

Wayne K Dawson

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

1,328
citations

623734

14
h-index

361022

35
g-index

51
all docs

51
docs citations

51
times ranked

1535
citing authors

#	ARTICLE	IF	CITATIONS
1	Developing an Updated Strategy for Estimating the Free-Energy Parameters in RNA Duplexes. International Journal of Molecular Sciences, 2021, 22, 9708.	4.1	3
2	Free energy-based model of CTCF-mediated chromatin looping in the human genome. Methods, 2020, 181-182, 35-51.	3.8	2
3	Chromatin: A Semi-Structured Polymer. , 2019, , 288-307.		1
4	One protein to rule them all: The role of CCCTC-binding factor in shaping human genome in health and disease. Seminars in Cell and Developmental Biology, 2019, 90, 114-127.	5.0	23
5	RNA structure interactions and ribonucleoprotein processes of the influenza A virus. Briefings in Functional Genomics, 2018, 17, 402-414.	2.7	10
6	OUP accepted manuscript. Briefings in Functional Genomics, 2018, 17, 415-427.	2.7	23
7	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
8	SuperRNAalign: a new tool for flexible superposition of homologous RNA structures and inference of accurate structure-based sequence alignments. Nucleic Acids Research, 2017, 45, e150-e150.	14.5	9
9	Electron Transport in a Dioxygenase-Ferredoxin Complex: Long Range Charge Coupling between the Rieske and Non-Heme Iron Center. PLoS ONE, 2016, 11, e0162031.	2.5	6
10	Coarse-grained modeling of RNA 3D structure. Methods, 2016, 103, 138-156.	3.8	42
11	SimRNA: a coarse-grained method for RNA folding simulations and 3D structure prediction. Nucleic Acids Research, 2016, 44, e63-e63.	14.5	281
12	SimRNAweb: a web server for RNA 3D structure modeling with optional restraints. Nucleic Acids Research, 2016, 44, W315-W319.	14.5	112
13	Modeling of Protein-RNA Complex Structures Using Computational Docking Methods. Methods in Molecular Biology, 2016, 1414, 353-372.	0.9	9
14	Computational modeling of RNA 3D structures and interactions. Current Opinion in Structural Biology, 2016, 37, 22-28.	5.7	43
15	Modeling of ribonucleic acid-ligand interactions. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2015, 5, 425-439.	14.6	12
16	A new entropy model for RNA: part IV, The Minimum Free Energy (mFE) and the thermodynamically most-probable folding pathway (TMPFP). Journal of Nucleic Acids Investigation, 2015, 6, .	0.8	1
17	A new entropy model for RNA: part V, Incorporating the Flory-Huggins model in structure prediction and folding. Journal of Nucleic Acids Investigation, 2015, 6, .	0.8	1
18	NPDock: a web server for protein-nucleic acid docking. Nucleic Acids Research, 2015, 43, W425-W430.	14.5	180

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19	A magnetic origin of cuprate superconductivity? A MaxEnt- $\hat{1}/4$ SR view. International Journal of Modern Physics B, 2015, 29, 1542026.	2.0	1
20	Computational modeling of RNA 3D structures, with the aid of experimental restraints. RNA Biology, 2014, 11, 522-536.	3.1	39
21	A new entropy model for RNA: part III. Is the folding free energy landscape of RNA funnel shaped?. Journal of Nucleic Acids Investigation, 2014, 5, .	0.8	11
22	A new entropy model for RNA: part II. Persistence-related entropic contributions to RNA secondary structure free energy calculations. Journal of Nucleic Acids Investigation, 2013, 4, 2.	0.8	3
23	A new entropy model for RNA: part I. A critique of the standard Jacobson-Stockmayer model applied to multiple cross links. Journal of Nucleic Acids Investigation, 2012, 3, 3.	0.8	2
24	A new entropy model for RNA: part I. A critique of the standard Jacobson-Stockmayer model applied to multiple cross links. Journal of Nucleic Acids Investigation, 2012, 3, 3.	0.8	2
25	Home Educating in an Extended Family Culture and Aging Society May Fare Best during a Pandemic. PLoS ONE, 2009, 4, e7221.	2.5	1
26	Modeling the Chain Entropy of Biopolymers: Unifying Two Different Random Walk Models under One Framework. Journal of Computer Science and Systems Biology, 2009, 02, .	0.0	10
27	A Consensus Approach for Intrinsic Disorder Analysis for Heat Shock Protein Family. Biotechnology, 2009, 8, 306-315.	0.1	0
28	2P-068 Dynamics of amino acids in the electron transfer pathways between Oxygenase and Ferredoxin components in Rieske oxygenase system(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S85.	0.1	0
29	Prediction of RNA Pseudoknots Using Heuristic Modeling with Mapping and Sequential Folding. PLoS ONE, 2007, 2, e905.	2.5	58
30	A method for finding optimal RNA secondary structures using a new entropy model (vsfold). Nucleosides, Nucleotides and Nucleic Acids, 2006, 25, 171-189.	1.1	24
31	A Physical Origin for Functional Domain Structure in Nucleic Acids as Evidenced by Cross-linking Entropy: I. Journal of Theoretical Biology, 2001, 213, 359-386.	1.7	9
32	A Physical Origin for Functional Domain Structure in Nucleic Acids as Evidenced by Cross-linking Entropy: II. Journal of Theoretical Biology, 2001, 213, 387-412.	1.7	9
33	Mean Free Energy Topology for Nucleotide Sequences of Varying Composition Based on Secondary Structure Calculations. Journal of Theoretical Biology, 1999, 201, 113-140.	1.7	9
34	Theoretical model for electron emission from the coating-layer on the ferroelectric disk. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 1997, 387, 315-318.	1.6	1
35	Muonium quadrupole interactions in $\hat{1}\pm$ -quartz under uniaxial pressure: room temperature anisotropy. Physics Letters, Section A: General, Atomic and Solid State Physics, 1996, 212, 290-298.	2.1	2
36	Muonium quadrupole interactions in $\hat{1}\pm$ -quartz at elevated temperatures. Physics Letters, Section A: General, Atomic and Solid State Physics, 1995, 198, 452-458.	2.1	2

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37	Redox reaction of H_2O in water determined by the chemical shift. <i>Hyperfine Interactions</i> , 1994, 87, 929-934.	0.5	1
38	Muon and hydrogen bonding, and magnetic resonance in pure and doped $\text{YBa}_2\text{Cu}_3\text{O}_{7-x}$. <i>Hyperfine Interactions</i> , 1994, 86, 519-524.	0.5	3
39	A study of diamagnetic muon bonding in α -quartz using muon spin resonance. <i>Hyperfine Interactions</i> , 1994, 86, 753-759.	0.5	2
40	Dynamics of muons in the ferroelectric material KDP. <i>Hyperfine Interactions</i> , 1994, 85, 85-90.	0.5	2
41	Magnetic frustration, muon probing, and hydrogen bonding in $\text{RBa}_2\text{Cu}_3\text{O}_y$. <i>Physica C: Superconductivity and Its Applications</i> , 1991, 185-189, 1221-1222.	1.2	4
42	Transverse and zero-field μSR investigation of magnetism and superconductivity in $(\text{Y}_{1-x}\text{Pr}_x)\text{Ba}_2\text{Cu}_3\text{O}_7$. <i>Hyperfine Interactions</i> , 1991, 63, 213-218.	0.5	10
43	Magnetism and candidate muon-probe sites in $\text{RBa}_2\text{Cu}_3\text{O}_y$. <i>Hyperfine Interactions</i> , 1991, 63, 219-226.	0.5	17
44	Zero-field muon spin relaxation in $(\text{Y}_{1-x}\text{Pr}_x)\text{Ba}_2\text{Cu}_3\text{O}_y$. <i>Journal of Applied Physics</i> , 1991, 69, 5385-5387.	2.5	5
45	Muon bonding and antiferromagnetism in the 123 cuprates. <i>Physica B: Condensed Matter</i> , 1990, 163, 453-457.	2.7	10
46	μSR investigation of magnetism and superconductivity in $(\text{Y}_{1-x}\text{Pr}_x)\text{Ba}_2\text{Cu}_3\text{O}_7$. <i>Physica B: Condensed Matter</i> , 1990, 163, 675-677.	2.7	8
47	Magnetic ordering in $(\text{Y}_{1-x}\text{Pr}_x)\text{Ba}_2\text{Cu}_3\text{O}_7$ as observed by muon-spin relaxation. <i>Physical Review B</i> , 1990, 41, 4801-4804.	3.2	92
48	Muon spin relaxation study of magnetism in $\text{ErBa}_2\text{Cu}_3\text{O}_{6.2}$. <i>Journal of Applied Physics</i> , 1990, 67, 5055-5057.	2.5	9
49	Magnetic ordering in $(\text{Y}_{1-x}\text{Pr}_x)\text{Ba}_2\text{Cu}_3\text{O}_7$ as evidenced by muon spin relaxation. <i>Journal of Applied Physics</i> , 1990, 67, 5061-5063.	2.5	21
50	Candidate muon probe sites in oxide superconductors. <i>Journal of Applied Physics</i> , 1988, 64, 5809-5811.	2.5	44