Richard Lavery

List of Publications by Year
in descending order

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237	13,981	24978	24179
papers	citations	57 h-index	110 g-index

245	245	245	7566
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Multiple protein-DNA interfaces unravelled by evolutionary information, physico-chemical and geometrical properties. PLoS Computational Biology, 2020, 16, e1007624.	1.5	18
2	Title is missing!. , 2020, 16, e1007624.		0
3	Title is missing!. , 2020, 16, e1007624.		0
4	Title is missing!. , 2020, 16, e1007624.		0
5	Title is missing!. , 2020, 16, e1007624.		0
6	The static and dynamic structural heterogeneities of B-DNA: extending Calladineâ€“Dickerson rules. Nucleic Acids Research, 2019, 47, 11090-11102.	6.5	45
7	Internal Coordinate Normal Mode Analysis: A Strategy To Predict Protein Conformational Transitions. Journal of Physical Chemistry B, 2019, 123, 1294-1301.	1.2	15
8	Sequence-dependent response of DNA to torsional stress: a potential biological regulation mechanism. Nucleic Acids Research, 2018, 46, 1684-1694.	6.5	40
9	A molecular dynamics study of adenylyl cyclase: The impact of ATP and G-protein binding. PLoS ONE, 2018, 13, e0196207.	1.1	19
10	Structure and Dynamics of a 197Âbp Nucleosome in Complex with Linker Histone H1. Molecular Cell, 2017, 66, 384-397.e8.	4.5	225
11	Analyzing DNA curvature and its impact on the ionic environment: application to molecular dynamics simulations of minicircles. Nucleic Acids Research, 2017, 45, 4269-4277.	6.5	22
12	The Role of Unconventional Hydrogen Bonds in Determining BII Propensities in B-DNA. Journal of Physical Chemistry Letters, 2017, 8, 21-28.	2.1	18
13	Decomposing proteinâ€“DNA binding and recognition using simplified protein models. Nucleic Acids Research, 2017, 45, 10270-10283.	6.5	12
14	Extra views on structure and dynamics of DNA loops on nucleosomes studied with molecular simulations. Nucleus, 2016, 7, 554-559.	0.6	3
15	Long-timescale dynamics of the Drewâ€“Dickerson dodecamer. Nucleic Acids Research, 2016, 44, 4052-4066.	6.5	86
16	Structure and dynamics of DNA loops on nucleosomes studied with atomistic, microsecond-scale molecular dynamics. Nucleic Acids Research, 2016, 44, 5450-5456.	6.5	42
17	DNA minicircles clarify the specific role of DNA structure on retroviral integration. Nucleic Acids Research, 2016, 44, 7830-7847.	6.5	22
18	Proteinâ€“DNA interfaces: a molecular dynamics analysis of time-dependent recognition processes for three transcription factors. Nucleic Acids Research, 2016, 44, gkw841.	6.5	31

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19	Dynamics and recognition within a proteinâ€“DNA complex: a molecular dynamics study of the SKN-1/DNA interaction. Nucleic Acids Research, 2016, 44, 1440-1448.	6.5	53
20	Improving the treatment of coarse-grain electrostatics: CVCEL. Journal of Chemical Physics, 2015, 143, 243118.	1.2	5
21	Analyzing ion distributions around DNA: sequence-dependence of potassium ion distributions from microsecond molecular dynamics. Nucleic Acids Research, 2015, 43, 2412-2423.	6.5	97
22	Internal Normal Mode Analysis (iNMA) Applied to Protein Conformational Flexibility. Journal of Chemical Theory and Computation, 2015, 11, 5503-5512.	2.3	19
23	Analyzing ion distributions around DNA. Nucleic Acids Research, 2014, 42, 8138-8149.	6.5	95
24	Î¼ABC: a systematic microsecond molecular dynamics study of tetranucleotide sequence effects in B-DNA. Nucleic Acids Research, 2014, 42, 12272-12283.	6.5	186
25	Unraveling the sequence-dependent polymorphic behavior of d(CpG) steps in B-DNA. Nucleic Acids Research, 2014, 42, 11304-11320.	6.5	81
26	Significance of Molecular Dynamics Simulations for Life Sciences. Israel Journal of Chemistry, 2014, 54, 1042-1051.	1.0	38
27	Temperature Dependence of the DNA Double Helix at the Nanoscale: Structure, Elasticity, and Fluctuations. Biophysical Journal, 2013, 105, 1904-1914.	0.2	34
28	PaLaCe: A Coarse-Grain Protein Model for Studying Mechanical Properties. Journal of Chemical Theory and Computation, 2013, 9, 785-793.	2.3	48
29	A Protein Solvation Model Based on Residue Burial. Journal of Chemical Theory and Computation, 2012, 8, 2141-2144.	2.3	16
30	Arbitrary proteinâ˜protein docking targets biologically relevant interfaces. BMC Biophysics, 2012, 5, 7.	4.4	34
31	Exploring polymorphisms in B-DNA helical conformations. Nucleic Acids Research, 2012, 40, 10668-10678.	6.5	89
32	Coarse-grain Protein Models. RSC Biomolecular Sciences, 2012, , 219-248.	0.4	1
33	Multistep Drug Intercalation: Molecular Dynamics and Free Energy Studies of the Binding of Daunomycin to DNA. Journal of the American Chemical Society, 2012, 134, 8588-8596.	6.6	78
34	Towards a molecular view of transcriptional control. Current Opinion in Structural Biology, 2012, 22, 160-167.	2.6	24
35	Proteinâ€“DNA Recognition Triggered by a DNA Conformational Switch. Angewandte Chemie - International Edition, 2011, 50, 6516-6518.	7.2	44
36	CURVES+ web server for analyzing and visualizing the helical, backbone and groove parameters of nucleic acid structures. Nucleic Acids Research, 2011, 39, W68-W73.	6.5	201

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37	A systematic molecular dynamics study of nearest-neighbor effects on base pair and base pair step conformations and fluctuations in B-DNA. Nucleic Acids Research, 2010, 38, 299-313.	6.5	349
38	Local and global effects of strong DNA bending induced during molecular dynamics simulations. Nucleic Acids Research, 2009, 37, 3766-3773.	6.5	78
39	Joint Evolutionary Trees: A Large-Scale Method To Predict Protein Interfaces Based on Sequence Sampling. PLoS Computational Biology, 2009, 5, e1000267.	1.5	79
40	Conformational analysis of nucleic acids revisited: Curves+. Nucleic Acids Research, 2009, 37, 5917-5929.	6.5	674
41	Modeling the Mechanical Response of Proteins to Anisotropic Deformation. ChemPhysChem, 2009, 10, 115-118.	1.0	21
42	Coarseâ€Grain Simulations of the Râ€SNARE Fusion Protein in its Membrane Environment Detect Longâ€Lived Conformational Subâ€States. ChemPhysChem, 2009, 10, 1548-1552.	1.0	30
43	Deforming DNA: From Physics to Biology. ChemPhysChem, 2009, 10, 1399-1404.	1.0	37
44	Model quantum-chemical studies on the reaction between the candidate proximate carcinogen benzo(a)pyrene-7,8-dihydrodiol-9,10-epoxide and guanine. International Journal of Quantum Chemistry, 2009, 14, 21-34.	1.0	0
45	Molecular electrostatic potential of the b-dna helix. VII. effect of screening by monovalent cations. International Journal of Quantum Chemistry, 2009, 18, 323-330.	1.0	0
46	The molecular electrostatic potential of DNA: The effect of countercation screening on various allomorphic forms. International Journal of Quantum Chemistry, 2009, 22, 103-110.	1.0	0
47	A Free Energy Pathway for the Interaction of the SRY Protein with Its Binding Site on DNA from Atomistic Simulations. Journal of the American Chemical Society, 2009, 131, 9864-9865.	6.6	29
48	Proteinâ€“DNA binding specificity: a grid-enabled computational approach applied to single and multiple protein assemblies. Physical Chemistry Chemical Physics, 2009, 11, 10712.	1.3	13
49	Simulation Study of the Molecular Mechanism of Intercalation of the Anti-Cancer Drug Daunomycin into DNA. Springer Series in Chemical Physics, 2009, , 165-180.	0.2	0
50	Proteinâ€“DNA recognition: Breaking the combinatorial barrier. Computer Physics Communications, 2008, 179, 112-119.	3.0	13
51	Interactions between Neuronal Fusion Proteins Explored by Molecular Dynamics. Biophysical Journal, 2008, 94, 3436-3446.	0.2	26
52	Identification of Protein Interaction Partners and Proteinâ€“Protein Interaction Sites. Journal of Molecular Biology, 2008, 382, 1276-1289.	2.0	52
53	On the Molecular Mechanism of Drug Intercalation into DNA: A Simulation Study of the Intercalation Pathway, Free Energy, and DNA Structural Changes. Journal of the American Chemical Society, 2008, 130, 9747-9755.	6.6	176
54	Coarse-Graining Protein Mechanics. , 2008, , 317-327.		0

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55	Probing the Flexibility of the Bacterial Reaction Center:â€‰ The Wild-Type Protein Is More Rigid Than Two Site-Specific Mutants. Biochemistry, 2007, 46, 14960-14968.	1.2	54
56	Locating the active sites of enzymes using mechanical properties. Proteins: Structure, Function and Bioinformatics, 2007, 67, 350-359.	1.5	96
57	Theory and simulation. Current Opinion in Structural Biology, 2007, 17, 147-148.	2.6	1
58	Protein mechanics: a route from structure to function. Journal of Biosciences, 2007, 32, 891-898.	0.5	73
59	Investigating the Local Flexibility of Functional Residues in Hemoproteins. Biophysical Journal, 2006, 90, 2706-2717.	0.2	92
60	Dynamics and Stability of E-Cadherin Dimers. Biophysical Journal, 2006, 91, 3964-3971.	0.2	29
61	ARTIST: An activated method in internal coordinate space for sampling protein energy landscapes. Proteins: Structure, Function and Bioinformatics, 2006, 63, 967-975.	1.5	14
62	Kinking Occurs during Molecular Dynamics Simulations of Small DNA Minicircles. Structure, 2006, 14, 1527-1534.	1.6	161
63	Modeling DNA Deformation. , 2006, , 169-210.		2
64	Wringing Out DNA. Physical Review Letters, 2006, 96, 178102.	2.9	144
65	Course 1 DNA structure, dynamics and recognition. Les Houches Summer School Proceedings, 2005, 82, 1-40.	0.2	0
66	Recognizing DNA. Quarterly Reviews of Biophysics, 2005, 38, 339-344.	2.4	28
67	Macromolecular recognition. Current Opinion in Structural Biology, 2005, 15, 171-175.	2.6	60
68	DNA/protein modeling. , 2005, , .		0
69	Non-additivity in protein-DNA binding. Bioinformatics, 2005, 21, 2254-2263.	1.8	52
70	Exciton States of Dynamic DNA Double Helices:Â Alternating dCdG Sequences. Journal of Physical Chemistry B, 2005, 109, 16109-16118.	1.2	71
71	Cadherin Mechanics and Complexation: The Importance of Calcium Binding. Biophysical Journal, 2005, 89, 3895-3903.	0.2	64
72	Molecular Dynamics Simulations of the 136 Unique Tetranucleotide Sequences of DNA Oligonucleotides. II: Sequence Context Effects on the Dynamical Structures of the 10 Unique Dinucleotide Steps. Biophysical Journal, 2005, 89, 3721-3740.	0.2	216

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73	Looking into DNA recognition: zinc finger binding specificity. Nucleic Acids Research, 2004, 32, 6673-6682.	6.5	33
74	Analyzing Protein-DNA Recognition Mechanisms. Structure, 2004, 12, 113-122.	1.6	108
75	Myosin flexibility: Structural domains and collective vibrations. Proteins: Structure, Function and Bioinformatics, 2004, 54, 384-393.	1.5	50
76	Probing Protein Mechanics: Residue-Level Properties and Their Use in Defining Domains. Biophysical Journal, 2004, 87, 1426-1435.	0.2	45
77	Molecular Dynamics Simulations of the 136 Unique Tetranucleotide Sequences of DNA Oligonucleotides. I. Research Design and Results on d(CpG) Steps. Biophysical Journal, 2004, 87, 3799-3813.	0.2	245
78	Motifs in nucleic acids: Molecular mechanics restraints for base pairing and base stacking. Journal of Computational Chemistry, 2003, 24, 1-9.	1.5	27
79	Docking macromolecules with flexible segments. Journal of Computational Chemistry, 2003, 24, 1910-1920.	1.5	32
80	Nucleic Acid Base Pair Dynamics:Â The Impact of Sequence and Structure Using Free-Energy Calculations. Journal of the American Chemical Society, 2003, 125, 4998-4999.	6.6	46
81	Influence of Conformational Dynamics on the Exciton States of DNA Oligomers. Journal of Physical Chemistry B, 2003, 107, 13512-13522.	1.2	118
82	Base pair opening within B-DNA: free energy pathways for GC and AT pairs from umbrella sampling simulations. Nucleic Acids Research, 2003, 31, 1434-1443.	6.5	153
83	Structure and mechanics of single biomolecules: experiment and simulation. Journal of Physics Condensed Matter, 2002, 14, R383-R414.	0.7	88
84	alpha/gamma Transitions in the B-DNA backbone. Nucleic Acids Research, 2002, 30, 5398-5406.	6.5	116
85	Base Flipping in DNA:â€‰ Pathways and Energetics Studied with Molecular Dynamic Simulations. Journal of the American Chemical Society, 2002, 124, 7272-7273.	6.6	84
86	Simulations of Nucleic Acids and Their Complexes. Accounts of Chemical Research, 2002, 35, 350-357.	7.6	116
87	Energetic and Conformational Aspects of A:T Base-Pair Opening within the DNA Double Helix. ChemPhysChem, 2001, 2, 673-677.	1.0	42
88	Modeling multi-component proteinâ€“DNA complexes: the role of bending and dimerization in the complex of p53 dimers with DNA. Protein Engineering, Design and Selection, 2001, 14, 233-243.	1.0	18
89	High-speed Molecular Mechanics Searches for Optimal DNA Interaction Sites. Combinatorial Chemistry and High Throughput Screening, 2001, 4, 707-717.	0.6	3
90	ADAPT: A molecular mechanics approach for studying the structural properties of long DNA sequences. Biopolymers, 2000, 56, 292-310.	1.2	18

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91	Perspective on "Stereochemistry of polypeptide chain conformations". Theoretical Chemistry Accounts, 2000, 103, 257-258.	0.5	4
92	The Impact of Abasic Sites on DNA Flexibility. Journal of Biomolecular Structure and Dynamics, 2000, 17, 645-653.	2.0	30
93	Methylene Blue Binding to DNA with Alternating GC Base Sequence:Â A Modeling Study. Journal of the American Chemical Society, 2000, 122, 2860-2866.	6.6	163
94	Optimization of Nucleic Acid Sequences. Biophysical Journal, 2000, 79, 680-685.	0.2	32
95	A Mechanism for RecA-Promoted Sequence Homology Recognition and Strand Exchange Between Single-Stranded DNA and Duplex DNA, via Triple-Helical Intermediates. Journal of Biomolecular Structure and Dynamics, 2000, 17, 147-153.	2.0	2
96	Perspective on â€œStereochemistry of polypeptide chain conformationsâ€• , 2000, , 257-258.		0
97	Twisting and stretching a DNA molecule leads to structural transitions. , 1999, , .		1
98	Modelling Protein-DNA Interactions. Theoretical and Computational Chemistry, 1999, 8, 441-483.	0.2	7
99	Phase coexistence in a single DNA molecule. Physica A: Statistical Mechanics and Its Applications, 1999, 263, 392-404.	1.2	56
100	Modelling DNA stretching for physics and biology. , 1999, 106, 75-84.		29
101	Collective variable modelling of nucleic acids. Current Opinion in Structural Biology, 1999, 9, 170-176.	2.6	27
102	Modeling DNA deformations induced by minor groove binding proteins. , 1999, 49, 341-353.		19
103	Free Energy Calculations of Watsonâ"Crick Base Pairing in Aqueous Solution. Journal of the American Chemical Society, 1999, 121, 9503-9508.	6.6	74
104	Experimental and Theoretical Studies of the Conformational Perturbations Induced by an Abasie Site. Journal of Biomolecular Structure and Dynamics, 1999, 17, 245-257.	2.0	9
105	Le jokari molÃ©culaire. Biofutur, 1999, 1999, 26-27.	0.0	1
106	A Molecular Model for RecA-Promoted Strand Exchange via Parallel Triple-Stranded Helices. Biophysical Journal, 1999, 77, 1562-1576.	0.2	35
107	From Atomic to Mesoscopic Descriptions of the Internal Dynamics of DNA. Biophysical Journal, 1999, 77, 2366-2376.	0.2	52
108	Abasic Sites in Duplex DNA: Molecular Modeling of Sequence-Dependent Effects on Conformation. Biophysical Journal, 1999, 77, 3218-3226.	0.2	35

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109	Unraveling Proteins: A Molecular Mechanics Study. Biophysical Journal, 1999, 76, 2760-2768.	0.2	103
110	Modelling DNA Stretching for Physics and Biology. , 1999, , 115-131.		0
111	Twisting a Single DNA Molecule: Experiments and Models. , 1999, , 735-765.		0
112	Modeling the Mechanics of a DNA Oligomer. Journal of Biomolecular Structure and Dynamics, 1998, 16, 593-604.	2.0	23
113	Sequence-Dependent Dynamics of TATA-Box Binding Sites. Biophysical Journal, 1998, 75, 372-381.	0.2	62
114	A Model for Parallel Triple Helix Formation by Ree A: Single-Strand Association with a Homologous Duple via the Minor Groove. Journal of Biomolecular Structure and Dynamics, 1998, 16, 535-546.	2.0	22
115	Stretched and overwound DNA forms a Pauling-like structure with exposed bases. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 14152-14157.	3.3	330
116	Distortions of the DNA Double Helix Induced by 1,3-trans-Diamminedichloroplatinum(II)-intrastrand Cross-link: An Internal Coordinate Molecular Modeling Study. Journal of Biomolecular Structure and Dynamics, 1997, 14, 703-714.	2.0	9
117	Local DNA stretching mimics the distortion caused by the TATA box-binding protein. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 2993-2998.	3.3	71
118	Conformational Properties of the TATA-Box Binding Sequence of DNA. Journal of Biomolecular Structure and Dynamics, 1997, 14, 757-765.	2.0	44
119	Unusual DNA conformations. Current Opinion in Structural Biology, 1997, 7, 348-354.	2.6	38
120	Modelling base pair opening: the role of helical twist. Computational and Theoretical Chemistry, 1997, 398-399, 473-482.	1.5	33
121	Internal coordinate modeling of DNA: Force field comparisons. Journal of Computational Chemistry, 1997, 18, 1043-1055.	1.5	40
122	Collective-variable Monte Carlo simulation of DNA. Journal of Computational Chemistry, 1997, 18, 2001-2011.	1.5	13
123	DNA: An Extensible Molecule. Science, 1996, 271, 792-794.	6.0	936
124	Poisson-Boltzmann calculations for nucleic acids and nucleic acids complexes. Chemical Physics, 1996, 204, 263-269.	0.9	21
125	DNA structural forms. Quarterly Reviews of Biophysics, 1996, 29, 309-368.	2.4	97
126	Molecular Modelling of (A4T4NN)n and (T4A4NN)n: Sequence Elements Responsible for Curvature. Nucleic Acids Research, 1996, 24, 1632-1637.	6.5	58

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127	Modelling Extreme Stretching of DNA. Nucleic Acids Research, 1996, 24, 2260-2267.	6.5	224
128	The Genetic Code â€" Passing from One Dimension to Three Dimensions. Data and Knowledge in A Changing World, 1996, , 179-190.	0.1	0
129	Low-frequency vibrations in ?-helices: Helicoidal analysis of polyalanine and deoxymyoglobin molecular dynamics trajectories. Biopolymers, 1995, 35, 555-571.	1.2	10
130	JUMNA (junction minimisation of nucleic acids). Computer Physics Communications, 1995, 91, 135-158.	3.0	194
131	Efficient conformational space sampling for nucleosides using internal coordinate Monte Carlo simulations and a modified furanose description. Journal of Computational Chemistry, 1995, 16, 667-680.	1.5	13
132	Modelling of transmembrane ?-helix bundles. Molecular Engineering, 1995, 5, 1-9.	0.2	0
133	Modeling A Strand Exchange Tetraplex Conformation. Journal of Biomolecular Structure and Dynamics, 1995, 13, 459-464.	2.0	14
134	Modelling the DNA double helix: techniques and results. , 1995, , 57-82.		4
135	Twists and Turns in DNA: Predicting Base Sequence Effects on the Conformation of the Double Helix. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1995, , 217-230.	0.2	3
136	Rotational Motions of Bases in DNA. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1995, , 231-239.	0.2	0
137	Modelling of Transmembrane Î±-Helix Bundles. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1995, , 1-9.	0.2	0
138	Theoretical studies of DNA-RNA hybrid conformations. Nucleic Acids Research, 1994, 22, 1444-1449.	6.5	22
139	Measuring the geometry of DNA grooves. Biopolymers, 1994, 34, 337-346.	1.2	101
140	Modelling DNA conformational mechanics. Biophysical Chemistry, 1994, 50, 33-45.	1.5	40
141	Prediction of the positioning of the seven transmembrane Î±-helices of bacteriorhodopsin. Journal of Molecular Biology, 1994, 236, 1105-1122.	2.0	32
142	Steps Towards Predicting the Structure of Membrane Proteins. NATO ASI Series Series B: Physics, 1994, , 239-252.	0.2	0
143	Persistence analysis of the static and dynamical helix deformations of DNA oligonucleotides: Application to the crystal structure and molecular dynamics simulation of d(CGCGAATTCGCG)2. Biopolymers, 1993, 33, 335-350.	1.2	22
144	Force field for platinum binding to adenine. Journal of Computational Chemistry, 1993, 14, 45-53.	1.5	28

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145	A critical comparison of search algorithms applied to the optimization of protein side-chain conformations. Journal of Computational Chemistry, 1993, 14, 790-798.	1.5	66
146	Packing and recognition of protein structural elements: A new approach applied to the 4-helix bundle of myohemerythrin. Proteins: Structure, Function and Bioinformatics, 1993, 15, 413-425.	1.5	17
147	An analysis of the conformational paths of citrate synthase. Proteins: Structure, Function and Bioinformatics, 1993, 16, 393-407.	1.5	12
148	Symmetry reduction in homopolymeric DNA: implications for DNA fine structure. Computational and Theoretical Chemistry, 1993, 286, 219-229.	1.5	8
149	A possible family of B-like triple helix structures: Comparison with the Arnott A-like triple helix. Biochemistry, 1993, 32, 2098-2103.	1.2	57
150	BI- BIItransitions in B-DNA. Nucleic Acids Research, 1993, 21, 561-568.	6.5	151
151	Conformations of DNA Duplexes Containing 8-Oxoguanine. Journal of Biomolecular Structure and Dynamics, 1993, 11, 293-301.	2.0	9
152	A comprehensive classification of nucleic acid structural families based on strand direction and base pairing. Nucleic Acids Research, 1992, 20, 5011-5016.	6.5	31
153	The fine structure of two DNA dodecamers containing the cAMP responsive element sequence and its inverse. Journal of Molecular Biology, 1992, 227, 852-875.	2.0	52
154	Conformational sub-states in B-DNA. Journal of Molecular Biology, 1992, 226, 775-794.	2.0	94
155	A new approach to the rapid determination of protein side-chain conformations. implications for the analysis of side-chain connectivity. Journal of Molecular Graphics, 1992, 10, 35-36.	1.7	0
156	Persistence analysis of the static and dynamical helix deformations of DNA oligonucleotides: application to the crystal structure and molecular dynamics simulation of d(CGCGAATTCGCG)2. Journal of Molecular Graphics, 1992, 10, 41-42.	1.7	0
157	A computational and experimental study of the bending induced at a double-triple helix junction. Biophysical Chemistry, 1992, 45, 143-152.	1.5	34
158	DNA flexibility as a function of allomorphic conformation and of base sequence. Biopolymers, 1992, 32, 1077-1103.	1.2	24
159	Strand orientation of [Î±]-oligodeoxynucleotides in triple helix structures: Dependence on nucleotide sequence. Journal of Molecular Recognition, 1992, 5, 93-98.	1.1	8
160	Evidence for the stochastic nature of base pair opening in DNA: a Brownian dynamics simulation. Journal of the American Chemical Society, 1991, 113, 2490-2493.	6.6	49
161	A New Approach to the Rapid Determination of Protein Side Chain Conformations. Journal of Biomolecular Structure and Dynamics, 1991, 8, 1267-1289.	2.0	320
162	Theoretical Study of Ethidium Intercalation in Triple-Stranded DNA and at Triplex-Duplex Junctions. Journal of Biomolecular Structure and Dynamics, 1991, 9, 425-436.	2.0	21

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163	Triple Helix Structures: Sequence Dependence, Flexibility and Mismatch Effects. Journal of Biomolecular Structure and Dynamics, 1991, 9, 411-424.	2.0	27
164	Modelling the B-DNA base pair opening reaction. Journal De Chimie Physique Et De Physico-Chimie Biologique, 1991, 88, 2567-2572.	0.2	0
165	Conformational and helicoidal analysis of the molecular dynamics of proteins: â€œCurves,â€•dials and windows for a 50 psec dynamic trajectory of BPTI. Proteins: Structure, Function and Bioinformatics, 1990, 8, 179-193.	1.5	34
166	Base Pair Opening Pathways in B-DNA. Journal of Biomolecular Structure and Dynamics, 1990, 7, 915-933.	2.0	36
167	The Conformation and Stability of Ribonucleic Acids: Modeling Base Sequence Effects in Double Stranded Helices. Journal of Biomolecular Structure and Dynamics, 1989, 7, 363-380.	2.0	3
168	Conformational and Helicoidal Analysis of 30 PS of Molecular Dynamics on the d(CGCGAATTCGCG) Double Helix: â€œCurvesâ€, Dials and Windows. Journal of Biomolecular Structure and Dynamics, 1989, 6, 669-699.	2.0	214
169	Modeling and measuring DNA deformation. Journal of Molecular Graphics, 1989, 7, 179.	1.7	0
170	Describing protein structure: A general algorithm yielding complete helicoidal parameters and a unique overall axis. Proteins: Structure, Function and Bioinformatics, 1989, 6, 46-60.	1.5	129
171	Theoretical prediction of base sequence effects in DNA. Journal of Molecular Biology, 1989, 207, 433-444.	2.0	26
172	Defining the Structure of Irregular Nucleic Acids: Conventions and Principles. Journal of Biomolecular Structure and Dynamics, 1989, 6, 655-667.	2.0	681
173	Sequence-targeted cleavage of nucleic acids by oligo-[.alpha.]thymidylate-phenanthroline conjugates: parallel and antiparallel double helices are formed with DNA and RNA, respectively. Biochemistry, 1988, 27, 6039-6045.	1.2	56
174	DNA stem-loop structures in oligopurine-oligopyrimidine triplexes. Nucleic Acids Research, 1988, 16, 11795-11809.	6.5	30
175	The Definition of Generalized Helicoidal Parameters and of Axis Curvature for Irregular Nucleic Acids. Journal of Biomolecular Structure and Dynamics, 1988, 6, 63-91.	2.0	874
176	Energetic coupling between DNA bending and base pair opening.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 7231-7235.	3.3	305
177	DNA Flexibility Under Control: The Jumna Algorithm and its Application to BZ Junctions. , 1988, , 189-206.		20
178	A Theoretical Study of the Sequence Specificity in Binding of Lexitropsins to B-DNA. Journal of Biomolecular Structure and Dynamics, 1987, 4, 833-843.	2.0	32
179	Theoretical studies on the interaction of proteins and nucleic acid. Biophysical Chemistry, 1986, 25, 201-213.	1.5	9
180	A General Approach to the Optimization of the Conformation of Ring Molecules with an Application to Valinomycin. Journal of Biomolecular Structure and Dynamics, 1986, 4, 443-462.	2.0	75

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181	The Flexibility of the Nucleic Acids: (I) â€œSIRâ€• a Novel Approach to the Variation of Polymer Geometry in Constrained Systems. Journal of Biomolecular Structure and Dynamics, 1986, 3, 967-987.	2.0	34
182	Binding of Non-Intercalating Antibiotics to B-DNA: A Theoretical Study Taking Into Account Nucleic Acid Flexibility. Journal of Biomolecular Structure and Dynamics, 1986, 3, 1155-1170.	2.0	34
183	The Flexibility of the Nucleic Acids: (II) The Calculation of Internal Energy and Applications to Mononucleotide Repeat DNA. Journal of Biomolecular Structure and Dynamics, 1986, 3, 989-1014.	2.0	165
184	The Flexibility of the Nucleic Acids: (III) The Interaction of an Aliphatic Diamine, Putrescine, with Flexible B-DNA. Journal of Biomolecular Structure and Dynamics, 1986, 3, 1015-1031.	2.0	22
185	Guanine and 7-methylguanine amino proton exchange rates as a function of buffer pK: implications for the exchange mechanism. Nucleic Acids Research, 1986, 14, 7083-92.	6.5	2
186	The Dependence of the Surface Electrostatic Potential of B-DNA on Environmental Factors. Journal of Biomolecular Structure and Dynamics, 1985, 2, 1021-1032.	2.0	101
187	The solvation contribution to the binding energy of DNA with non-intercalating antibiotics. Nucleic Acids Research, 1984, 12, 6559-6574.	6.5	38
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