variability of the Gut Microbiota. Cell Reports, 2016, 14, 945-955.	2.9	49
88	DNA-loop-extruding SMC complexes can traverse one another in vivo. Nature Structural and Molecular Biology, 2021, 28, 642-651.	3.6	49
89	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data. Nature Communications, 2022, 13, 2365.	5.8	49
90	Intrinsic Fluctuations, Robustness, and Tunability in Signaling Cycles. Biophysical Journal, 2007, 92, 4473-4481.	0.2	48

#	ARTICLE	IF	CITATIONS
91	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
92	The genome-wide multi-layered architecture of chromosome pairing in early Drosophila embryos. Nature Communications, 2019, 10, 4486.	5.8	38
93	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
94	Host proteostasis modulates influenza evolution. ELife, 2017, 6, .	2.8	34
95	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
96	Diminished <i>PRRX1</i> Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	33
97	Viewing Nuclear Architecture through the Eyes of Nocturnal Mammals. Trends in Cell Biology, 2020, 30, 276-289.	3.6	30
98	ZFX Controls Propagation and Prevents Differentiation of Acute T-Lymphoblastic and Myeloid Leukemia. Cell Reports, 2014, 6, 528-540.	2.9	29
99	Keeping chromatin in the loop(s). Nature Reviews Molecular Cell Biology, 2021, 22, 439-440.	16.1	26
100	Cell commuters avoid delays. Nature Physics, 2008, 4, 93-95.	6.5	23
101	Oncogene-triggered suppression of DNA repair leads to DNA instability in cancer. Oncotarget, 2014, 5, 8367-8378.	0.8	22
102	Using genome-wide measurements for computational prediction of SH2-peptide interactions. Nucleic Acids Research, 2009, 37, 4629-4641.	6.5	18
103	Understanding conserved amino acids in proteins. Physica A: Statistical Mechanics and Its Applications, 2002, 314, 600-606.	1.2	17
104	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
105	Chromosomes captured one by one. Nature, 2013, 502, 45-46.	13.7	16
106	The interplay between asymmetric and symmetric DNA loop extrusion. ELife, 2020, 9, .	2.8	16
107	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
108	Predicting transcription factor specificity with all-atom models. Nucleic Acids Research, 2008, 36, 6209-6217.	6.5	14

#	ARTICLE	IF	CITATIONS
109	Using Evolutionary Information to Find Specificity-Determining and Co-evolving Residues. <i>Methods in Molecular Biology</i> , 2009, 541, 421-448.	0.4	12
110	CoC: a database of universally conserved residues in protein folds. <i>Bioinformatics</i> , 2005, 21, 2539-2540.	1.8	11
111	Quantitative Characterization of Filament Dynamics by Single-Molecule Lifetime Measurements. <i>Methods in Cell Biology</i> , 2010, 95, 582-600.	0.5	11
112	Nucleome programming is required for the foundation of totipotency in mammalian germline development. <i>EMBO Journal</i> , 2022, 41, .	3.5	9
113	Detection of $\hat{1}\pm/\hat{1}^2$ -hydrolase fold in the cell surface esterases of <i>Acinetobacter</i> species using an analysis of 3D profiles. <i>FEBS Letters</i> , 1995, 371, 231-235.	1.3	8
114	Monte Carlo modeling of epidemiological studies. <i>Human and Ecological Risk Assessment (HERA)</i> , 1996, 2, 920-938.	1.7	8
115	Limits of Chromosome Compaction by Loop-Extruding Motors. <i>Physical Review X</i> , 2019, 9, .	2.8	8
116	Cells use loop extrusion to weave and tie the genome. <i>Nature</i> , 2021, 590, 554-555.	13.7	8
117	Chromatin Organization by an Interplay of Loop Extrusion and Compartmental Segregation. <i>Biophysical Journal</i> , 2018, 114, 30a.	0.2	6
118	Fold recognition with minimal gaps. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 531-543.	1.5	5
119	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
120	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
121	Abstract 24: A genetic model of metastatic evolution: Driver and passenger mutations affect metastatic fitness. , 2011, , .		3
122	Sequence-Dependent Kinetics of One-Dimensional Diffusion of p53 on DNA. <i>Biophysical Journal</i> , 2009, 96, 416a.	0.2	1
123	High-order chromatin architecture determines the landscape of chromosomal alterations in cancer. <i>Nature Precedings</i> , 2011, , .	0.1	1
124	Abstract 18865: Identification of a Functional SNP Regulating PRRX1 at the 1q24 Locus for Atrial Fibrillation. <i>Circulation</i> , 2014, 130, .	1.6	1
125	Fundamentally different strategies for transcriptional regulation are revealed by analysis of binding motifs. <i>Nature Precedings</i> , 2008, , .	0.1	0
126	Chromosomal architecture changes upon cell differentiation. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	0

#	ARTICLE	IF	CITATIONS
127	Polymer models of yeast <i>S. cerevisiae</i> genome organization. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	0
128	<i>S. cerevisiae</i> genome as a confined equilibrium polymer brush. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	0
129	Polymer Models Integrate Inverted Nuclear Geometry with Conventional HI-C Compartmentalization. <i>Biophysical Journal</i> , 2017, 112, 373a.	0.2	0
130	Elucidating the Role of Transcription in Shaping the 3D Structure of the Bacterial Genome. <i>Biophysical Journal</i> , 2017, 112, 69a.	0.2	0
131	Compaction and Segregation of Sister Chromatids by Loop-Extruding Enzymes. <i>Biophysical Journal</i> , 2017, 112, 373a.	0.2	0
132	RNAP as a Moving Barrier to Loop Extrusion. <i>Biophysical Journal</i> , 2019, 116, 22a.	0.2	0
133	Chromosome Organization by Loop Extrusion and Phase Separation. <i>Biophysical Journal</i> , 2019, 116, 171a.	0.2	0
134	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
135	THE PROTEIN-FOLDING NUCLEUS: FROM SIMPLE MODELS TO REAL PROTEINS. , 2004, , .		0