

Molecular dynamics simulations demonstrate the regulation of histone tail acetylations and mutations

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Role of Histone Tails in the Nucleosome: A Computational Study. <i>Biophysical Journal</i> , 2014, 107, 2911-2922.	0.2	70
2	A Coarse-Grained DNA Model Parameterized from Atomistic Simulations by Inverse Monte Carlo. <i>Polymers</i> , 2014, 6, 1655-1675.	2.0	55
3	Shearing of the CENP-A dimerization interface mediates plasticity in the octameric centromeric nucleosome. <i>Scientific Reports</i> , 2015, 5, 17038.	1.6	35
4	Computational Modeling to Elucidate Molecular Mechanisms of Epigenetic Memory. , 2015, , 245-264.		0
5	Thermodynamic model of heterochromatin formation through epigenetic regulation. <i>Journal of Physics Condensed Matter</i> , 2015, 27, 064109.	0.7	19
6	Chromatin Unfolding by Epigenetic Modifications Explained by Dramatic Impairment of Internucleosome Interactions: A Multiscale Computational Study. <i>Journal of the American Chemical Society</i> , 2015, 137, 10205-10215.	6.6	135
7	The Acetylation Landscape of the H4 Histone Tail: Disentangling the Interplay between the Specific and Cumulative Effects. <i>Journal of the American Chemical Society</i> , 2015, 137, 6245-6253.	6.6	64
8	Distinct Roles of Histone H3 and H2A Tails in Nucleosome Stability. <i>Scientific Reports</i> , 2016, 6, 31437.	1.6	79
9	Chromatin Modifications in DNA Repair and Cancer. , 2016, , 487-509.		0
10	Atomistic Simulation of Stacked Nucleosome Core Particles: Tail Bridging, the H4 Tail, and Effect of Hydrophobic Forces. <i>Journal of Physical Chemistry B</i> , 2016, 120, 3048-3060.	1.2	30
11	Coupling between Histone Conformations and DNA Geometry in Nucleosomes on a Microsecond Timescale: Atomistic Insights into Nucleosome Functions. <i>Journal of Molecular Biology</i> , 2016, 428, 221-237.	2.0	131
12	Nucleosome Histone Tail Conformation and Dynamics: Impacts of Lysine Acetylation and a Nearby Minor Groove Benzo[<i>a</i>]pyrene-Derived Lesion. <i>Biochemistry</i> , 2017, 56, 1963-1973.	1.2	20
13	All-Atom MD Simulation of DNA Condensation Using <i>Ab Initio</i> Derived Force Field Parameters of Cobalt(III)-Hexammine. <i>Journal of Physical Chemistry B</i> , 2017, 121, 7761-7770.	1.2	16
14	Sequence-dependent DNA condensation as a driving force of DNA phase separation. <i>Nucleic Acids Research</i> , 2018, 46, 9401-9413.	6.5	55
15	Cryo-EM of nucleosome core particle interactions in trans. <i>Scientific Reports</i> , 2018, 8, 7046.	1.6	55
16	Effects of alternating electric field on the imaging of DNA double-helix structure by atomic force microscope. <i>Applied Nanoscience (Switzerland)</i> , 2020, 10, 3517-3524.	1.6	2
17	Molecular dynamics simulations reveal how H3K56 acetylation impacts nucleosome structure to promote DNA exposure for lesion sensing. <i>DNA Repair</i> , 2021, 107, 103201.	1.3	8
18	Is the H4 histone tail intrinsically disordered or intrinsically multifunctional?. <i>Physical Chemistry Chemical Physics</i> , 2021, 23, 5134-5142.	1.3	2

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19	Free energy profiles for unwrapping the outer superhelical turn of nucleosomal DNA. PLoS Computational Biology, 2018, 14, e1006024.	1.5	25
20	Two Arginine Residues Suppress the Flexibility of Nucleosomal DNA in the Canonical Nucleosome Core. PLoS ONE, 2015, 10, e0120635.	1.1	30
22	Histone tail electrostatics modulate E2â€E3 enzyme dynamics: a gateway to regulate ubiquitination machinery. Physical Chemistry Chemical Physics, 2023, 25, 3361-3374.	1.3	1