

Gerd P Pfeifer

List of Publications by Year in descending order

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Version: 2024-02-01

115
papers

15,333
citations

20817

60
h-index

26613

107
g-index

119
all docs

119
docs citations

119
times ranked

18151
citing authors

#	ARTICLE	IF	CITATIONS
1	Lack of Major Genome-Wide DNA Methylation Changes in Succinate-Treated Human Epithelial Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5663.	4.1	0
2	Concordance of hydrogen peroxide-induced 8-oxo-guanine patterns with two cancer mutation signatures of upper GI tract tumors. <i>Science Advances</i> , 2022, 8, .	10.3	10
3	Purification of TET Proteins. <i>Methods in Molecular Biology</i> , 2021, 2272, 225-237.	0.9	2
4	The chromosomal protein SMCHD1 regulates DNA methylation and the 2c-like state of embryonic stem cells by antagonizing TET proteins. <i>Science Advances</i> , 2021, 7, .	10.3	28
5	The epigenetic DNA modification 5-carboxylcytosine promotes high levels of cyclobutane pyrimidine dimer formation upon UVB irradiation. <i>Genome Instability & Disease</i> , 2021, 2, 59-69.	1.1	7
6	DNA repair in neurons and its possible link to the epigenetic machinery at enhancers. <i>Epigenomics</i> , 2021, 13, 913-917.	2.1	1
7	The major mechanism of melanoma mutations is based on deamination of cytosine in pyrimidine dimers as determined by circle damage sequencing. <i>Science Advances</i> , 2021, 7, .	10.3	23
8	3â€²HS1 CTCF binding site in human Î²-globin locus regulates fetal hemoglobin expression. <i>ELife</i> , 2021, 10, .	6.0	5
9	High-Resolution Analysis of 5-Hydroxymethylcytosine by TET-Assisted Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2021, 2198, 321-331.	0.9	4
10	The ups and downs of DNA methylation: an interview with Gerd Pfeifer. <i>Epigenomics</i> , 2021, , .	2.1	1
11	Protein Interactions at Oxidized 5-Methylcytosine Bases. <i>Journal of Molecular Biology</i> , 2020, 432, 1718-1730.	4.2	25
12	Mechanisms of UV-induced mutations and skin cancer. <i>Genome Instability & Disease</i> , 2020, 1, 99-113.	1.1	53
13	Smoke signals in the DNA of normal lung cells. <i>Nature</i> , 2020, 578, 224-226.	27.8	6
14	Reprogramming of DNA methylation at NEUROD2-bound sequences during cortical neuron differentiation. <i>Science Advances</i> , 2019, 5, eaax0080.	10.3	32
15	Suppressor of hepatocellular carcinoma RASSF1A activates autophagy initiation and maturation. <i>Cell Death and Differentiation</i> , 2019, 26, 1379-1395.	11.2	30
16	5-Methylcytosine and Its Oxidized Derivatives. , 2019, , 65-86.		0
17	Gene body profiles of 5-hydroxymethylcytosine: potential origin, function and use as a cancer biomarker. <i>Epigenomics</i> , 2018, 10, 1029-1032.	2.1	14
18	Defining Driver DNA Methylation Changes in Human Cancer. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1166.	4.1	238

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19	An Intrinsic Epigenetic Barrier for Functional Axon Regeneration. <i>Neuron</i> , 2017, 94, 337-346.e6.	8.1	130
20	Dynamics of RNA Polymerase II Pausing and Bivalent Histone H3 Methylation during Neuronal Differentiation in Brain Development. <i>Cell Reports</i> , 2017, 20, 1307-1318.	6.4	47
21	Methods for Assessing DNA Cytosine Modifications Genome-Wide. , 2017, , 125-134.		0
22	Properly dividing with YAP. <i>Science Signaling</i> , 2016, 9, fs3.	3.6	1
23	Are there specific readers of oxidized 5-methylcytosine bases?. <i>BioEssays</i> , 2016, 38, 1038-1047.	2.5	34
24	Somatic TP53 Mutations in the Era of Genome Sequencing. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2016, 6, a026179.	6.2	176
25	Switching enhancer methylation in metastatic melanoma. <i>Pigment Cell and Melanoma Research</i> , 2016, 29, 491-493.	3.3	0
26	How tobacco smoke changes the (epi)genome. <i>Science</i> , 2016, 354, 549-550.	12.6	10
27	Analysis of Liver Tumor-Prone Mouse Models of the Hippo Kinase Scaffold Proteins RASSF1A and SAV1. <i>Cancer Research</i> , 2016, 76, 2824-2835.	0.9	22
28	Tet3 Reads 5-Carboxylcytosine through Its CXXC Domain and Is a Potential Guardian against Neurodegeneration. <i>Cell Reports</i> , 2016, 14, 493-505.	6.4	109
29	Single Base Resolution Analysis of 5-Methylcytosine and 5-Hydroxymethylcytosine by RRBS and TAB-RRBS. <i>Methods in Molecular Biology</i> , 2015, 1238, 273-287.	0.9	31
30	Longitudinal epigenetic and gene expression profiles analyzed by three-component analysis reveal down-regulation of genes involved in protein translation in human aging. <i>Nucleic Acids Research</i> , 2015, 43, e100-e100.	14.5	35
31	Aging and DNA methylation. <i>BMC Biology</i> , 2015, 13, 7.	3.8	397
32	How the environment shapes cancer genomes. <i>Current Opinion in Oncology</i> , 2015, 27, 71-77.	2.4	31
33	Genome-wide mapping of 5-hydroxymethylcytosine in three rice cultivars reveals its preferential localization in transcriptionally silent transposable element genes. <i>Journal of Experimental Botany</i> , 2015, 66, 6651-6663.	4.8	26
34	The DNA methylation landscape of human melanoma. <i>Genomics</i> , 2015, 106, 322-330.	2.9	50
35	MIRA-seq for DNA methylation analysis of CpG islands. <i>Epigenomics</i> , 2015, 7, 695-706.	2.1	37
36	<i>Drosophila</i> genomic methylation: new evidence and new questions. <i>Epigenomics</i> , 2014, 6, 459-461.	2.1	35

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37	The tumour suppressor Ras-association domain family protein 1A (RASSF1A) regulates TNF- α signalling in cardiomyocytes. <i>Cardiovascular Research</i> , 2014, 103, 47-59.	3.8	10
38	5-Hydroxymethylcytosine: A stable or transient DNA modification?. <i>Genomics</i> , 2014, 104, 314-323.	2.9	114
39	The role of 5-hydroxymethylcytosine in human cancer. <i>Cell and Tissue Research</i> , 2014, 356, 631-641.	2.9	87
40	Loss of the Polycomb Mark from Bivalent Promoters Leads to Activation of Cancer-Promoting Genes in Colorectal Tumors. <i>Cancer Research</i> , 2014, 74, 3617-3629.	0.9	43
41	Formation of cyclobutane pyrimidine dimers at dipyrimidines containing 5-hydroxymethylcytosine. <i>Photochemical and Photobiological Sciences</i> , 2013, 12, 1409-1415.	2.9	24
42	Dynamics of 5-Hydroxymethylcytosine and Chromatin Marks in Mammalian Neurogenesis. <i>Cell Reports</i> , 2013, 3, 291-300.	6.4	385
43	5-hydroxymethylcytosine and its potential roles in development and cancer. <i>Epigenetics and Chromatin</i> , 2013, 6, 10.	3.9	157
44	Detection of Oxidation Products of 5-Methyl-2-Deoxycytidine in Arabidopsis DNA. <i>PLoS ONE</i> , 2013, 8, e84620.	2.5	27
45	UVB irradiation does not directly induce detectable changes of DNA methylation in human keratinocytes. <i>F1000Research</i> , 2013, 2, 45.	1.6	21
46	Interactions between hepatitis B virus and aflatoxin B1: effects on p53 induction in HepaRG cells. <i>Journal of General Virology</i> , 2012, 93, 640-650.	2.9	26
47	UV wavelength-dependent DNA damage and human non-melanoma and melanoma skin cancer. <i>Photochemical and Photobiological Sciences</i> , 2012, 11, 90-97.	2.9	346
48	DNA methylation biomarkers for lung cancer. <i>Tumor Biology</i> , 2012, 33, 287-296.	1.8	116
49	The role of Tet3 DNA dioxygenase in epigenetic reprogramming by oocytes. <i>Nature</i> , 2011, 477, 606-610.	27.8	969
50	Reprogramming of the paternal genome upon fertilization involves genome-wide oxidation of 5-methylcytosine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3642-3647.	7.1	618
51	5-Hydroxymethylcytosine Is Strongly Depleted in Human Cancers but Its Levels Do Not Correlate with <i>IDH1</i> Mutations. <i>Cancer Research</i> , 2011, 71, 7360-7365.	0.9	400
52	Uveal Melanoma and <i>GNA11</i> Mutations: a new piece added to the puzzle. <i>Pigment Cell and Melanoma Research</i> , 2011, 24, 18-20.	3.3	11
53	Relationship between Gene Body DNA Methylation and Intragenic H3K9me3 and H3K36me3 Chromatin Marks. <i>PLoS ONE</i> , 2011, 6, e18844.	2.5	131
54	Next-generation sequencing: emerging lessons on the origins of human cancer. <i>Current Opinion in Oncology</i> , 2011, 23, 62-68.	2.4	36

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55	Wavelength dependence of ultraviolet radiation-induced DNA damage as determined by laser irradiation suggests that cyclobutane pyrimidine dimers are the principal DNA lesions produced by terrestrial sunlight. <i>FASEB Journal</i> , 2011, 25, 3079-3091.	0.5	118
56	Genomic mapping of 5-hydroxymethylcytosine in the human brain. <i>Nucleic Acids Research</i> , 2011, 39, 5015-5024.	14.5	344
57	Epigenetic changes of DNA repair genes in cancer. <i>Journal of Molecular Cell Biology</i> , 2011, 3, 51-58.	3.3	168
58	The Tumor Suppressor RASSF1A Prevents Dephosphorylation of the Mammalian STE20-like Kinases MST1 and MST2. <i>Journal of Biological Chemistry</i> , 2011, 286, 6253-6261.	3.4	99
59	RASSF proteins. <i>Current Biology</i> , 2010, 20, R344-R345.	3.9	11
60	CpG Island Hypermethylation in Human Astrocytomas. <i>Cancer Research</i> , 2010, 70, 2718-2727.	0.9	122
61	Examination of the specificity of DNA methylation profiling techniques towards 5-methylcytosine and 5-hydroxymethylcytosine. <i>Nucleic Acids Research</i> , 2010, 38, e125-e125.	14.5	389
62	Identification of Driver and Passenger DNA Methylation in Cancer by Epigenomic Analysis. <i>Advances in Genetics</i> , 2010, 70, 277-308.	1.8	128
63	DNA methylation profiling using the methylated-CpG island recovery assay (MIRA). <i>Methods</i> , 2010, 52, 213-217.	3.8	48
64	Environmental exposures and mutational patterns of cancer genomes. <i>Genome Medicine</i> , 2010, 2, 54.	8.2	58
65	A human B cell methylome at 100~base pair resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 671-678.	7.1	319
66	DNA methylation patterns in lung carcinomas. <i>Seminars in Cancer Biology</i> , 2009, 19, 181-187.	9.6	100
67	The RASSF proteins in cancer; from epigenetic silencing to functional characterization. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2009, 1796, 114-128.	7.4	197
68	Mutational spectra of human cancer. <i>Human Genetics</i> , 2009, 125, 493-506.	3.8	160
69	Sunlight ultraviolet irradiation and <i>BRAF</i> V600 mutagenesis in human melanoma. <i>Human Mutation</i> , 2008, 29, 983-991.	2.5	50
70	High-resolution mapping of DNA hypermethylation and hypomethylation in lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 252-257.	7.1	322
71	Homeobox gene methylation in lung cancer studied by genome-wide analysis with a microarray-based methylated CpG island recovery assay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5527-5532.	7.1	260
72	Methylated-CpG island recovery assay-assisted microarrays for cancer diagnosis. <i>Expert Opinion on Medical Diagnostics</i> , 2007, 1, 99-108.	1.6	0

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73	Frequent hypermethylation ofMST1 andMST2 in soft tissue sarcoma. <i>Molecular Carcinogenesis</i> , 2007, 46, 865-871.	2.7	144
74	RASSF1A Is Part of a Complex Similar to the Drosophila Hippo/Salvador/Lats Tumor-Suppressor Network. <i>Current Biology</i> , 2007, 17, 700-705.	3.9	191
75	MIRA-Assisted Microarray Analysis, a New Technology for the Determination of DNA Methylation Patterns, Identifies Frequent Methylation of Homeodomain-Containing Genes in Lung Cancer Cells. <i>Cancer Research</i> , 2006, 66, 7939-7947.	0.9	276
76	Measuring the Formation and Repair of DNA Damage by Ligation-Mediated PCR. <i>Methods in Molecular Biology</i> , 2006, 314, 201-214.	0.9	6
77	Involvement of the <i>RASSF1A</i> Tumor Suppressor Gene in Controlling Cell Migration. <i>Cancer Research</i> , 2005, 65, 7653-7659.	0.9	78
78	DNA Damage and Mutagenesis Induced by Polycyclic Aromatic Hydrocarbons. , 2005, , 171-210.		3
79	Mutations induced by ultraviolet light. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2005, 571, 19-31.	1.0	656
80	DNA lesions induced by UV A1 and B radiation in human cells: Comparative analyses in the overall genome and in the p53 tumor suppressor gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10058-10063.	7.1	139
81	The role of DNA polymerase β in UV mutational spectra. <i>DNA Repair</i> , 2005, 4, 211-220.	2.8	60
82	Tumor susceptibility of <i>Rassf1a</i> knockout mice. <i>Cancer Research</i> , 2005, 65, 92-8.	0.9	154
83	On the origin of G \rightarrow T transversions in lung cancer. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2003, 526, 39-43.	1.0	73
84	Frequent epigenetic inactivation of the RASSF1A gene in hepatocellular carcinoma. <i>Oncogene</i> , 2003, 22, 1866-1871.	5.9	174
85	Control of microtubule stability by the RASSF1A tumor suppressor. <i>Oncogene</i> , 2003, 22, 8125-8136.	5.9	179
86	Deamination of 5-Methylcytosines within Cyclobutane Pyrimidine Dimers Is an Important Component of UVB Mutagenesis. <i>Journal of Biological Chemistry</i> , 2003, 278, 10314-10321.	3.4	89
87	Deamination of 5-methylcytosines within cyclobutane pyrimidine dimers is an important component of UVB mutagenesis.. <i>Journal of Biological Chemistry</i> , 2003, 278, 16454.	3.4	6
88	Epigenetic inactivation of RAS association domain family protein 1 (RASSF1A) in malignant cutaneous melanoma. <i>Cancer Research</i> , 2003, 63, 1639-43.	0.9	119
89	Methylation of the RASSF1A Gene in Human Cancers. <i>Biological Chemistry</i> , 2002, 383, 907-14.	2.5	106
90	The putative tumor suppressor RASSF1A homodimerizes and heterodimerizes with the Ras-GTP binding protein Nore1. <i>Oncogene</i> , 2002, 21, 1381-1390.	5.9	205

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91	Tobacco smoke carcinogens, DNA damage and p53 mutations in smoking-associated cancers. <i>Oncogene</i> , 2002, 21, 7435-7451.	5.9	961
92	Similarities in sunlight-induced mutational spectra of CpG-methylated transgenes and the p53 gene in skin cancer point to an important role of 5-methylcytosine residues in solar UV mutagenesis ¹¹ Edited by J. Miller. <i>Journal of Molecular Biology</i> , 2001, 305, 389-399.	4.2	95
93	Sequence-specific detection of aristolochic acid-DNA adducts in the human p53 gene by terminal transferase-dependent PCR. <i>Carcinogenesis</i> , 2001, 22, 133-140.	2.8	85
94	Hypermethylation of the CpG island of the RASSF1A gene in ovarian and renal cell carcinomas. <i>International Journal of Cancer</i> , 2001, 94, 212-217.	5.1	148
95	A new verdict for an old convict. <i>Nature Genetics</i> , 2001, 29, 3-4.	21.4	15
96	The CpG island of the novel tumor suppressor gene RASSF1A is intensely methylated in primary small cell lung carcinomas. <i>Oncogene</i> , 2001, 20, 3563-3567.	5.9	159
97	Cyclobutane Pyrimidine Dimers Are Responsible for the Vast Majority of Mutations Induced by UVB Irradiation in Mammalian Cells. <i>Journal of Biological Chemistry</i> , 2001, 276, 44688-44694.	3.4	245
98	Genomic structure and mutation screening of the E2F4 gene in human tumors. , 2000, 86, 672-677.		35
99	Epigenetic inactivation of a RAS association domain family protein from the lung tumour suppressor locus 3p21.3. <i>Nature Genetics</i> , 2000, 25, 315-319.	21.4	994
100	Targeting of Lung Cancer Mutational Hotspots by Polycyclic Aromatic Hydrocarbons. <i>Journal of the National Cancer Institute</i> , 2000, 92, 803-811.	6.3	262
101	Cyclobutane pyrimidine dimers form preferentially at the major p53 mutational hotspot in UVB-induced mouse skin tumors. <i>Carcinogenesis</i> , 2000, 21, 2113-2117.	2.8	95
102	Cell cycle-independent removal of UV-induced pyrimidine dimers from the promoter and the transcription initiation domain of the human CDC2 gene. <i>Nucleic Acids Research</i> , 2000, 28, 3991-3998.	14.5	25
103	The DNA damage spectrum produced by simulated sunlight ¹ Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2000, 299, 681-693.	4.2	149
104	Involvement of 5-methylcytosine in sunlight-induced mutagenesis ¹ Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1999, 293, 493-503.	4.2	88
105	The p53 codon 249 mutational hotspot in hepatocellular carcinoma is not related to selective formation or persistence of aflatoxin B1 adducts. <i>Oncogene</i> , 1998, 17, 3007-3014.	5.9	104
106	Formation and repair of DNA lesions in the p53 gene: Relation to cancer mutations?. , 1998, 31, 197-205.		60
107	Sequence and time-dependent deamination of cytosine bases in UVB-induced cyclobutane pyrimidine dimers in vivo. <i>Journal of Molecular Biology</i> , 1998, 284, 297-311.	4.2	91
108	In vivo evidence for binding of p53 to consensus binding sites in the p21 and GADD45 genes in response to ionizing radiation. <i>Oncogene</i> , 1997, 15, 87-99.	5.9	83

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109	Formation and Processing of UV Photoproducts: Effects of DNA Sequence and Chromatin Environment. <i>Photochemistry and Photobiology</i> , 1997, 65, 270-283.	2.5	276
110	Genomic sequencing by ligation-mediated PCR. <i>Molecular Biotechnology</i> , 1996, 5, 281-288.	2.4	16
111	A high-resolution analysis of chromatin structure along p53 sequences. <i>Molecular Carcinogenesis</i> , 1996, 17, 192-201.	2.7	16
112	UV damage and repair mechanisms in mammalian cells. <i>BioEssays</i> , 1996, 18, 221-228.	2.5	156
113	In vivo protein-DNA interactions at the c-jun promoter in quiescent and serum-stimulated fibroblasts. <i>Journal of Cellular Biochemistry</i> , 1995, 57, 479-487.	2.6	29
114	UV Light as a Footprinting Agent: Modulation of UV-induced DNA Damage by Transcription Factors Bound at the Promoters of Three Human Genes. <i>Journal of Molecular Biology</i> , 1995, 249, 714-728.	4.2	127
115	X-chromosome inactivation and cell memory. <i>Trends in Genetics</i> , 1992, 8, 169-174.	6.7	295