Thomas W Kirby

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Phosphopeptide interactions of the Nbs1 N-terminal FHA-BRCT1/2 domains. Scientific Reports, 2021, 11, 9046.	1.6	7
2	Ligand binding characteristics of the Ku80 von Willebrand domain. DNA Repair, 2020, 85, 102739.	1.3	14
3	Variations in nuclear localization strategies among pol X family enzymes. Traffic, 2018, 19, 723-735.	1.3	3
4	Transitions in DNA polymerase β μs-ms dynamics related to substrate binding and catalysis. Nucleic Acids Research, 2018, 46, 7309-7322.	6.5	3
5	DNA polymerase β contains a functional nuclear localization signal at its N-terminus. Nucleic Acids Research, 2017, 45, 1958-1970.	6.5	13
6	Characterization of the APLF FHA–XRCC1 phosphopeptide interaction and its structural and functional implications. Nucleic Acids Research, 2017, 45, 12374-12387.	6.5	9
7	Nuclear Localization of the DNA Repair Scaffold XRCC1: Uncovering the Functional Role of a Bipartite NLS. Scientific Reports, 2015, 5, 13405.	1.6	30
8	Characterization of the Redox Transition of the XRCC1 N-terminal Domain. Structure, 2014, 22, 1754-1763.	1.6	6
9	Substrate Rescue of DNA Polymerase β Containing a Catastrophic L22P Mutation. Biochemistry, 2014, 53, 2413-2422.	1.2	12
10	Metal-induced DNA translocation leads to DNA polymerase conformational activation. Nucleic Acids Research, 2012, 40, 2974-2983.	6.5	30
11	NMR study of the effect of Zn on conformational activation of rat DNA polymerase β. FASEB Journal, 2010, 24, 876.6.	0.2	0
12	NMR analysis of [methyl-13C]methionine UvrB from Bacillus caldotenax reveals UvrB–domain 4 heterodimer formation in solution. Journal of Molecular Biology, 2007, 373, 282-295.	2.0	24
13	NMR assignment of polymerase β labeled with 2H, 13C, and 15N in complex with substrate DNA. Biomolecular NMR Assignments, 2007, 1, 33-35.	0.4	5
14	NMR Determination of Lysine pKaValues in the Pol λ Lyase Domain: Mechanistic Implications. Biochemistry, 2006, 45, 1785-1794.	1.2	21
15	Structure of the Escherichia coli DNA Polymerase ΙΙΙ Ϊμ-HOT Proofreading Complex. Journal of Biological Chemistry, 2006, 281, 38466-38471.	1.6	30
16	Structure of a Complex of <i>E. coli</i> DNA Polymerase III ε Subunit with Phage P1 Homolog of Î, . FASEB Journal, 2006, 20, .	0.2	0
17	Nuclear Magnetic Resonance Solution Structure of the Escherichia coli DNA Polymerase III Î, Subunit. Journal of Bacteriology, 2005, 187, 7081-7089.	1.0	19
18	A Thymine Isostere in the Templating Position Disrupts Assembly of the Closed DNA Polymerase β Ternary Complex. Biochemistry, 2005, 44, 15230-15237.	1.2	29

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19	Phage Like It HOT. Structure, 2004, 12, 2221-2231.	1.6	12
20	Dynamic Characterization of a DNA Repair Enzyme:Â NMR Studies of [methyl-13C]Methionine-Labeled DNA Polymerase β. Biochemistry, 2004, 43, 8911-8922.	1.2	53
21	Backbone Dynamics of the RNase H Domain of HIV-1 Reverse Transcriptase. Biochemistry, 2004, 43, 9332-9342.	1.2	24
22	Metabolic transformation of AZTp4A by Ap4A hydrolase regenerates AZT triphosphate. Antiviral Research, 2003, 58, 227-233.	1.9	5
23	NMR assignment of protein side chains using residue-correlated labeling and NOE spectra. Journal of Magnetic Resonance, 2003, 165, 237-247.	1.2	2
24	Solution Structure of the RNase H Domain of the HIV-1 Reverse Transcriptase in the Presence of Magnesiumâ€. Biochemistry, 2003, 42, 639-650.	1.2	53
25	Solution Structure of the Lyase Domain of Human DNA Polymerase λ. Biochemistry, 2003, 42, 9564-9574.	1.2	27
26	The Nuclease A Inhibitor Represents a New Variation of the Rare PR-1 Fold. Journal of Molecular Biology, 2002, 320, 771-782.	2.0	20
27	A picomolar spectrophotometric assay for superoxide dismutase. Analytical Biochemistry, 1982, 127, 435-440.	1.1	49
28	Isolation and characterization of the iron-containing superoxide dismutase of Methanobacterium bryantii. Archives of Biochemistry and Biophysics, 1981, 210, 140-148.	1.4	131
29	Distinguishing between Mn-containing and Fe-containing superoxide dismutases in crude extracts of cells. Archives of Biochemistry and Biophysics, 1980, 201, 551-555.	1.4	97
30	Application of a partially automated solid-phase peptide synthesis apparatus to the synthesis of a protected peptide fragment of cytochrome c. Analytical Biochemistry, 1978, 85, 367-376.	1.1	5