

Ashok S Bhagwat

List of Publications by Year in descending order

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76
papers

4,158
citations

136950

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62
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78
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78
docs citations

78
times ranked

4138
citing authors

#	ARTICLE	IF	CITATIONS
1	Human activation-induced deaminase lacks strong replicative strand bias or preference for cytosines in hairpin loops. <i>Nucleic Acids Research</i> , 2022, 50, 5145-5157.	14.5	8
2	An extended APOBEC3A mutation signature in cancer. <i>Nature Communications</i> , 2021, 12, 1602.	12.8	69
3	FAM72A antagonizes UNG2 to promote mutagenic repair during antibody maturation. <i>Nature</i> , 2021, 600, 324-328.	27.8	29
4	Visualization of uracils created by APOBEC3A using UdgX shows colocalization with RPA at stalled replication forks. <i>Nucleic Acids Research</i> , 2020, 48, e118-e118.	14.5	19
5	APOBEC3 enzymes mediate efficacy of cisplatin and are epistatic with base excision repair and mismatch repair in platinum response. <i>NAR Cancer</i> , 2020, 2, zcaa033.	3.1	5
6	Genome-wide mapping of regions preferentially targeted by the human DNA-cytosine deaminase APOBEC3A using uracil-DNA pulldown and sequencing. <i>Journal of Biological Chemistry</i> , 2019, 294, 15037-15051.	3.4	18
7	Human Herpes Simplex Virus-1 depletes APOBEC3A from nuclei. <i>Virology</i> , 2019, 537, 104-109.	2.4	21
8	A Tumor-Promoting Phorbol Ester Causes a Large Increase in APOBEC3A Expression and a Moderate Increase in APOBEC3B Expression in a Normal Human Keratinocyte Cell Line without Increasing Genomic Uracils. <i>Molecular and Cellular Biology</i> , 2019, 39, .	2.3	22
9	Unscheduled DNA synthesis leads to elevated uracil residues at highly transcribed genomic loci in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2018, 14, e1007516.	3.5	10
10	A novel class of chemicals that react with abasic sites in DNA and specifically kill B cell cancers. <i>PLoS ONE</i> , 2017, 12, e0185010.	2.5	9
11	Abstract 3802: A novel uracil-DNA glycosylase, UdgX, as a new biochemical tool to directly detect uracils in DNA. , 2017, , .		0
12	Functions and Malfunctions of Mammalian DNA-Cytosine Deaminases. <i>Chemical Reviews</i> , 2016, 116, 12688-12710.	47.7	104
13	Strand-biased cytosine deamination at the replication fork causes cytosine to thymine mutations in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2176-2181.	7.1	94
14	APOBEC3A damages the cellular genome during DNA replication. <i>Cell Cycle</i> , 2016, 15, 998-1008.	2.6	69
15	Abstract 3757: A novel class of chemicals that react with damaged DNA and specifically kill B-cell cancers. , 2016, , .		0
16	A versatile new tool to quantify abasic sites in DNA and inhibit base excision repair. <i>DNA Repair</i> , 2015, 27, 9-18.	2.8	28
17	Characterization of the Catalytic Domain of Human APOBEC3B and the Critical Structural Role for a Conserved Methionine. <i>Journal of Molecular Biology</i> , 2015, 427, 3042-3055.	4.2	28
18	Abstract 3016: APOBEC3 enzymes induce damage to the cellular genome during DNA replication. , 2015, , .		0

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19	Transcription-Associated Mutagenesis. <i>Annual Review of Genetics</i> , 2014, 48, 341-359.	7.6	104
20	Genomic Uracil Homeostasis during Normal B Cell Maturation and Loss of This Balance during B Cell Cancer Development. <i>Molecular and Cellular Biology</i> , 2014, 34, 4019-4032.	2.3	23
21	The COMBREX Project: Design, Methodology, and Initial Results. <i>PLoS Biology</i> , 2013, 11, e1001638.	5.6	54
22	Base Damage within Single-Strand DNA Underlies In Vivo Hypermutability Induced by a Ubiquitous Environmental Agent. <i>PLoS Genetics</i> , 2012, 8, e1003149.	3.5	76
23	Efficient deamination of 5-methylcytosines in DNA by human APOBEC3A, but not by AID or APOBEC3G. <i>Nucleic Acids Research</i> , 2012, 40, 9206-9217.	14.5	100
24	Excision of 5-hydroxymethyluracil and 5-carboxylcytosine by the thymine DNA glycosylase domain: its structural basis and implications for active DNA demethylation. <i>Nucleic Acids Research</i> , 2012, 40, 10203-10214.	14.5	134
25	Use of <i>Drosophila</i> deoxynucleoside kinase to study mechanism of toxicity and mutagenicity of deoxycytidine analogs in <i>Escherichia coli</i> . <i>DNA Repair</i> , 2010, 9, 153-160.	2.8	7
26	Determinants of sequence-specificity within human AID and APOBEC3G. <i>DNA Repair</i> , 2010, 9, 579-587.	2.8	85
27	Importance of the tmRNA system for cell survival when transcription is blocked by DNA-protein crosslinks. <i>Molecular Microbiology</i> , 2010, 78, 686-700.	2.5	9
28	Comment on "Deoxyuridine Triphosphate Incorporation during Somatic Hypermutation of Mouse V _H Ox Genes after Immunization with Phenyloxazolone". <i>Journal of Immunology</i> , 2010, 185, 7130.2-7131.	0.8	1
29	Transcriptional pausing and stalling causes multiple clustered mutations by human activation-induced deaminase. <i>FASEB Journal</i> , 2009, 23, 34-44.	0.5	38
30	DNA flipping by restriction endonucleases. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s153-s153.	0.3	0
31	<i>Escherichia coli</i> DNA glycosylase Mug: a growth-regulated enzyme required for mutation avoidance in stationary-phase cells. <i>Molecular Microbiology</i> , 2008, 41, 1101-1111.	2.5	28
32	Is AID a monomer in solution?. <i>DNA Repair</i> , 2008, 7, 349-350.	2.8	8
33	Transcription increases methylmethane sulfonate-induced mutations in alkB strains of <i>Escherichia coli</i> . <i>DNA Repair</i> , 2008, 7, 1289-1297.	2.8	13
34	DNA base flipping by both members of the PspGI restriction-modification system. <i>Nucleic Acids Research</i> , 2008, 36, 5417-5425.	14.5	6
35	Central base pair flipping and discrimination by PspGI. <i>Nucleic Acids Research</i> , 2008, 36, 6109-6117.	14.5	32
36	Evaluation of Molecular Models for the Affinity Maturation of Antibodies: Roles of Cytosine Deamination by AID and DNA Repair. <i>Chemical Reviews</i> , 2006, 106, 700-719.	47.7	28

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37	Sequence-dependent enhancement of hydrolytic deamination of cytosines in DNA by the restriction enzyme PspGI. <i>Nucleic Acids Research</i> , 2006, 34, 3762-3770.	14.5	13
38	Transcription promotes guanine to thymine mutations in the non-transcribed strand of an <i>Escherichia coli</i> gene. <i>DNA Repair</i> , 2005, 4, 806-813.	2.8	22
39	Interaction of the <i>Escherichia coli</i> Vsr with DNA and Mismatch Repair Proteins. , 2005, , .		0
40	DNA-cytosine deaminases: from antibody maturation to antiviral defense. <i>DNA Repair</i> , 2004, 3, 85-89.	2.8	24
41	Phylogenomic identification of five new human homologs of the DNA repair enzyme AlkB. <i>BMC Genomics</i> , 2003, 4, 48.	2.8	180
42	A nomenclature for restriction enzymes, DNA methyltransferases, homing endonucleases and their genes. <i>Nucleic Acids Research</i> , 2003, 31, 1805-1812.	14.5	634
43	Mismatch Repair in Methylated DNA. <i>Journal of Biological Chemistry</i> , 2003, 278, 5285-5291.	3.4	68
44	Human activation-induced cytidine deaminase causes transcription-dependent, strand-biased C to U deaminations. <i>Nucleic Acids Research</i> , 2003, 31, 2990-2994.	14.5	247
45	Mismatch Uracil Glycosylase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 20526-20532.	3.4	53
46	Transcription-Dependent Increase in Multiple Classes of Base Substitution Mutations in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2002, 184, 6866-6872.	2.2	37
47	Protection of DNA by $\hat{I}\pm/\hat{I}^2$ -Type Small, Acid-Soluble Proteins from <i>Bacillus subtilis</i> Spores Against Cytosine Deamination. <i>Biochemistry</i> , 2002, 41, 11325-11330.	2.5	22
48	Lack of dependance of transcription-induced cytosine deaminations on protein synthesis. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2002, 508, 131-136.	1.0	4
49	Cooperation and competition in mismatch repair: very short-patch repair and methyl-directed mismatch repair in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2002, 44, 1421-1428.	2.5	67
50	Interaction of MutS and Vsr: Some Dominant-Negative mutS Mutations That Disable Methyladenine-Directed Mismatch Repair Are Active in Very-Short-Patch Repair. <i>Journal of Bacteriology</i> , 2001, 183, 6487-6490.	2.2	13
51	Transcription-Induced Cytosine-to-Thymine Mutations Are Not Dependent on Sequence Context of the Target Cytosine. <i>Journal of Bacteriology</i> , 2001, 183, 6491-6493.	2.2	33
52	Mutations induced by bacteriophage T7 RNA polymerase and their effects on the composition of the T7 genome ¹¹ Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 2000, 300, 1057-1065.	4.2	46
53	Reviving a Dead Enzyme:â€‰ Cytosine Deaminations Promoted by an Inactive DNA Methyltransferase and an S-Adenosylmethionine Analogue. <i>Biochemistry</i> , 2000, 39, 14611-14616.	2.5	27
54	The Role of the <i>Escherichia coli</i> Mug Protein in the Removal of Uracil and 3,N 4-Ethenocytosine from DNA. <i>Journal of Biological Chemistry</i> , 1999, 274, 31034-31038.	3.4	59

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55	Principal causes of hot spots for cytosine to thymine mutations at sites of cytosine methylation in growing cells. <i>Mutation Research - Reviews in Mutation Research</i> , 1999, 437, 11-20.	5.5	82
56	Mechanism of Avoidance of 5-methylcytosine to Thymine Mutations in Bacteria. , 1998, , 119-129.		0
57	Very short patch repair: reducing the cost of cytosine methylation. <i>Molecular Microbiology</i> , 1996, 20, 467-473.	2.5	99
58	Overproduction of DNA Cytosine Methyltransferases Causes Methylation and C → T Mutations at Non-canonical Sites. <i>Journal of Biological Chemistry</i> , 1996, 271, 7851-7859.	3.4	47
59	Determination of methylation specificity of DsaV methyltransferase by a simple biochemical method. <i>Nucleic Acids Research</i> , 1995, 23, 29-35.	14.5	3
60	Cytosine methyltransferase from <i>Escherichia coli</i> in which active site cysteine is replaced with serine is partially active. <i>Biochemistry</i> , 1995, 34, 8914-8923.	2.5	46
61	Cloning and characterization of the gene encoding the DsaV methyltransferase. <i>Gene</i> , 1995, 157, 61-63.	2.2	0
62	A novel repetitive sequence lies near the gene encoding a cytosine methyltransferase in the cyanobacterium <i>Dactylococcus salina</i> . <i>Gene</i> , 1995, 164, 71-74.	2.2	2
63	A Cytosine Methyltransferase Converts 5-Methylcytosine in DNA to Thymine. <i>Biochemistry</i> , 1995, 34, 14752-14757.	2.5	83
64	DsaV methyltransferase and its isoschizomers contain a conserved segment that is similar to the segment in HhaI methyltransferase that is in contact with DNA bases. <i>Nucleic Acids Research</i> , 1994, 22, 4482-4488.	14.5	10
65	A DNA repair process in <i>Escherichia coli</i> corrects U:G and T:G mismatches to C:G at sites of cytosine methylation. <i>Molecular Genetics and Genomics</i> , 1994, 243, 244-248.	2.4	16
66	Mechanism of expression of DNA repair gene <i>vsr</i> , an <i>Escherichia coli</i> gene that overlaps the DNA cytosine methylase gene, <i>dcm</i> . <i>Molecular Microbiology</i> , 1993, 9, 823-833.	2.5	34
67	The cysteine conserved among DNA cytosine methylases required for methyl transfer, but not for specific DNA binding. <i>Nucleic Acids Research</i> , 1993, 21, 295-301.	14.5	79
68	A rapid and sensitive method to measure DNA endonuclease activity. <i>Nucleic Acids Research</i> , 1993, 21, 5797-5798.	14.5	2
69	Substitutions of a cysteine conserved among DNA cytosine methylases result in a variety of phenotypes. <i>Nucleic Acids Research</i> , 1992, 20, 319-326.	14.5	65
70	DNA mismatch correction by Very Short Patch repair may have altered the abundance of oligonucleotides in the <i>E. coli</i> genome. <i>Nucleic Acids Research</i> , 1992, 20, 1663-1668.	14.5	60
71	[21] Restriction enzymes: Properties and use. <i>Methods in Enzymology</i> , 1992, 216, 199-224.	1.0	27
72	Predictive motifs derived from cytosine methyltransferases. <i>Nucleic Acids Research</i> , 1989, 17, 2421-2435.	14.5	513

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73	Sequence motifs specific for cytosine methyltransferases. <i>Gene</i> , 1988, 74, 261-265.	2.2	26
74	A new gene involved in mismatch correction in <i>Escherichia coli</i> . <i>Gene</i> , 1988, 74, 153-156.	2.2	12
75	Nucleotide sequence and expression of the gene encoding the EcoRII modification enzyme. <i>Nucleic Acids Research</i> , 1987, 15, 313-332.	14.5	111
76	Structure and properties of the region of homology between plasmids pMB1 and ColE1. <i>Molecular Genetics and Genomics</i> , 1981, 182, 505-507.	2.4	11