

Alexander C Drohat

List of Publications by Year in descending order

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40
papers

2,533
citations

172207

29
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288905

40
g-index

40
all docs

40
docs citations

40
times ranked

2318
citing authors

#	ARTICLE	IF	CITATIONS
1	TET-TDG Active DNA Demethylation at CpG and Non-CpG Sites. <i>Journal of Molecular Biology</i> , 2021, 433, 166877.	2.0	21
2	Structural Insights into the Mechanism of Base Excision by MBD4. <i>Journal of Molecular Biology</i> , 2021, 433, 167097.	2.0	13
3	Excision of 5-Carboxylcytosine by Thymine DNA Glycosylase. <i>Journal of the American Chemical Society</i> , 2019, 141, 18851-18861.	6.6	21
4	Defining the Role of Nucleotide Flipping in Enzyme Specificity Using 19F NMR. <i>Journal of the American Chemical Society</i> , 2019, 141, 4952-4962.	6.6	23
5	Kinetic Methods for Studying DNA Glycosylases Functioning in Base Excision Repair. <i>Methods in Enzymology</i> , 2017, 592, 357-376.	0.4	13
6	Characterizing Requirements for Small Ubiquitin-like Modifier (SUMO) Modification and Binding on Base Excision Repair Activity of Thymine-DNA Glycosylase in Vivo. <i>Journal of Biological Chemistry</i> , 2016, 291, 9014-9024.	1.6	15
7	Structural basis of damage recognition by thymine DNA glycosylase: Key roles for N-terminal residues. <i>Nucleic Acids Research</i> , 2016, 44, gkw768.	6.5	44
8	Role of Base Excision "Repair" Enzymes in Erasing Epigenetic Marks from DNA. <i>Chemical Reviews</i> , 2016, 116, 12711-12729.	23.0	87
9	Role of base excision repair in maintaining the genetic and epigenetic integrity of CpG sites. <i>DNA Repair</i> , 2015, 32, 33-42.	1.3	79
10	Lesion search and recognition by thymine DNA glycosylase revealed by single molecule imaging. <i>Nucleic Acids Research</i> , 2015, 43, 2716-2729.	6.5	36
11	Thymine DNA glycosylase exhibits negligible affinity for nucleobases that it removes from DNA. <i>Nucleic Acids Research</i> , 2015, 43, 9541-9552.	6.5	28
12	E2-mediated Small Ubiquitin-like Modifier (SUMO) Modification of Thymine DNA Glycosylase Is Efficient but Not Selective for the Enzyme-Product Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 15810-15819.	1.6	17
13	Mechanisms for enzymatic cleavage of the N-glycosidic bond in DNA. <i>Organic and Biomolecular Chemistry</i> , 2014, 12, 8367-8378.	1.5	63
14	Divergent Mechanisms for Enzymatic Excision of 5-Formylcytosine and 5-Carboxylcytosine from DNA. <i>Journal of the American Chemical Society</i> , 2013, 135, 15813-15822.	6.6	69
15	Coordination of MYH DNA glycosylase and APE1 endonuclease activities via physical interactions. <i>DNA Repair</i> , 2013, 12, 1043-1052.	1.3	33
16	Structure of human apurinic/aprimidinic endonuclease 1 with the essential Mg ²⁺ cofactor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2555-2562.	2.5	39
17	Functional Assessment of Population and Tumor-Associated APE1 Protein Variants. <i>PLoS ONE</i> , 2013, 8, e65922.	1.1	30
18	How a mismatch repair enzyme balances the needs for efficient lesion processing and minimal action on undamaged DNA. <i>Cell Cycle</i> , 2012, 11, 3345-3346.	1.3	2

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19	Lesion processing by a repair enzyme is severely curtailed by residues needed to prevent aberrant activity on undamaged DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8091-8096.	3.3	48
20	Crystal Structure of Human Methyl-Binding Domain IV Glycosylase Bound to Abasic DNA. <i>Journal of Molecular Biology</i> , 2012, 420, 164-175.	2.0	34
21	Thymine DNA Glycosylase Can Rapidly Excise 5-Formylcytosine and 5-Carboxylcytosine. <i>Journal of Biological Chemistry</i> , 2011, 286, 35334-35338.	1.6	704
22	Dependence of substrate binding and catalysis on pH, ionic strength, and temperature for thymine DNA glycosylase: Insights into recognition and processing of G•T mispairs. <i>DNA Repair</i> , 2011, 10, 545-553.	1.3	34
23	Stoichiometry and affinity for thymine DNA glycosylase binding to specific and nonspecific DNA. <i>Nucleic Acids Research</i> , 2011, 39, 2319-2329.	6.5	43
24	Chemical shift assignments for human apurinic/apyrimidinic endonuclease 1. <i>Biomolecular NMR Assignments</i> , 2010, 4, 5-8.	0.4	10
25	Role of Two Strictly Conserved Residues in Nucleotide Flipping and N-Glycosylic Bond Cleavage by Human Thymine DNA Glycosylase. <i>Journal of Biological Chemistry</i> , 2009, 284, 36680-36688.	1.6	52
26	Structural Studies of RNA/DNA Polypurine Tracts. <i>Chemistry and Biology</i> , 2008, 15, 203-204.	6.2	5
27	Crystal structure of human thymine DNA glycosylase bound to DNA elucidates sequence-specific mismatch recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8890-8895.	3.3	103
28	Coordinating the Initial Steps of Base Excision Repair. <i>Journal of Biological Chemistry</i> , 2008, 283, 32680-32690.	1.6	86
29	Excision of 5-Halogenated Uracils by Human Thymine DNA Glycosylase. <i>Journal of Biological Chemistry</i> , 2007, 282, 27578-27586.	1.6	87
30	The human checkpoint sensor Rad9•Rad1•Hus1 interacts with and stimulates DNA repair enzyme TDG glycosylase. <i>Nucleic Acids Research</i> , 2007, 35, 6207-6218.	6.5	57
31	Specificity of Human Thymine DNA Glycosylase Depends on N-Glycosidic Bond Stability. <i>Journal of the American Chemical Society</i> , 2006, 128, 12510-12519.	6.6	149
32	Solution Structure and Base Perturbation Studies Reveal a Novel Mode of Alkylated Base Recognition by 3-Methyladenine DNA Glycosylase I. <i>Journal of Biological Chemistry</i> , 2003, 278, 48012-48020.	1.6	33
33	Probing the Limits of Electrostatic Catalysis by Uracil DNA Glycosylase Using Transition State Mimicry and Mutagenesis. <i>Journal of Biological Chemistry</i> , 2002, 277, 15385-15392.	1.6	37
34	3-methyladenine DNA glycosylase I is an unexpected helix-hairpin-helix superfamily member. <i>Nature Structural Biology</i> , 2002, 9, 659-664.	9.7	49
35	Uracil DNA Glycosylase: Insights from a Master Catalyst. <i>Archives of Biochemistry and Biophysics</i> , 2001, 396, 1-9.	1.4	53
36	NMR Evidence for an Unusually Low N1 pK _a for Uracil Bound to Uracil DNA Glycosylase: Implications for Catalysis. <i>Journal of the American Chemical Society</i> , 2000, 122, 1840-1841.	6.6	74

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37	Structural changes in the C-terminus of Ca ²⁺ -bound rat S100B(β^2) upon binding to a peptide derived from the C-terminal regulatory domain of p53. Protein Science, 1999, 8, 1743-1751.	3.1	41
38	The use of dipolar couplings for determining the solution structure of rat apo-S100B(β^2). Protein Science, 1999, 8, 800-809.	3.1	77
39	S100B(β^2) inhibits the protein kinase C-dependent phosphorylation of a peptide derived from p53 in a Ca ²⁺ -dependent manner. Protein Science, 1998, 7, 794-798.	3.1	67
40	Oligomerization state of S100B at nanomolar concentration determined by large-angle analytical gel filtration chromatography. Protein Science, 1997, 6, 1577-1582.	3.1	57