Geeta J Narlikar

List of Publications by Year
in descending order

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67	8,952	101543	114465
papers	citations	36 h-index	63 g-index

85	85	85	9286
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Cooperation between Complexes that Regulate Chromatin Structure and Transcription. Cell, 2002, 108, 475-487.	28.9	1,370
2	Liquid droplet formation by HP1Î± suggests a role for phase separation in heterochromatin. Nature, 2017, 547, 236-240.	27.8	1,351
3	Reconstitution of a Core Chromatin Remodeling Complex from SWI/SNF Subunits. Molecular Cell, 1999, 3, 247-253.	9.7	557
4	Mechanisms and Functions of ATP-Dependent Chromatin-Remodeling Enzymes. Cell, 2013, 154, 490-503.	28.9	522
5	The Site-Specific Installation of Methyl-Lysine Analogs into Recombinant Histones. Cell, 2007, 128, 1003-1012.	28.9	446
6	HP1 reshapes nucleosome core to promote phase separation of heterochromatin. Nature, 2019, 575, 390-394.	27.8	358
7	MECHANISTIC ASPECTS OF ENZYMATIC CATALYSIS:Lessons from Comparison of RNA and Protein Enzymes. Annual Review of Biochemistry, 1997, 66, 19-59.	11.1	262
8	Chromodomain-Mediated Oligomerization of HP1 Suggests a Nucleosome-Bridging Mechanism for Heterochromatin Assembly. Molecular Cell, 2011, 41, 67-81.	9.7	262
9	Structural Basis of Silencing: Sir3 BAH Domain in Complex with a Nucleosome at 3.0 Ã... Resolution. Science, 2011, 334, 977-982.	12.6	241
10	Nucleosome breathing and remodeling constrain CRISPR-Cas9 function. ELife, 2016, 5, .	6.0	193
11	The chromatin-remodeling enzyme ACF is an ATP-dependent DNA length sensor that regulates nucleosome spacing. Nature Structural and Molecular Biology, 2006, 13, 1078-1083.	8.2	185
12	Dynamics of nucleosome remodelling by individual ACF complexes. Nature, 2009, 462, 1022-1027.	27.8	184
13	Mechanisms of functional promiscuity by HP1 proteins. Trends in Cell Biology, 2014, 24, 377-386.	7.9	165
14	The chromatin remodeller ACF acts as a dimeric motor to space nucleosomes. Nature, 2009, 462, 1016-1021.	27.8	160
15	Distinct Strategies to Make Nucleosomal DNA Accessible. Molecular Cell, 2003, 11, 1311-1322.	9.7	149
16	The Role of Phase Separation in Heterochromatin Formation, Function, and Regulation. Biochemistry, 2018, 57, 2540-2548.	2.5	144
17	A conformational switch in HP1 releases auto-inhibition to drive heterochromatin assembly. Nature, 2013, 496, 377-381.	27.8	141
18	Division of Labor between the Chromodomains of HP1 and Suv39 Methylase Enables Coordination of Heterochromatin Spread. Molecular Cell, 2013, 51, 80-91.	9.7	125

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19	Generation and Interconversion of Multiple Distinct Nucleosomal States as a Mechanism for Catalyzing Chromatin Fluidity. Molecular Cell, 2001, 8, 1219-1230.	9.7	122
20	Mechanisms of ATP-Dependent Chromatin Remodeling Motors. Annual Review of Biophysics, 2016, 45, 153-181.	10.0	120
21	HP1 proteins compact DNA into mechanically and positionally stable phase separated domains. ELife, 2021, 10, .	6.0	119
22	Rvb1p and Rvb2p Are Essential Components of a Chromatin Remodeling Complex That Regulates Transcription of over 5% of Yeast Genes. Journal of Biological Chemistry, 2001, 276, 16279-16288.	3.4	103
23	Chromatin topology, condensates and gene regulation: shifting paradigms or just a phase?. Development (Cambridge), 2019, 146, .	2.5	93
24	Distortion of histone octamer core promotes nucleosome mobilization by a chromatin remodeler. Science, 2017, 355, .	12.6	92
25	Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. Cell, 2020, 180, 263-277.e20.	28.9	87
26	ATP-dependent chromatin remodeling enzymes: two heads are not better, just different. Current Opinion in Genetics and Development, 2008, 18, 137-144.	3.3	81
27	Functional Differences between the Human ATP-dependent Nucleosome Remodeling Proteins BRG1 and SNF2H. Journal of Biological Chemistry, 2001, 276, 34270-34278.	3.4	76
28	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. PLoS ONE, 2015, 10, e0126420.	2.5	71
29	Cryo-EM structures of remodeler-nucleosome intermediates suggest allosteric control through the nucleosome. ELife, 2019, 8, .	6.0	70
30	Stable Remodeling of Tailless Nucleosomes by the Human SWI-SNF Complex. Molecular and Cellular Biology, 1999, 19, 2088-2097.	2.3	61
31	A Nucleotide-Driven Switch Regulates Flanking DNA Length Sensing by a Dimeric Chromatin Remodeler. Molecular Cell, 2015, 57, 850-859.	9.7	58
32	Human ACF1 Alters the Remodeling Strategy of SNF2h. Journal of Biological Chemistry, 2006, 281, 28636-28647.	3.4	55
33	The nucleosomal acidic patch relieves auto-inhibition by the ISWI remodeler SNF2h. ELife, 2018, 7, .	6.0	55
34	Massively multiplex single-molecule oligonucleosome footprinting. ELife, 2020, 9, .	6.0	55
35	Phase-separation in chromatin organization. Journal of Biosciences, 2020, 45, 1.	1.1	50
36	Enzymatic Reactions inside Biological Condensates. Journal of Molecular Biology, 2021, 433, 166624.	4.2	50

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37	Chromatin Remodelers Act Globally, Sequence Positions Nucleosomes Locally. Journal of Molecular Biology, 2009, 391, 12-25.	4.2	48
38	The Yeast INO80 Complex Operates as a Tunable DNA Length-Sensitive Switch to Regulate Nucleosome Sliding. Molecular Cell, 2018, 69, 677-688.e9.	9.7	45
39	Nucleosome Remodeling by the Human SWI/SNF Complex Requires Transient Global Disruption of Histone-DNA Interactions. Molecular and Cellular Biology, 2002, 22, 3653-3662.	2.3	44
40	A proposal for kinetic proof reading by ISWI family chromatin remodeling motors. Current Opinion in Chemical Biology, 2010, 14, 660-665.	6.1	43
41	Regulation of Rvb1/Rvb2 by a Domain within the INO80 Chromatin Remodeling Complex Implicates the Yeast Rvbs as Protein Assembly Chaperones. Cell Reports, 2017, 19, 2033-2044.	6.4	43
42	Ion counting demonstrates a high electrostatic field generated by the nucleosome. ELife, 2019, 8, .	6.0	43
43	Zscan4 binds nucleosomal microsatellite DNA and protects mouse two-cell embryos from DNA damage. Science Advances, 2020, 6, eaaz9115.	10.3	39
44	Stability of a Human SWI-SNF Remodeled Nucleosomal Array. Molecular and Cellular Biology, 2001, 21, 1132-1144.	2.3	36
45	Assembly of Nucleosomal Templates by Salt Dialysis. , 2001, Chapter 21, Unit 21.6.		33
46	A Nucleosome Bridging Mechanism for Activation of a Maintenance DNA Methyltransferase. Molecular Cell, 2019, 73, 73-83.e6.	9.7	33
47	The Histone H4 Tail Regulates the Conformation of the ATP-Binding Pocket in the SNF2h Chromatin Remodeling Enzyme. Journal of Molecular Biology, 2014, 426, 2034-2044.	4.2	30
48	Liquid-like interactions in heterochromatin: Implications for mechanism and regulation. Current Opinion in Cell Biology, 2020, 64, 90-96.	5.4	29
49	The ATP-Dependent Remodeler RSC Transfers Histone Dimers and Octamers through the Rapid Formation of an Unstable Encounter Intermediate. Biochemistry, 2010, 49, 9882-9890.	2.5	26
50	Topical collection on Chromatin Biology and Epigenetics. Journal of Biosciences, 2020, 45, 1.	1.1	25
51	Biochemical Basis for Distinct Roles of the Heterochromatin Proteins Swi6 and Chp2. Journal of Molecular Biology, 2017, 429, 3666-3677.	4.2	24
52	FRET-based methods to study ATP-dependent changes in chromatin structure. Methods, 2007, 41, 291-295.	3.8	23
53	Topical collection on Chromatin Biology and Epigenetics. Journal of Biosciences, 2020, 45, .	1.1	16
54	Satellite repeat transcripts modulate heterochromatin condensates and safeguard chromosome stability in mouse embryonic stem cells. Nature Communications, 2022, 13, .	12.8	16

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55	ATP Hydrolysis by the SNF2 Domain of Dnmt5 Is Coupled to Both Specific Recognition and Modification of Hemimethylated DNA. Molecular Cell, 2020, 79, 127-139.e4.	9.7	15
56	Analysis of Changes in Nucleosome Conformation Using Fluorescence Resonance Energy Transfer. Methods in Molecular Biology, 2012, 833, 337-349.	0.9	13
57	Visualization and Quantitation of Phase-Separated Droplet Formation by Human HP1Î±. Methods in Enzymology, 2018, 611, 51-66.	1.0	13
58	Phase-separation in chromatin organization. Journal of Biosciences, 2020, 45, .	1.1	12
59	Biophysical Properties of HP1-Mediated Heterochromatin. Cold Spring Harbor Symposia on Quantitative Biology, 2019, 84, 217-225.	1.1	11
60	Collaboration through chromatin: motors of transcription and chromatin structure. Journal of Molecular Biology, 2021, 433, 166876.	4.2	11
61	A hexasome is the preferred substrate for the INO80 chromatin remodeling complex, allowing versatility of function. Molecular Cell, 2022, 82, 2098-2112.e4.	9.7	11
62	Generation and Biochemical Characterization of Phaseâ€Separated Droplets Formed by Nucleic Acid Binding Proteins: Using HP1 as a Model System. Current Protocols, 2021, 1, e109.	2.9	6
63	Histone dynamics play a critical role in SNF2h-mediated nucleosome sliding. Nature Structural and Molecular Biology, 2021, 28, 548-551.	8.2	3
64	ATP Hydrolysis Coordinates the Activities of Two Motors in a Dimeric Chromatin Remodeling Enzyme. Journal of Molecular Biology, 2022, 434, 167653.	4.2	3
65	Mechanism of the ATPâ€dependent chromatin remodeling complex ACF. FASEB Journal, 2007, 21, A39.	0.5	0
66	Mechanisms of ATPâ€dependent Chromatin Remodeling Enzymes. FASEB Journal, 2009, 23, 325.2.	0.5	0
67	Mechanistic Analysis of HP1 heterochromatin assembly. FASEB Journal, 2013, 27, 456.3.	0.5	0