

# David Mj Lilley

## List of Publications by Year in descending order

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126  
papers

8,637  
citations

34016

52  
h-index

45213

90  
g-index

126  
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126  
docs citations

126  
times ranked

4751  
citing authors

#	ARTICLE	IF	CITATIONS
1	Human ANKLE1 Is a Nuclease Specific for Branched DNA. <i>Journal of Molecular Biology</i> , 2020, 432, 5825-5834.	2.0	12
2	Structure-guided design of a high-affinity ligand for a riboswitch. <i>Rna</i> , 2019, 25, 423-430.	1.6	10
3	The role of RNA structure in translational regulation by L7Ae protein in archaea. <i>Rna</i> , 2019, 25, 60-69.	1.6	7
4	Biochemical and Structural Properties of Fungal Holliday Junction-Resolving Enzymes. <i>Methods in Enzymology</i> , 2018, 600, 543-568.	0.4	1
5	Control of box C/D snoRNP assembly by N <sup>6</sup> -methylation of adenine. <i>EMBO Reports</i> , 2017, 18, 1631-1645.	2.0	51
6	How RNA acts as a nuclease: some mechanistic comparisons in the nucleolytic ribozymes. <i>Biochemical Society Transactions</i> , 2017, 45, 683-691.	1.6	28
7	The Structure of the Guanidine-II Riboswitch. <i>Cell Chemical Biology</i> , 2017, 24, 695-702.e2.	2.5	55
8	Sequence determinants of the folding properties of box C/D kink-turns in RNA. <i>Rna</i> , 2017, 23, 1927-1935.	1.6	8
9	Structure of the Guanidine III Riboswitch. <i>Cell Chemical Biology</i> , 2017, 24, 1407-1415.e2.	2.5	47
10	Crystal Structures of Cyanine Fluorophores Stacked onto the End of Double-Stranded RNA. <i>Biophysical Journal</i> , 2017, 113, 2336-2343.	0.2	8
11	The Kink Turn, a Key Architectural Element in RNA Structure. <i>Journal of Molecular Biology</i> , 2016, 428, 790-801.	2.0	43
12	RNA catalysis is that it?. <i>Rna</i> , 2015, 21, 534-537.	1.6	21
13	GEN1 from a Thermophilic Fungus Is Functionally Closely Similar to Non-Eukaryotic Junction-Resolving Enzymes. <i>Journal of Molecular Biology</i> , 2014, 426, 3946-3959.	2.0	18
14	Structure of a rare non-standard sequence k-turn bound by L7Ae protein. <i>Nucleic Acids Research</i> , 2014, 42, 4734-4740.	6.5	15
15	The K-turn motif in riboswitches and other RNA species. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 995-1004.	0.9	30
16	The Importance of the N-Terminus of T7 Endonuclease I in the Interaction with DNA Junctions. <i>Journal of Molecular Biology</i> , 2013, 425, 395-410.	2.0	13
17	A Mechanistic Comparison of the Varkud Satellite and Hairpin Ribozymes. <i>Progress in Molecular Biology and Translational Science</i> , 2013, 120, 93-121.	0.9	5
18	The functional exchangeability of pk- and k-turns in RNA structure. <i>RNA Biology</i> , 2013, 10, 445-452.	1.5	9

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19	Synthesis of novel tetrazole C5-linked C0- and C2-ribonucleoside phosphoramidites using MePOM and POM groups for probing RNA catalysis. <i>Tetrahedron Letters</i> , 2012, 53, 5891-5894.	0.7	12
20	Identification of KIAA1018/FAN1, a DNA Repair Nuclease Recruited to DNA Damage by Monoubiquitinated FANCD2. <i>Cell</i> , 2010, 142, 65-76.	13.5	284
21	Comparative Gel Electrophoresis Analysis of Helical Junctions in RNA. <i>Methods in Enzymology</i> , 2009, 469, 143-157.	0.4	6
22	The Structure and Folding of Branched RNA Analyzed by Fluorescence Resonance Energy Transfer. <i>Methods in Enzymology</i> , 2009, 469, 159-187.	0.4	13
23	Coordination of Structure-Specific Nucleases by Human SLX4/BTBD12 Is Required for DNA Repair. <i>Molecular Cell</i> , 2009, 35, 116-127.	4.5	300
24	Four-Way Helical Junctions in DNA Molecules. <i>The IMA Volumes in Mathematics and Its Applications</i> , 2009, , 213-224.	0.5	3
25	New insight into the recognition of branched DNA structure by junction-resolving enzymes. <i>Current Opinion in Structural Biology</i> , 2008, 18, 86-95.	2.6	71
26	The Complete VS Ribozyme in Solution Studied by Small-Angle X-Ray Scattering. <i>Structure</i> , 2008, 16, 1357-1367.	1.6	78
27	The Importance of GÂ:A Hydrogen Bonding in the Metal Ion- and Protein-induced Folding of a Kink Turn RNA. <i>Journal of Molecular Biology</i> , 2008, 381, 431-442.	2.0	39
28	RNA folding and the origins of catalytic activity in the hairpin ribozyme. <i>Blood Cells, Molecules, and Diseases</i> , 2007, 38, 8-14.	0.6	23
29	A chemo-genetic approach for the study of nucleobase participation in nucleolytic ribozymes. <i>Biological Chemistry</i> , 2007, 388, 699-704.	1.2	9
30	Structural Recognition between a Four-way DNA Junction and a Resolving Enzyme. <i>Journal of Molecular Biology</i> , 2006, 359, 1261-1276.	2.0	20
31	Folding of the Adenine Riboswitch. <i>Chemistry and Biology</i> , 2006, 13, 857-868.	6.2	255
32	Mass Determination of Phosphoramidites. , 2006, Chapter 10, 10.11.1-10.11.16.		2
33	Nucleobase catalysis in the hairpin ribozyme. <i>Rna</i> , 2006, 12, 980-987.	1.6	61
34	Accurate molecular weight measurements of nucleoside phosphoramidites: a suitable matrix of mass spectrometry. <i>Tetrahedron</i> , 2005, 61, 4689-4699.	1.0	18
35	Synthesis of novel C4-linked imidazole ribonucleoside phosphoramidites for probing general acid and base catalysis in ribozyme. <i>Tetrahedron</i> , 2005, 61, 11976-11985.	1.0	15
36	Stereospecific Effects Determine the Structure of a Four-Way DNA Junction. <i>Chemistry and Biology</i> , 2005, 12, 217-228.	6.2	18

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37	Structure, folding and mechanisms of ribozymes. <i>Current Opinion in Structural Biology</i> , 2005, 15, 313-323.	2.6	143
38	Induced fit of RNA on binding the L7Ae protein to the kink-turn motif. <i>Rna</i> , 2005, 11, 1192-1200.	1.6	97
39	Folding of the natural hammerhead ribozyme is enhanced by interaction of auxiliary elements. <i>Rna</i> , 2004, 10, 880-888.	1.6	138
40	The kink-turn motif in RNA is dimorphic, and metal ion-dependent. <i>Rna</i> , 2004, 10, 254-264.	1.6	140
41	Synthesis of C4-linked imidazole ribonucleoside phosphoramidite with pivaloyloxymethyl (POM) group. <i>Tetrahedron Letters</i> , 2004, 45, 2657-2661.	0.7	25
42	Vesicle Encapsulation Studies Reveal that Single Molecule Ribozyme Heterogeneities Are Intrinsic. <i>Biophysical Journal</i> , 2004, 87, 2798-2806.	0.2	189
43	Conformational Flexibility of Four-way Junctions in RNA. <i>Journal of Molecular Biology</i> , 2004, 336, 69-79.	2.0	86
44	Exploring Rare Conformational Species and Ionic Effects in DNA Holliday Junctions Using Single-molecule Spectroscopy. <i>Journal of Molecular Biology</i> , 2004, 341, 739-751.	2.0	111
45	Electrostatic Interactions and the Folding of the Four-way DNA Junction: Analysis by Selective Methyl Phosphonate Substitution. <i>Journal of Molecular Biology</i> , 2004, 343, 851-864.	2.0	17
46	The origins of RNA catalysis in ribozymes. <i>Trends in Biochemical Sciences</i> , 2003, 28, 495-501.	3.7	99
47	Structural dynamics of individual Holliday junctions. <i>Nature Structural Biology</i> , 2003, 10, 93-97.	9.7	311
48	Metal Ion Binding in the Active Site of the Junction-resolving Enzyme T7 Endonuclease I in the Presence and in the Absence of DNA. <i>Journal of Molecular Biology</i> , 2003, 333, 59-73.	2.0	9
49	The dynamic nature of the four-way junction of the hepatitis C virus IRES. <i>Rna</i> , 2003, 9, 809-820.	1.6	31
50	Holliday Junction Resolution Is Modulated by Archaeal Chromatin Components in Vitro. <i>Journal of Biological Chemistry</i> , 2002, 277, 2992-2996.	1.6	20
51	Functional Group Requirements in the Probable Active Site of the VS Ribozyme. <i>Journal of Molecular Biology</i> , 2002, 323, 23-34.	2.0	64
52	Folding and catalysis by the VS ribozyme. <i>Biochimie</i> , 2002, 84, 889-896.	1.3	10
53	Metal ion binding and the folding of the hairpin ribozyme. <i>Rna</i> , 2002, 8, 587-600.	1.6	49
54	The active site of the junction-resolving enzyme T7 endonuclease I 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 2001, 307, 1145-1158.	2.0	30

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55	The A730 loop is an important component of the active site of the VS ribozyme 1 Edited by J. Karn. Journal of Molecular Biology, 2001, 312, 663-674.	2.0	73
56	Distortion of DNA junctions imposed by the binding of resolving enzymes: a fluorescence study. Journal of Molecular Biology, 2001, 313, 751-764.	2.0	36
57	Structure, folding and activity of the VS ribozyme: importance of the 2-3-6 helical junction. EMBO Journal, 2001, 20, 1415-1424.	3.5	83
58	Crystal structure of the Holliday junction resolving enzyme T7 endonuclease I. Nature Structural Biology, 2001, 8, 62-67.	9.7	84
59	[23] Analysis of global conformation of branched RNA species using electrophoresis and fluorescence. Methods in Enzymology, 2000, 317, 368-393.	0.4	16
60	Fluorescence resonance energy transfer as a structural tool for nucleic acids. Current Opinion in Chemical Biology, 2000, 4, 507-517.	2.8	133
61	The folding of the hairpin ribozyme: Dependence on the loops and the junction. Rna, 2000, 6, 1833-1846.	1.6	47
62	Extensive central disruption of a four-way junction on binding CCE1 resolving enzyme 1 Edited by M. Yaniv. Journal of Molecular Biology, 2000, 296, 421-433.	2.0	47
63	Generation of Superhelical Torsion by ATP-Dependent Chromatin Remodeling Activities. Cell, 2000, 103, 1133-1142.	13.5	241
64	The influence of junction conformation on RNA cleavage by the hairpin ribozyme in its natural junction form. Rna, 1999, 5, 180-187.	1.6	26
65	The Holliday junction is finally seen with crystal clarity. , 1999, 6, 897-899.		24
66	RNA folding and catalysis. , 1999, 106, 95-102.		5
67	Structure, folding and catalysis of the small nucleolytic ribozymes. Current Opinion in Structural Biology, 1999, 9, 330-338.	2.6	78
68	Folding and catalysis by the hairpin ribozyme. FEBS Letters, 1999, 452, 26-30.	1.3	10
69	Binding of U1A protein to the 3' untranslated region of its pre-mRNA 1 Edited by J. Karn. Journal of Molecular Biology, 1999, 288, 585-594.	2.0	18
70	Folding of the Hairpin Ribozyme in Its Natural Conformation Achieves Close Physical Proximity of the Loops. Molecular Cell, 1998, 1, 873-881.	4.5	156
71	Structural recognition and distortion by the DNA junction-resolving enzyme RusA. Journal of Molecular Biology, 1998, 278, 117-133.	2.0	63
72	Global structure of four-way RNA junctions studied using fluorescence resonance energy transfer. Rna, 1998, 4, 719-728.	1.6	58

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73	111 A Holliday junction endonuclease from fission yeast. <i>Biochemical Society Transactions</i> , 1997, 25, S645-S645.	1.6	0
74	186 The interaction of HMG-box proteins with the four-way DNA junction. <i>Biochemical Society Transactions</i> , 1997, 25, S647-S647.	1.6	2
75	The resolving enzyme CCE1 of yeast opens the structure of the four-way DNA junction 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 1997, 266, 122-134.	2.0	88
76	Recognition and manipulation of branched DNA structure by junction-resolving enzymes 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1997, 269, 647-664.	2.0	101
77	Severe axial bending of RNA induced by the U1A binding element present in the 3' untranslated region of the U1A mRNA. <i>Journal of Molecular Biology</i> , 1997, 273, 84-92.	2.0	16
78	The crystal structure of a parallel-stranded guanine tetraplex at 0.95 Å resolution. <i>Journal of Molecular Biology</i> , 1997, 273, 171-182.	2.0	423
79	The junction-resolving enzyme T7 endonuclease I: quaternary structure and interaction with DNA. <i>Journal of Molecular Biology</i> , 1997, 270, 169-178.	2.0	43
80	Not such a bad book. <i>Nature</i> , 1997, 385, 672-672.	13.7	0
81	Near-simultaneous DNA cleavage by the subunits of the junction-resolving enzyme T4 endonuclease VII. <i>EMBO Journal</i> , 1997, 16, 2528-2534.	3.5	45
82	Site-specific recombination caught in the act. <i>Chemistry and Biology</i> , 1997, 4, 717-720.	6.2	7
83	Nucleic acid structure and recognition. <i>Biophysical Chemistry</i> , 1997, 68, 53-62.	1.5	10
84	A Nomenclature of Junctions and Branchpoints in Nucleic Acids. Recommendations 1994. <i>Journal of Molecular Biology</i> , 1996, 255, 554-555.	2.0	6
85	The Structure-selectivity and Sequence-preference of the Junction-resolving Enzyme CCE1 of <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1996, 257, 330-341.	2.0	97
86	T4 Endonuclease VII Selects and Alters the Structure of the Four-way DNA Junction; Binding of a Resolution-defective Mutant Enzyme. <i>Journal of Molecular Biology</i> , 1996, 260, 678-696.	2.0	81
87	A critical junction for RuvA. <i>Nature Structural Biology</i> , 1996, 3, 984-986.	9.7	2
88	Effect of Flanking Sequences on the Right- to Left- Handed Transition of a (dA-dT) <sub>n</sub> Tract in Supercoiled DNA. <i>Journal of Biomolecular Structure and Dynamics</i> , 1996, 13, 1007-1014.	2.0	6
89	T4 Endonuclease VII. <i>Journal of Biological Chemistry</i> , 1996, 271, 33148-33155.	1.6	46
90	Ionic interactions and the global conformations of the hammerhead ribozyme. <i>Nature Structural Biology</i> , 1995, 2, 45-55.	9.7	137

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91	The global folding of four-way helical junctions in RNA, including that in U1 snRNA. <i>Cell</i> , 1995, 83, 1027-1036.	13.5	80
92	Binding of the Junction-resolving Enzyme Bacteriophage T7 Endonuclease I to DNA: Separation of Binding and Catalysis by Mutation. <i>Journal of Molecular Biology</i> , 1995, 246, 95-107.	2.0	69
93	Two Inequivalent Folding Isomers of the Three-way DNA Junction with Unpaired Bases: Sequence-dependence of the Folded Conformation. <i>Journal of Molecular Biology</i> , 1995, 251, 507-519.	2.0	41
94	The Modular Character of a DNA Junction-resolving Enzyme: A Zinc-binding Motif in Bacteriophage T4 Endonuclease VII. <i>Journal of Molecular Biology</i> , 1995, 252, 596-610.	2.0	31
95	Mutational analysis of the DNA binding domain A of chromosomal protein HMG1. <i>Nucleic Acids Research</i> , 1994, 22, 285-292.	6.5	65
96	Large-scale opening of A+T rich regions within supercoiled DNA molecules is suppressed by salt. <i>Nucleic Acids Research</i> , 1994, 22, 2042-2050.	6.5	33
97	Structure of Four-way DNA Junctions containing a Nick in One Strand. <i>Journal of Molecular Biology</i> , 1994, 238, 62-74.	2.0	24
98	Solution Structure of a Parallel-stranded Tetraplex Formed by d(TG4T) in the Presence of Sodium Ions by Nuclear Magnetic Resonance Spectroscopy. <i>Journal of Molecular Biology</i> , 1994, 243, 458-471.	2.0	143
99	T4 Endonuclease VII Cleaves DNA Containing a Cisplatin Adduct. <i>Journal of Molecular Biology</i> , 1993, 233, 77-85.	2.0	34
100	Structures of bulged three-way DNA junctions. <i>Nucleic Acids Research</i> , 1993, 21, 4548-4555.	6.5	63
101	[8] Supercoiled DNA and cruciform structures. <i>Methods in Enzymology</i> , 1992, 211, 158-180.	0.4	55
102	Retinoblastoma susceptibility genes contain 5' sequences with a high propensity to form guanine-tetrad structures. <i>Nucleic Acids Research</i> , 1992, 20, 49-53.	6.5	118
103	[5] Two-dimensional gel electrophoresis of circular DNA topoisomers. <i>Methods in Enzymology</i> , 1992, 212, 105-120.	0.4	49
104	[7] Probes of DNA structure. <i>Methods in Enzymology</i> , 1992, 212, 133-139.	0.4	25
105	Gel Electrophoresis and the Structure of RNA Molecules. <i>Biotechnology and Genetic Engineering Reviews</i> , 1992, 10, 379-402.	2.4	8
106	Kinking of RNA helices by bulged bases, and the structure of the human immunodeficiency virus transactivator response element. <i>Journal of Molecular Biology</i> , 1992, 226, 305-310.	2.0	66
107	Helix opening transitions in supercoiled DNA. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1992, 1131, 1-15.	2.4	39
108	Effects of base mismatches on the structure of the four-way DNA junction. <i>Journal of Molecular Biology</i> , 1991, 221, 147-161.	2.0	41

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109	Model for the interaction of DNA junctions and resolving enzymes. <i>Journal of Molecular Biology</i> , 1991, 221, 1191-1207.	2.0	93
110	Structural alteration in alternating adenine-thymine sequences in positively supercoiled DNA. <i>Journal of Molecular Biology</i> , 1991, 219, 145-149.	2.0	24
111	The tertiary structure of the four-way DNA junction affords protection against DNase I Cleavage. <i>Nucleic Acids Research</i> , 1990, 18, 2599-2606.	6.5	46
112	The stereochemistry of a four-way DNA junction: a theoretical study. <i>Nucleic Acids Research</i> , 1990, 18, 2671-2683.	6.5	150
113	The contrasting structures of mismatched DNA sequences containing looped-out bases (bulges) and multiple mismatches (bubbles). <i>Nucleic Acids Research</i> , 1989, 17, 6821-6840.	6.5	200
114	Single base mismatches in DNA long- and short-range structure probed by analysis of axis trajectory and local chemical reactivity. <i>Journal of Molecular Biology</i> , 1989, 209, 583-597.	2.0	64
115	Base methylation and local DNA helix stability. <i>Journal of Molecular Biology</i> , 1989, 205, 593-602.	2.0	40
116	The structure of the holliday junction, and its resolution. <i>Cell</i> , 1988, 55, 79-89.	13.5	507
117	Helix stability and the mechanism of cruciform extrusion in supercoiled DNA molecules. <i>Nucleic Acids Research</i> , 1988, 16, 1079-1093.	6.5	26
118	The mechanism of cruciform formation in supercoiled DNA: initial opening of central basepairs in salt-dependent extrusion. <i>Nucleic Acids Research</i> , 1987, 15, 9641-9654.	6.5	59
119	A two-state conformational equilibrium for alternating (A-T) <sub>n</sub> sequences in negatively supercoiled DNA. <i>Journal of Molecular Biology</i> , 1987, 197, 707-721.	2.0	57
120	Influence of cation size and charge on the extrusion of a salt-dependent cruciform. <i>Journal of Molecular Biology</i> , 1987, 193, 397-404.	2.0	83
121	A dominant influence of flanking sequences on a local structural transition in DNA. <i>Cell</i> , 1986, 47, 817-827.	13.5	110
122	The kinetic properties of cruciform extrusion are determined by DNA base-sequence. <i>Nucleic Acids Research</i> , 1985, 13, 1443-1465.	6.5	102
123	Facile cruciform formation by an (A-T) <sub>34</sub> sequence from a <i>Xenopus</i> globin gene. <i>Journal of Molecular Biology</i> , 1985, 185, 461-478.	2.0	195
124	Thermodynamics of the ColE1 cruciform. <i>Journal of Molecular Biology</i> , 1984, 180, 179-200.	2.0	79
125	Cruciform-resolvase interactions in supercoiled DNA. <i>Cell</i> , 1984, 36, 413-422.	13.5	196
126	Hairpin-loop formation by inverted repeats in supercoiled DNA is a local and transmissible property. <i>Nucleic Acids Research</i> , 1981, 9, 1271-1290.	6.5	137