

Richard Lavery

List of Publications by Year in descending order

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237
papers

13,981
citations

28736

57
h-index

27587

110
g-index

245
all docs

245
docs citations

245
times ranked

8611
citing authors

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

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19	Dynamics and recognition within a protein-DNA complex: a molecular dynamics study of the SKN-1/DNA interaction. <i>Nucleic Acids Research</i> , 2016, 44, 1440-1448.	6.5	53
20	Improving the treatment of coarse-grain electrostatics: CVCEL. <i>Journal of Chemical Physics</i> , 2015, 143, 243118.	1.2	5
21	Analyzing ion distributions around DNA: sequence-dependence of potassium ion distributions from microsecond molecular dynamics. <i>Nucleic Acids Research</i> , 2015, 43, 2412-2423.	6.5	97
22	Internal Normal Mode Analysis (iNMA) Applied to Protein Conformational Flexibility. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 5503-5512.	2.3	19
23	Analyzing ion distributions around DNA. <i>Nucleic Acids Research</i> , 2014, 42, 8138-8149.	6.5	95
24	¼ABC: a systematic microsecond molecular dynamics study of tetranucleotide sequence effects in B-DNA. <i>Nucleic Acids Research</i> , 2014, 42, 12272-12283.	6.5	186
25	Unraveling the sequence-dependent polymorphic behavior of d(CpC) steps in B-DNA. <i>Nucleic Acids Research</i> , 2014, 42, 11304-11320.	6.5	81
26	Significance of Molecular Dynamics Simulations for Life Sciences. <i>Israel Journal of Chemistry</i> , 2014, 54, 1042-1051.	1.0	38
27	Temperature Dependence of the DNA Double Helix at the Nanoscale: Structure, Elasticity, and Fluctuations. <i>Biophysical Journal</i> , 2013, 105, 1904-1914.	0.2	34
28	PaLaCe: A Coarse-Grain Protein Model for Studying Mechanical Properties. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 785-793.	2.3	48
29	A Protein Solvation Model Based on Residue Burial. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 2141-2144.	2.3	16
30	Arbitrary protein-protein docking targets biologically relevant interfaces. <i>BMC Biophysics</i> , 2012, 5, 7.	4.4	34
31	Exploring polymorphisms in B-DNA helical conformations. <i>Nucleic Acids Research</i> , 2012, 40, 10668-10678.	6.5	89
32	Coarse-grain Protein Models. <i>RSC Biomolecular Sciences</i> , 2012, , 219-248.	0.4	1
33	Multistep Drug Intercalation: Molecular Dynamics and Free Energy Studies of the Binding of Daunomycin to DNA. <i>Journal of the American Chemical Society</i> , 2012, 134, 8588-8596.	6.6	78
34	Towards a molecular view of transcriptional control. <i>Current Opinion in Structural Biology</i> , 2012, 22, 160-167.	2.6	24
35	Protein-DNA Recognition Triggered by a DNA Conformational Switch. <i>Angewandte Chemie - International Edition</i> , 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. <i>Nucleic Acids Research</i> , 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. <i>Nucleic Acids Research</i> , 2010, 38, 299-313.	6.5	349
38	Local and global effects of strong DNA bending induced during molecular dynamics simulations. <i>Nucleic Acids Research</i> , 2009, 37, 3766-3773.	6.5	78
39	Joint Evolutionary Trees: A Large-Scale Method To Predict Protein Interfaces Based on Sequence Sampling. <i>PLoS Computational Biology</i> , 2009, 5, e1000267.	1.5	79
40	Conformational analysis of nucleic acids revisited: Curves+. <i>Nucleic Acids Research</i> , 2009, 37, 5917-5929.	6.5	674
41	Modeling the Mechanical Response of Proteins to Anisotropic Deformation. <i>ChemPhysChem</i> , 2009, 10, 115-118.	1.0	21
42	Coarse-Grain Simulations of the R α -SNARE Fusion Protein in its Membrane Environment Detect Long-Lived Conformational Substates. <i>ChemPhysChem</i> , 2009, 10, 1548-1552.	1.0	30
43	Deforming DNA: From Physics to Biology. <i>ChemPhysChem</i> , 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. <i>International Journal of Quantum Chemistry</i> , 2009, 14, 21-34.	1.0	0
45	Molecular electrostatic potential of the b-dna helix. VII. effect of screening by monovalent cations. <i>International Journal of Quantum Chemistry</i> , 2009, 18, 323-330.	1.0	0
46	The molecular electrostatic potential of DNA: The effect of counteraction screening on various allomorphic forms. <i>International Journal of Quantum Chemistry</i> , 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. <i>Journal of the American Chemical Society</i> , 2009, 131, 9864-9865.	6.6	29
48	Protein-DNA binding specificity: a grid-enabled computational approach applied to single and multiple protein assemblies. <i>Physical Chemistry Chemical Physics</i> , 2009, 11, 10712.	1.3	13
49	Simulation Study of the Molecular Mechanism of Intercalation of the Anti-Cancer Drug Daunomycin into DNA. <i>Springer Series in Chemical Physics</i> , 2009, , 165-180.	0.2	0
50	Protein-DNA recognition: Breaking the combinatorial barrier. <i>Computer Physics Communications</i> , 2008, 179, 112-119.	3.0	13
51	Interactions between Neuronal Fusion Proteins Explored by Molecular Dynamics. <i>Biophysical Journal</i> , 2008, 94, 3436-3446.	0.2	26
52	Identification of Protein Interaction Partners and Protein-Protein Interaction Sites. <i>Journal of Molecular Biology</i> , 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. <i>Journal of the American Chemical Society</i> , 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: The Wild-Type Protein Is More Rigid Than Two Site-Specific Mutants. <i>Biochemistry</i> , 2007, 46, 14960-14968.	1.2	54
56	Locating the active sites of enzymes using mechanical properties. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 350-359.	1.5	96
57	Theory and simulation. <i>Current Opinion in Structural Biology</i> , 2007, 17, 147-148.	2.6	1
58	Protein mechanics: a route from structure to function. <i>Journal of Biosciences</i> , 2007, 32, 891-898.	0.5	73
59	Investigating the Local Flexibility of Functional Residues in Hemoproteins. <i>Biophysical Journal</i> , 2006, 90, 2706-2717.	0.2	92
60	Dynamics and Stability of E-Cadherin Dimers. <i>Biophysical Journal</i> , 2006, 91, 3964-3971.	0.2	29
61	ARTIST: An activated method in internal coordinate space for sampling protein energy landscapes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 967-975.	1.5	14
62	Kinking Occurs during Molecular Dynamics Simulations of Small DNA Minicircles. <i>Structure</i> , 2006, 14, 1527-1534.	1.6	161
63	Modeling DNA Deformation. , 2006, , 169-210.		2
64	Wringing Out DNA. <i>Physical Review Letters</i> , 2006, 96, 178102.	2.9	144
65	Course 1 DNA structure, dynamics and recognition. <i>Les Houches Summer School Proceedings</i> , 2005, 82, 1-40.	0.2	0
66	Recognizing DNA. <i>Quarterly Reviews of Biophysics</i> , 2005, 38, 339-344.	2.4	28
67	Macromolecular recognition. <i>Current Opinion in Structural Biology</i> , 2005, 15, 171-175.	2.6	60
68	DNA/protein modeling. , 2005, , .		0
69	Non-additivity in protein-DNA binding. <i>Bioinformatics</i> , 2005, 21, 2254-2263.	1.8	52
70	Exciton States of Dynamic DNA Double Helices: Alternating dCdG Sequences. <i>Journal of Physical Chemistry B</i> , 2005, 109, 16109-16118.	1.2	71
71	Cadherin Mechanics and Complexation: The Importance of Calcium Binding. <i>Biophysical Journal</i> , 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. <i>Biophysical Journal</i> , 2005, 89, 3721-3740.	0.2	216

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73	Looking into DNA recognition: zinc finger binding specificity. <i>Nucleic Acids Research</i> , 2004, 32, 6673-6682.	6.5	33
74	Analyzing Protein-DNA Recognition Mechanisms. <i>Structure</i> , 2004, 12, 113-122.	1.6	108
75	Myosin flexibility: Structural domains and collective vibrations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 384-393.	1.5	50
76	Probing Protein Mechanics: Residue-Level Properties and Their Use in Defining Domains. <i>Biophysical Journal</i> , 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. <i>Biophysical Journal</i> , 2004, 87, 3799-3813.	0.2	245
78	Motifs in nucleic acids: Molecular mechanics restraints for base pairing and base stacking. <i>Journal of Computational Chemistry</i> , 2003, 24, 1-9.	1.5	27
79	Docking macromolecules with flexible segments. <i>Journal of Computational Chemistry</i> , 2003, 24, 1910-1920.	1.5	32
80	Nucleic Acid Base Pair Dynamics: The Impact of Sequence and Structure Using Free-Energy Calculations. <i>Journal of the American Chemical Society</i> , 2003, 125, 4998-4999.	6.6	46
81	Influence of Conformational Dynamics on the Exciton States of DNA Oligomers. <i>Journal of Physical Chemistry B</i> , 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. <i>Nucleic Acids Research</i> , 2003, 31, 1434-1443.	6.5	153
83	Structure and mechanics of single biomolecules: experiment and simulation. <i>Journal of Physics Condensed Matter</i> , 2002, 14, R383-R414.	0.7	88
84	alpha/gamma Transitions in the B-DNA backbone. <i>Nucleic Acids Research</i> , 2002, 30, 5398-5406.	6.5	116
85	Base Flipping in DNA: Pathways and Energetics Studied with Molecular Dynamic Simulations. <i>Journal of the American Chemical Society</i> , 2002, 124, 7272-7273.	6.6	84
86	Simulations of Nucleic Acids and Their Complexes. <i>Accounts of Chemical Research</i> , 2002, 35, 350-357.	7.6	116
87	Energetic and Conformational Aspects of A:T Base-Pair Opening within the DNA Double Helix. <i>ChemPhysChem</i> , 2001, 2, 673-677.	1.0	42
88	Modeling multi-component protein-DNA complexes: the role of bending and dimerization in the complex of p53 dimers with DNA. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 233-243.	1.0	18
89	High-speed Molecular Mechanics Searches for Optimal DNA Interaction Sites. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2001, 4, 707-717.	0.6	3
90	ADAPT: A molecular mechanics approach for studying the structural properties of long DNA sequences. <i>Biopolymers</i> , 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: 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 "Stereochemistry of polypeptide chain conformations", 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 Watson-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 Abasic Site. Journal of Biomolecular Structure and Dynamics, 1999, 17, 245-257.	2.0	9
105	Le jokari moléculaire. 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. <i>Biophysical Journal</i> , 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. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998, 16, 593-604.	2.0	23
113	Sequence-Dependent Dynamics of TATA-Box Binding Sites. <i>Biophysical Journal</i> , 1998, 75, 372-381.	0.2	62
114	A Model for Parallel Triple Helix Formation by Rec A: Single-Strand Association with a Homologous Duplex via the Minor Groove. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998, 16, 535-546.	2.0	22
115	Stretched and overwound DNA forms a Pauling-like structure with exposed bases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 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. <i>Journal of Biomolecular Structure and Dynamics</i> , 1997, 14, 703-714.	2.0	9
117	Local DNA stretching mimics the distortion caused by the TATA box-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 2993-2998.	3.3	71
118	Conformational Properties of the TATA-Box Binding Sequence of DNA. <i>Journal of Biomolecular Structure and Dynamics</i> , 1997, 14, 757-765.	2.0	44
119	Unusual DNA conformations. <i>Current Opinion in Structural Biology</i> , 1997, 7, 348-354.	2.6	38
120	Modelling base pair opening: the role of helical twist. <i>Computational and Theoretical Chemistry</i> , 1997, 398-399, 473-482.	1.5	33
121	Internal coordinate modeling of DNA: Force field comparisons. <i>Journal of Computational Chemistry</i> , 1997, 18, 1043-1055.	1.5	40
122	Collective-variable Monte Carlo simulation of DNA. <i>Journal of Computational Chemistry</i> , 1997, 18, 2001-2011.	1.5	13
123	DNA: An Extensible Molecule. <i>Science</i> , 1996, 271, 792-794.	6.0	936
124	Poisson-Boltzmann calculations for nucleic acids and nucleic acids complexes. <i>Chemical Physics</i> , 1996, 204, 263-269.	0.9	21
125	DNA structural forms. <i>Quarterly Reviews of Biophysics</i> , 1996, 29, 309-368.	2.4	97
126	Molecular Modelling of (A4T4NN) _n and (T4A4NN) _n : Sequence Elements Responsible for Curvature. <i>Nucleic Acids Research</i> , 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 " 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 α -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 α -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 α -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 α -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. <i>Journal of Computational Chemistry</i> , 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. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 413-425.	1.5	17
147	An analysis of the conformational paths of citrate synthase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 16, 393-407.	1.5	12
148	Symmetry reduction in homopolymeric DNA: implications for DNA fine structure. <i>Computational and Theoretical Chemistry</i> , 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. <i>Biochemistry</i> , 1993, 32, 2098-2103.	1.2	57
150	BI-BII transitions in B-DNA. <i>Nucleic Acids Research</i> , 1993, 21, 561-568.	6.5	151
151	Conformations of DNA Duplexes Containing 8-Oxoguanine. <i>Journal of Biomolecular Structure and Dynamics</i> , 1993, 11, 293-301.	2.0	9
152	A comprehensive classification of nucleic acid structural families based on strand direction and base pairing. <i>Nucleic Acids Research</i> , 1992, 20, 5011-5016.	6.5	31
153	The fine structure of two DNA dodecamers containing the cAMP responsive element sequence and its inverse. <i>Journal of Molecular Biology</i> , 1992, 227, 852-875.	2.0	52
154	Conformational sub-states in B-DNA. <i>Journal of Molecular Biology</i> , 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. <i>Journal of Molecular Graphics</i> , 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 . <i>Journal of Molecular Graphics</i> , 1992, 10, 41-42.	1.7	0
157	A computational and experimental study of the bending induced at a double-triple helix junction. <i>Biophysical Chemistry</i> , 1992, 45, 143-152.	1.5	34
158	DNA flexibility as a function of allomorphic conformation and of base sequence. <i>Biopolymers</i> , 1992, 32, 1077-1103.	1.2	24
159	Strand orientation of [±]-oligodeoxynucleotides in triple helix structures: Dependence on nucleotide sequence. <i>Journal of Molecular Recognition</i> , 1992, 5, 93-98.	1.1	8
160	Evidence for the stochastic nature of base pair opening in DNA: a Brownian dynamics simulation. <i>Journal of the American Chemical Society</i> , 1991, 113, 2490-2493.	6.6	49
161	A New Approach to the Rapid Determination of Protein Side Chain Conformations. <i>Journal of Biomolecular Structure and Dynamics</i> , 1991, 8, 1267-1289.	2.0	320
162	Theoretical Study of Ethidium Intercalation in Triple-Stranded DNA and at Triplex-Duplex Junctions. <i>Journal of Biomolecular Structure and Dynamics</i> , 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: "Curves," 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: "Curves," 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
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