Lars NordenskiÃ¶ld

List of Publications by Year
in descending order

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117	4,062	101543	138484
papers	citations	36 h-index	58 g-index

123	123	123	3363
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Recent Advances in Investigating Functional Dynamics of Chromatin. Frontiers in Genetics, 2022, 13, 870640.	2.3	5
2	A Bottom-Up Coarse-Grained Model for Nucleosomeâ€“Nucleosome Interactions with Explicit Ions. Journal of Chemical Theory and Computation, 2022, 18, 3948-3960.	5.3	12
3	Hydrophobic interactions control the self-assembly of DNA and cellulose. Quarterly Reviews of Biophysics, 2021, 54, e3.	5.7	56
4	Linker histone defines structure and self-association behaviour of the 177Âbp human chromatosome. Scientific Reports, 2021, 11, 380.	3.3	16
5	Bottom-Up Coarse-Grained Modeling of DNA. Frontiers in Molecular Biosciences, 2021, 8, 645527.	3.5	22
6	Histone H4 lysine 20 mono-methylation directly facilitates chromatin openness and promotes transcription of housekeeping genes. Nature Communications, 2021, 12, 4800.	12.8	56
7	Solid-state NMR 13C, 15N assignments of human histone H3 in the nucleosome core particle. Biomolecular NMR Assignments, 2020, 14, 99-104.	0.8	12
8	Modeling DNA Flexibility: Comparison of Force Fields from Atomistic to Multiscale Levels. Journal of Physical Chemistry B, 2020, 124, 38-49.	2.6	37
9	Dynamic networks observed in the nucleosome core particles couple the histone globular domains with DNA. Communications Biology, 2020, 3, 639.	4.4	25
10	The human telomeric nucleosome displays distinct structural and dynamic properties. Nucleic Acids Research, 2020, 48, 5383-5396.	14.5	23
11	Compaction and self-association of megabase-sized chromatin are induced by anionic protein crowding. Soft Matter, 2020, 16, 4366-4372.	2.7	9
12	Internal Motion of Chromatin Fibers Is Governed by Dynamics of Uncompressed Linker Strands. Biophysical Journal, 2020, 119, 2326-2334.	0.5	5
13	A multiscale analysis of DNA phase separation: from atomistic to mesoscale level. Nucleic Acids Research, 2019, 47, 5550-5562.	14.5	24
14	Structure and Dynamics of the Telomeric Nucleosome and Chromatin. Biophysical Journal, 2019, 116, 71a.	0.5	1
15	Magic v.3: An integrated software package for systematic structure-based coarse-graining. Computer Physics Communications, 2019, 237, 263-273.	7.5	22
16	A Systematic Study of Nucleosome Core Particle and Nucleosome-Nucleosome Stacking Structure. Biophysical Journal, 2018, 114, 254a.	0.5	0
17	A systematic analysis of nucleosome core particle and nucleosome-nucleosome stacking structure. Scientific Reports, 2018, 8, 1543.	3.3	43
18	Stretch and Dynamics of Single Chromatin Molecules Confined in Nanofluidic Channels. Biophysical Journal, 2018, 114, 599a.	0.5	0

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19	Single-molecule compaction of megabase-long chromatin molecules by multivalent cations. Nucleic Acids Research, 2018, 46, 635-649.	14.5	24
20	EZH2 promotes neoplastic transformation through VAV interaction-dependent extranuclear mechanisms. Oncogene, 2018, 37, 461-477.	5.9	15
21	Structure and Dynamics in the Nucleosome Revealed by Solidâ€State NMR. Angewandte Chemie, 2018, 130, 9882-9886.	2.0	5
22	Multiscale Modeling and Simulation of Multivalent Cation Induced DNA Condensation. Biophysical Journal, 2018, 114, 29a.	0.5	0
23	Compaction of Single-Molecule Megabase-Long Chromatin under the Influence of Macromolecular Crowding. Biophysical Journal, 2018, 114, 2326-2335.	0.5	16
24	The effect of linker DNA on the structure and interaction of nucleosome core particles. Soft Matter, 2018, 14, 9096-9106.	2.7	10
25	Structure and Dynamics in the Nucleosome Revealed by Solidâ€State NMR. Angewandte Chemie - International Edition, 2018, 57, 9734-9738.	13.8	30
26	Regulation of Nucleosome Stacking and Chromatin Compaction by the Histone H4 N-Terminal Tailâ€“H2A Acidic Patch Interaction. Journal of Molecular Biology, 2017, 429, 2075-2092.	4.2	56
27	Single-molecule force spectroscopy on histone H4 tail-cross-linked chromatin reveals fiber folding. Journal of Biological Chemistry, 2017, 292, 17506-17513.	3.4	33
28	All-Atom MD Simulation of DNA Condensation Using Ab Initio Derived Force Field Parameters of Cobalt(III)-Hexammine. Journal of Physical Chemistry B, 2017, 121, 7761-7770.	2.6	16
29	3.9â€…Ã… phase plate cryo-EM reconstruction of the nucleosome core particle. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C1293-C1293.	0.1	0
30	Unravelling the Role of Linker Histone H1 and the H4-Tail in Chromatin (Un-)Folding. Biophysical Journal, 2016, 110, 68a.	0.5	0
31	Elucidating the DNAâ€“Histone Interaction in Nucleosome from the DNAâ€“Dendrimer Complex. Macromolecules, 2016, 49, 4277-4285.	4.8	10
32	The Influence of Ionic Environment and Histone Tails on Columnar Order of Nucleosome Core Particles. Biophysical Journal, 2016, 110, 1720-1731.	0.5	27
33	3.9 Ã… structure of the nucleosome core particle determined by phase-plate cryo-EM. Nucleic Acids Research, 2016, 44, 8013-8019.	14.5	78
34	Multiscale coarse-grained modelling of chromatin components: DNA and the nucleosome. Advances in Colloid and Interface Science, 2016, 232, 36-48.	14.7	19
35	Chromatin compaction under mixed salt conditions: Opposite effects of sodium and potassium ions on nucleosome array folding. Scientific Reports, 2015, 5, 8512.	3.3	66
36	Multiscale modelling of nucleosome core particle aggregation. Journal of Physics Condensed Matter, 2015, 27, 064111.	1.8	10

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37	ISWI Remodelling of Physiological Chromatin Fibres Acetylated at Lysine 16 of Histone H4. PLoS ONE, 2014, 9, e88411.	2.5	24
38	Molecular dynamics simulations demonstrate the regulation of DNAâ€DNA attraction by H4 histone tail acetylations and mutations. Biopolymers, 2014, 101, 1051-1064.	2.4	22
39	A Coarse-Grained DNA Model Parameterized from Atomistic Simulations by Inverse Monte Carlo. Polymers, 2014, 6, 1655-1675.	4.5	55
40	Principles of electrostatic interactions and self-assembly in lipid/peptide/DNA systems: Applications to gene delivery. Advances in Colloid and Interface Science, 2014, 205, 221-229.	14.7	18
41	Conformation-dependent DNA attraction. Nanoscale, 2014, 6, 7085-7092.	5.6	13
42	Interactions and Stacking in Ordered Mononucleosomes and Folded Chromatin: Effects of Histone Tail Modifications. Biophysical Journal, 2014, 106, 74a.	0.5	0
43	Selective Acetylation Reveals Distinct Roles of Histones H3 and H4 in Nucleosome Dynamics - a FRET Study. Biophysical Journal, 2014, 106, 430a.	0.5	0
44	How Histone Modifications Change Nucleosome Stability â€“ FRET Studies on Single Molecules and in Bulk. Microscopy and Microanalysis, 2014, 20, 1204-1205.	0.4	0
45	Nucleosome-Nucleosome Stacking: A Major Element of Chromatin Structure. Biophysical Journal, 2013, 104, 580a.	0.5	0
46	An Advanced Coarse-Grained Nucleosome Core Particle Model for Computer Simulations of Nucleosome-Nucleosome Interactions under Varying Ionic Conditions. PLoS ONE, 2013, 8, e54228.	2.5	46
47	A universal description for the experimental behavior of salt-(in)dependent oligocation-induced DNA condensation. Nucleic Acids Research, 2012, 40, 2807-2821.	14.5	25
48	The Effectcs of Histone H4 Acetylations in Nucleosome-Nucleosome Interactions and on Chromatin Folding and Fibre-Fibre Association. Biophysical Journal, 2012, 102, 481a.	0.5	0
49	Biophysical Characterization of a Recombinant Chromatin-Liposome Aggregates. Biophysical Journal, 2012, 102, 479a.	0.5	0
50	Supramolecular Organization in Self-Assembly of Chromatin and Cationic Lipid Bilayers is Controlled by Membrane Charge Density. Biomacromolecules, 2012, 13, 4146-4157.	5.4	7
51	Structure and internal organization of overcharged cationic-lipid/peptide/DNA self-assembly complexes. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 1794-1800.	2.6	14
52	The effect of salt on oligocation-induced chromatin condensation. Biochemical and Biophysical Research Communications, 2012, 418, 205-210.	2.1	18
53	Biophysical Properties and Supramolecular Structure of Self-Assembled Liposome/Îµ-Peptide/DNA Nanoparticles: Correlation with Gene Delivery. Biomacromolecules, 2012, 13, 124-131.	5.4	15
54	The polyelectrolyte properties of chromatin. Soft Matter, 2012, 8, 9322.	2.7	76

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55	Modelling chromatin structure and dynamics: status and prospects. Current Opinion in Structural Biology, 2012, 22, 151-159.	5.7	36
56	The effects of histone H4 tail acetylations on cation-induced chromatin folding and self-association. Nucleic Acids Research, 2011, 39, 1680-1691.	14.5	178
57	Sequence-Specific Mg²⁺â€“DNA Interactions: A Molecular Dynamics Simulation Study. Journal of Physical Chemistry B, 2011, 115, 14713-14720.	2.6	57
58	Influence of Histone Tails and H4 Tail Acetylations on Nucleosomeâ€“Nucleosome Interactions. Journal of Molecular Biology, 2011, 414, 749-764.	4.2	62
59	A Direct Method for Siteâ€Specific Protein Acetylation. Angewandte Chemie - International Edition, 2011, 50, 9611-9614.	13.8	124
60	Effects of cholesterol on pore formation in lipid bilayers induced by human islet amyloid polypeptide fragments: A coarse-grained molecular dynamics study. Physical Review E, 2011, 84, 051922.	2.1	27
61	Cation-induced polyelectrolyteâ€“polyelectrolyte attraction in solutions of DNA and nucleosome core particles. Advances in Colloid and Interface Science, 2010, 158, 32-47.	14.7	43
62	Self-Assembly in Phospholipid DNA - Protein Mixtures With Applications To Complex Formation in Cationic Liposome-Chromatin Systems. Biophysical Journal, 2010, 98, 78a.	0.5	0
63	Electrostatic Origin of Salt-Induced Nucleosome Array Compaction. Biophysical Journal, 2010, 99, 1896-1905.	0.5	54
64	Interactions between Cationic Lipid Bilayers and Model Chromatin. Langmuir, 2010, 26, 12488-12492.	3.5	11
65	A universal description for the experimental behavior of salt-(in)dependent oligocation-induced DNA condensation. Nucleic Acids Research, 2009, 37, 7137-7150.	14.5	58
66	Computer Modeling Reveals that Modifications of the Histone Tail Charges Define Salt-Dependent Interaction of the Nucleosome Core Particles. Biophysical Journal, 2009, 96, 2082-2094.	0.5	26
67	Counterion Induced Electrostatic Condensation Of Nucleosomes And Chromatin Arrays. Biophysical Journal, 2009, 96, 54a.	0.5	0
68	Influence of Nitroxide Spin Labels on RNA Structure: A Molecular Dynamics Simulation Study. Journal of Chemical Theory and Computation, 2008, 4, 1781-1787.	5.3	12
69	Design and Biophysical Characterization of Novel Polycationic Ïµ-Peptides for DNA Compaction and Delivery. Biomacromolecules, 2008, 9, 321-330.	5.4	35
70	Global optimisation by replica exchange with scaled hybrid Hamiltonians. Molecular Simulation, 2008, 34, 575-590.	2.0	7
71	Molecular Dynamics Simulation of Multivalent-Ion Mediated Attraction between DNA Molecules. Physical Review Letters, 2008, 100, 118301.	7.8	99
72	Charge Structure and Counterion Distribution in Hexagonal DNA Liquid Crystal. Biophysical Journal, 2007, 92, 947-958.	0.5	12

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73	H4 histone tail mediated DNA-DNA interaction and effects on DNA structure, flexibility, and counterion binding. A molecular dynamics study. Biopolymers, 2007, 86, 409-423.	2.4	17
74	Physicochemical analysis of electrostatic foundation for DNAâ€“protein interactions in chromatin transformations. Progress in Biophysics and Molecular Biology, 2007, 95, 23-49.	2.9	72
75	Folding, Misfolding, and Amyloid Protofibril Formation of WW Domain FBP28. Biophysical Journal, 2006, 90, 3983-3992.	0.5	48
76	Computer Modeling Demonstrates that Electrostatic Attraction of Nucleosomal DNA is Mediated by Histone Tails. Biophysical Journal, 2006, 90, 4305-4316.	0.5	67
77	Similarities and differences in interaction of K + and Na + with condensed ordered DNA. A molecular dynamics computer simulation study. Nucleic Acids Research, 2006, 34, 686-696.	14.5	148
78	Molecular Simulation of an Î±/É›-Peptide Dendrimer. , 2006, , 585-586.		0
79	A molecular dynamics simulation study of polyamine? and sodium?DNA. Interplay between polyamine binding and DNA structure. European Biophysics Journal, 2004, 33, 671-682.	2.2	31
80	Molecular dynamics simulation study of oriented polyamine- and Na-DNA: Sequence specific interactions and effects on DNA structure. Biopolymers, 2004, 73, 542-555.	2.4	31
81	Application of the Poisson Boltzmann polyelectrolyte model for analysis of thermal denaturation of DNA in the presence of Na+ and polyamine cations. Biophysical Chemistry, 2003, 104, 55-66.	2.8	15
82	A molecular dynamics simulation study of oriented DNA with polyamine and sodium counterions: diffusion and averaged binding of water and cations. Nucleic Acids Research, 2003, 31, 5971-5981.	14.5	75
83	Polyamine-nucleic acid interactions and the effects on structure in oriented DNA fibers. Nucleic Acids Research, 2002, 30, 419-428.	14.5	90
84	Application of the Poisson Boltzmann Polyelectrolyte Model for Analysis of Equilibria Between Single-, Double-, and Triple-Stranded Polynucleotides in the Presence of K⁺, Na⁺, and Mg²⁺ions. Journal of Biomolecular Structure and Dynamics, 2002, 20, 275-290.	3.5	15
85	Metal Ion-Induced Lateral Aggregation of Filamentous Viruses fd and M13. Biophysical Journal, 2002, 83, 566-581.	0.5	68
86	On the Competition between Water, Sodium Ions, and Spermine in Binding to DNA: A Molecular Dynamics Computer Simulation Study. Biophysical Journal, 2002, 82, 2860-2875.	0.5	118
87	Spermine: an â€œinvisibleâ€•component in the crystals of B-DNA. A grand canonical Monte Carlo and molecular dynamics simulation study. Journal of Molecular Biology, 2001, 308, 907-917.	4.2	78
88	Competitive substitution of hexammine cobalt(III) for Na+ and K+ ions in oriented DNA fibers. Biopolymers, 2001, 58, 268-278.	2.4	25
89	Influence of Alkali Cation Nature on Structural Transitions and Reactions of Biopolyelectrolytes. Biomacromolecules, 2000, 1, 648-655.	5.4	17
90	Interactions of polyamines with the DNA octamers d(m5CG)4 and d(GGAATTCC): A1H-NMR investigation. Biopolymers, 1999, 49, 41-53.	2.4	9

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91	Competitive Binding of Mg2+, Ca2+, Na+, and K+ Ions to DNA in Oriented DNA Fibers: Experimental and Monte Carlo Simulation Results. Biophysical Journal, 1999, 77, 2736-2749.	0.5	108
92	Experimental and Monte Carlo Simulation Studies on the Competitive Binding of Li+, Na+, and K+Ions to DNA in Oriented DNA Fibersâ€. Journal of Physical Chemistry B, 1999, 103, 9008-9019.	2.6	30
93	An NMR self-diffusion study of the interactions between spermidine and oligonucleotides. , 1998, 38, 505-513.		3
94	Self-Diffusion and Association of Li+, Cs+, and H2O in Oriented DNA Fibers. An NMR and MD Simulation Study. Journal of Physical Chemistry B, 1998, 102, 10636-10642.	2.6	21
95	Application of Polyelectrolyte Theories for Analysis of DNA Melting in the Presence of Na+ and Mg2+ Ions. Biophysical Journal, 1998, 75, 3041-3056.	0.5	61
96	Electrostatically Induced Polyelectrolyte Association of Rodlike Virus Particles. Physical Review Letters, 1998, 81, 5465-5468.	7.8	80
97	Electrostatically Induced Bundle Formation of Rodlike Polyelectrolytes: Comparison of Predictions from Monte Carlo Simulations with Experiments on Fd And M13 Virus Particles.. Materials Research Society Symposia Proceedings, 1997, 489, 61.	0.1	0
98	Monte Carlo Simulation Study of DNA Polyelectrolyte Properties in the Presence of Multivalent Polyamine Ions. Journal of Physical Chemistry B, 1997, 101, 4335-4342.	2.6	86
99	Multiple-quantum pulsed gradient NMR diffusion experiments on quadrupolar (I >) spins. Chemical Physics Letters, 1996, 262, 737-743.	2.6	14
100	An NMR selfâ€‰diffusion study of the interactions between spermidine and oligonucleotides. Biopolymers, 1996, 38, 505-513.	2.4	3
101	Mechanochemical study of conformational transitions and melting of Li-, Na-, K-, and CsDNA fibers in ethanol-water solutions. Biopolymers, 1994, 34, 897-920.	2.4	43
102	Li+counterion self-diffusion in ordered DNA. Biopolymers, 1994, 34, 1605-1614.	2.4	8
103	Ca²⁺Binding Environments on Natural and Synthetic Polymeric DNA's. Journal of Biomolecular Structure and Dynamics, 1992, 10, 333-343.	3.5	25
104	A study of the quadrupolar NMR splittings of7Li+,23Na+, and133Cs+counterions in macroscopically oriented DNA fibers. Biopolymers, 1992, 32, 1631-1642.	2.4	20
105	A reexamination of25Mg2+nmr in DNA solution: Site heterogeneity and cation competition effects. Biopolymers, 1991, 31, 1343-1346.	2.4	31
106	Evaluation of the electrostatic osmotic pressure in an infinite system of hexagonally oriented DNA molecules. Molecular Physics, 1991, 72, 177-192.	1.7	35
107	Preparation of Oriented Ca- and Mg-DNA by Means of the Wet Spinning Method.. Acta Chemica Scandinavica, 1991, 45, 216-218.	0.7	6
108	The interaction of calcium (II) with DNA probed by43Ca-NMR is not influenced by terminal phosphate groups at ends and nicks. Biopolymers, 1989, 28, 1339-1342.	2.4	20

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109	A43Ca-nmr study of Ca(II)-DNA interactions. Biopolymers, 1987, 26, 1047-1062.	2.4	48
110	A Monte Carlo simulation study of electrostatic forces between hexagonally packed DNA double helices. Journal of Chemical Physics, 1986, 85, 6686-6698.	3.0	127
111	Theory of nuclear spin relaxation in paramagnetic systems in solution. Progress in Nuclear Magnetic Resonance Spectroscopy, 1985, 17, 141-185.	7.5	200
112	A potassium-39 NMR study of potassium binding to double-helical DNA. FEBS Journal, 1984, 142, 133-137.	0.2	31
113	Dipole-dipole nuclear spin relaxation. Molecular Physics, 1983, 50, 515-530.	1.7	41
114	Applicability of the Solomon-Bloembergen equation to the study of paramagnetic transition metal-water complexes. An ab initio SCF-MO study. Journal of the American Chemical Society, 1982, 104, 379-382.	13.7	62
115	A nonempirical SCFâ€“MO study of the validity of the Solomonâ€“Bloembergen equation for the hexaâ€aquonickel (II) ion. Journal of Chemical Physics, 1981, 74, 2927-2930.	3.0	40
116	Kinetics for ligand exchange in paramagnetic complexes of Ni(DPM)2 with nitrogen, oxygen and sulfur ligands. A carbon-13 NMR relaxation study. Inorganica Chimica Acta, 1980, 40, X97-X98.	2.4	0
117	DNAâ€“DNA Interactions. , 0, , 209-237.		5