Gerd P Pfeifer

List of Publications by Year in descending order

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115	15,333	60	107
papers	citations	h-index	g-index
119	119	119	18151 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	Epigenetic inactivation of a RAS association domain family protein from the lung tumour suppressor locus 3p21.3. Nature Genetics, 2000, 25, 315-319.	9.4	994
2	The role of Tet3 DNA dioxygenase in epigenetic reprogramming by oocytes. Nature, 2011, 477, 606-610.	13.7	969
3	Tobacco smoke carcinogens, DNA damage and p53 mutations in smoking-associated cancers. Oncogene, 2002, 21, 7435-7451.	2.6	961
4	Mutations induced by ultraviolet light. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2005, 571, 19-31.	0.4	656
5	Reprogramming of the paternal genome upon fertilization involves genome-wide oxidation of 5-methylcytosine. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3642-3647.	3.3	618
6	5-Hydroxymethylcytosine Is Strongly Depleted in Human Cancers but Its Levels Do Not Correlate with <i>IDH1</i> Mutations. Cancer Research, 2011, 71, 7360-7365.	0.4	400
7	Aging and DNA methylation. BMC Biology, 2015, 13, 7.	1.7	397
8	Examination of the specificity of DNA methylation profiling techniques towards 5-methylcytosine and 5-hydroxymethylcytosine. Nucleic Acids Research, 2010, 38, e125-e125.	6. 5	389
9	Dynamics of 5-Hydroxymethylcytosine and Chromatin Marks in Mammalian Neurogenesis. Cell Reports, 2013, 3, 291-300.	2.9	385
10	UV wavelength-dependent DNA damage and human non-melanoma and melanoma skin cancer. Photochemical and Photobiological Sciences, 2012, 11, 90-97.	1.6	346
11	Genomic mapping of 5-hydroxymethylcytosine in the human brain. Nucleic Acids Research, 2011, 39, 5015-5024.	6.5	344
12	High-resolution mapping of DNA hypermethylation and hypomethylation in lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 252-257.	3.3	322
13	A human B cell methylome at 100â^'base pair resolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 671-678.	3.3	319
14	X-chromosome inactivation and cell memory. Trends in Genetics, 1992, 8, 169-174.	2.9	295
15	Formation and Processing of UV Photoproducts: Effects of DNA Sequence and Chromatin Environment. Photochemistry and Photobiology, 1997, 65, 270-283.	1.3	276
16	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. Cancer Research, 2006, 66, 7939-7947.	0.4	276
17	Targeting of Lung Cancer Mutational Hotspots by Polycyclic Aromatic Hydrocarbons. Journal of the National Cancer Institute, 2000, 92, 803-811.	3.0	262
18	Homeobox gene methylation in lung cancer studied by genome-wide analysis with a microarray-based methylated CpG island recovery assay. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5527-5532.	3.3	260

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19	Cyclobutane Pyrimidine Dimers Are Responsible for the Vast Majority of Mutations Induced by UVB Irradiation in Mammalian Cells. Journal of Biological Chemistry, 2001, 276, 44688-44694.	1.6	245
20	Defining Driver DNA Methylation Changes in Human Cancer. International Journal of Molecular Sciences, 2018, 19, 1166.	1.8	238
21	The putative tumor suppressor RASSF1A homodimerizes and heterodimerizes with the Ras-GTP binding protein Nore1. Oncogene, 2002, 21, 1381-1390.	2.6	205
22	The RASSF proteins in cancer; from epigenetic silencing to functional characterization. Biochimica Et Biophysica Acta: Reviews on Cancer, 2009, 1796, 114-128.	3.3	197
23	RASSF1A Is Part of a Complex Similar to the Drosophila Hippo/Salvador/Lats Tumor-Suppressor Network. Current Biology, 2007, 17, 700-705.	1.8	191
24	Control of microtubule stability by the RASSF1A tumor suppressor. Oncogene, 2003, 22, 8125-8136.	2.6	179
25	Somatic <i>TP53</i> Mutations in the Era of Genome Sequencing. Cold Spring Harbor Perspectives in Medicine, 2016, 6, a026179.	2.9	176
26	Frequent epigenetic inactivation of the RASSF1A gene in hepatocellular carcinoma. Oncogene, 2003, 22, 1866-1871.	2.6	174
27	Epigenetic changes of DNA repair genes in cancer. Journal of Molecular Cell Biology, 2011, 3, 51-58.	1.5	168
28	Mutational spectra of human cancer. Human Genetics, 2009, 125, 493-506.	1.8	160
29	The CpG island of the novel tumor suppressor gene RASSF1A is intensely methylated in primary small cell lung carcinomas. Oncogene, 2001, 20, 3563-3567.	2.6	159
30	5-hydroxymethylcytosine and its potential roles in development and cancer. Epigenetics and Chromatin, 2013, 6, 10.	1.8	157
31	UV damage and repair mechanisms in mammalian cells. BioEssays, 1996, 18, 221-228.	1.2	156
32	Tumor susceptibility of Rassf1a knockout mice. Cancer Research, 2005, 65, 92-8.	0.4	154
33	The DNA damage spectrum produced by simulated sunlight 1 1Edited by I. Tinoco. Journal of Molecular Biology, 2000, 299, 681-693.	2.0	149
34	Hypermethylation of the CpG island of the RASSF1A gene in ovarian and renal cell carcinomas. International Journal of Cancer, 2001, 94, 212-217.	2.3	148
35	Frequent hypermethylation of MST1 and MST2 in soft tissue sarcoma. Molecular Carcinogenesis, 2007, 46, 865-871.	1.3	144
36	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. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10058-10063.	3.3	139

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37	Relationship between Gene Body DNA Methylation and Intragenic H3K9me3 and H3K36me3 Chromatin Marks. PLoS ONE, 2011, 6, e18844.	1.1	131
38	An Intrinsic Epigenetic Barrier for Functional Axon Regeneration. Neuron, 2017, 94, 337-346.e6.	3.8	130
39	Identification of Driver and Passenger DNA Methylation in Cancer by Epigenomic Analysis. Advances in Genetics, 2010, 70, 277-308.	0.8	128
40	UV Light as a Footprinting Agent: Modulation of UV-induced DNA Damage by Transcription Factors Bound at the Promoters of Three Human Genes. Journal of Molecular Biology, 1995, 249, 714-728.	2.0	127
41	CpG Island Hypermethylation in Human Astrocytomas. Cancer Research, 2010, 70, 2718-2727.	0.4	122
42	Epigenetic inactivation of RAS association domain family protein 1 (RASSF1A) in malignant cutaneous melanoma. Cancer Research, 2003, 63, 1639-43.	0.4	119
43	Wavelength dependence of ultraviolet radiationâ€induced DNA damage as determined by laser irradiation suggests that cyclobutane pyrimidine dimers are the principal DNA lesions produced by terrestrial sunlight. FASEB Journal, 2011, 25, 3079-3091.	0.2	118
44	DNA methylation biomarkers for lung cancer. Tumor Biology, 2012, 33, 287-296.	0.8	116
45	5-Hydroxymethylcytosine: A stable or transient DNA modification?. Genomics, 2014, 104, 314-323.	1.3	114
46	Tet3 Reads 5-Carboxylcytosine through Its CXXC Domain and Is a Potential Guardian against Neurodegeneration. Cell Reports, 2016, 14, 493-505.	2.9	109
47	Methylation of the RASSF1A Gene in Human Cancers. Biological Chemistry, 2002, 383, 907-14.	1.2	106
48	The p53 codon 249 mutational hotspot in hepatocellular carcinoma is not related to selective formation or persistence of aflatoxin B1 adducts. Oncogene, 1998, 17, 3007-3014.	2.6	104
49	DNA methylation patterns in lung carcinomas. Seminars in Cancer Biology, 2009, 19, 181-187.	4.3	100
50	The Tumor Suppressor RASSF1A Prevents Dephosphorylation of the Mammalian STE20-like Kinases MST1 and MST2. Journal of Biological Chemistry, 2011, 286, 6253-6261.	1.6	99
51	Cyclobutane pyrimidine dimers form preferentially at the major p53 mutational hotspot in UVB-induced mouse skin tumors. Carcinogenesis, 2000, 21, 2113-2117.	1.3	95
52	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 mutagenesis11Edited by J. Miller. Journal of Molecular Biology, 2001, 305, 389-399.	2.0	95
53	Sequence and time-dependent deamination of cytosine bases in UVB-induced cyclobutane pyrimidine dimers in vivo. Journal of Molecular Biology, 1998, 284, 297-311.	2.0	91
54	Deamination of 5-Methylcytosines within Cyclobutane Pyrimidine Dimers Is an Important Component of UVB Mutagenesis. Journal of Biological Chemistry, 2003, 278, 10314-10321.	1.6	89

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55	Involvement of 5-methylcytosine in sunlight-induced mutagenesis 1 1Edited by J. Karn. Journal of Molecular Biology, 1999, 293, 493-503.	2.0	88
56	The role of 5-hydroxymethylcytosine in human cancer. Cell and Tissue Research, 2014, 356, 631-641.	1.5	87
57	Sequence-specific detection of aristolochic acid-DNA adducts in the human p53 gene by terminal transferase-dependent PCR. Carcinogenesis, 2001, 22, 133-140.	1.3	85
58	In vivo evidence for binding of p53 to consensus binding sites in the p21 and GADD45 genes in response to ionizing radiation. Oncogene, 1997, 15, 87-99.	2.6	83
59	Involvement of the <i>RASSF1A</i> Tumor Suppressor Gene in Controlling Cell Migration. Cancer Research, 2005, 65, 7653-7659.	0.4	78
60	On the origin of G→T transversions in lung cancer. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2003, 526, 39-43.	0.4	73
61	Formation and repair of DNA lesions in thep53 gene: Relation to cancer mutations?., 1998, 31, 197-205.		60
62	The role of DNA polymerase $\hat{\textbf{l}}\cdot$ in UV mutational spectra. DNA Repair, 2005, 4, 211-220.	1.3	60
63	Environmental exposures and mutational patterns of cancer genomes. Genome Medicine, 2010, 2, 54.	3.6	58
64	Mechanisms of UV-induced mutations and skin cancer. Genome Instability & Disease, 2020, 1, 99-113.	0.5	53
65	Sunlight ultraviolet irradiation and <i>BRAF </i> V600 mutagenesis in human melanoma. Human Mutation, 2008, 29, 983-991.	1.1	50
66	The DNA methylation landscape of human melanoma. Genomics, 2015, 106, 322-330.	1.3	50
67	DNA methylation profiling using the methylated-CpG island recovery assay (MIRA). Methods, 2010, 52, 213-217.	1.9	48
68	Dynamics of RNA Polymerase II Pausing and Bivalent Histone H3 Methylation during Neuronal Differentiation in Brain Development. Cell Reports, 2017, 20, 1307-1318.	2.9	47
69	Loss of the Polycomb Mark from Bivalent Promoters Leads to Activation of Cancer-Promoting Genes in Colorectal Tumors. Cancer Research, 2014, 74, 3617-3629.	0.4	43
70	MIRA-seq for DNA methylation analysis of CpG islands. Epigenomics, 2015, 7, 695-706.	1.0	37
71	Next-generation sequencing: emerging lessons on the origins of human cancer. Current Opinion in Oncology, 2011, 23, 62-68.	1.1	36
72	Genomic structure and mutation screening of the E2F4 gene in human tumors., 2000, 86, 672-677.		35

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73	<i>Drosophila</i> genomic methylation: new evidence and new questions. Epigenomics, 2014, 6, 459-461.	1.0	35
74	Longitudinal epigenetic and gene expression profiles analyzed by three-component analysis reveal down-regulation of genes involved in protein translation in human aging. Nucleic Acids Research, 2015, 43, e100-e100.	6.5	35
75	Are there specific readers of oxidized 5â€methylcytosine bases?. BioEssays, 2016, 38, 1038-1047.	1.2	34
76	Reprogramming of DNA methylation at NEUROD2-bound sequences during cortical neuron differentiation. Science Advances, 2019, 5, eaax0080.	4.7	32
77	Single Base Resolution Analysis of 5-Methylcytosine and 5-Hydroxymethylcytosine by RRBS and TAB-RRBS. Methods in Molecular Biology, 2015, 1238, 273-287.	0.4	31
78	How the environment shapes cancer genomes. Current Opinion in Oncology, 2015, 27, 71-77.	1.1	31
79	Suppressor of hepatocellular carcinoma RASSF1A activates autophagy initiation and maturation. Cell Death and Differentiation, 2019, 26, 1379-1395.	5.0	30
80	In vivo protein-DNA interactions at the c-jun promoter in quiescent and serum-stimulated fibroblasts. Journal of Cellular Biochemistry, 1995, 57, 479-487.	1.2	29
81	The chromosomal protein SMCHD1 regulates DNA methylation and the 2c-like state of embryonic stem cells by antagonizing TET proteins. Science Advances, 2021, 7, .	4.7	28
82	Detection of Oxidation Products of 5-Methyl-2′-Deoxycytidine in Arabidopsis DNA. PLoS ONE, 2013, 8, e84620.	1.1	27
83	Interactions between hepatitis B virus and aflatoxin B1: effects on p53 induction in HepaRG cells. Journal of General Virology, 2012, 93, 640-650.	1.3	26
84	Genome-wide mapping of 5-hydroxymethylcytosine in three rice cultivars reveals its preferential localization in transcriptionally silent transposable element genes. Journal of Experimental Botany, 2015, 66, 6651-6663.	2.4	26
85	Cell cycle-independent removal of UV-induced pyrimidine dimers from the promoter and the transcription initiation domain of the human CDC2 gene. Nucleic Acids Research, 2000, 28, 3991-3998.	6.5	25
86	Protein Interactions at Oxidized 5-Methylcytosine Bases. Journal of Molecular Biology, 2020, 432, 1718-1730.	2.0	25
87	Formation of cyclobutane pyrimidine dimers at dipyrimidines containing 5-hydroxymethylcytosine. Photochemical and Photobiological Sciences, 2013, 12, 1409-1415.	1.6	24
88	The major mechanism of melanoma mutations is based on deamination of cytosine in pyrimidine dimers as determined by circle damage sequencing. Science Advances, 2021, 7, .	4.7	23
89	Analysis of Liver Tumor-Prone Mouse Models of the Hippo Kinase Scaffold Proteins RASSF1A and SAV1. Cancer Research, 2016, 76, 2824-2835.	0.4	22
90	UVB irradiation does not directly induce detectable changes of DNA methylation in human keratinocytes. F1000Research, 2013, 2, 45.	0.8	21

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91	Genomic sequencing by ligation-mediated PCR. Molecular Biotechnology, 1996, 5, 281-288.	1.3	16
92	A high-resolution analysis of chromatin structure alongp53 sequences. Molecular Carcinogenesis, 1996, 17, 192-201.	1.3	16
93	A new verdict for an old convict. Nature Genetics, 2001, 29, 3-4.	9.4	15
94	Gene body profiles of 5-hydroxymethylcytosine: potential origin, function and use as a cancer biomarker. Epigenomics, 2018, 10, 1029-1032.	1.0	14
95	RASSF proteins. Current Biology, 2010, 20, R344-R345.	1.8	11
96	Uveal Melanoma and <i>GNA11</i> Mutations: a new piece added to the puzzle. Pigment Cell and Melanoma Research, 2011, 24, 18-20.	1.5	11
97	The tumour suppressor Ras-association domain family protein 1A (RASSF1A) regulates TNF-α signalling in cardiomyocytes. Cardiovascular Research, 2014, 103, 47-59.	1.8	10
98	How tobacco smoke changes the (epi)genome. Science, 2016, 354, 549-550.	6.0	10
99	Concordance of hydrogen peroxide–induced 8-oxo-guanine patterns with two cancer mutation signatures of upper GI tract tumors. Science Advances, 2022, 8, .	4.7	10
100	The epigenetic DNA modification 5-carboxylcytosine promotes high levels of cyclobutane pyrimidine dimer formation upon UVB irradiation. Genome Instability & Disease, 2021, 2, 59-69.	0.5	7
101	Measuring the Formation and Repair of DNA Damage by Ligation-Mediated PCR. Methods in Molecular Biology, 2006, 314, 201-214.	0.4	6
102	Smoke signals in the DNA of normal lung cells. Nature, 2020, 578, 224-226.	13.7	6
103	Deamination of 5-methylcytosines within cyclobutane pyrimidine dimers is an important component of UVB mutagenesis Journal of Biological Chemistry, 2003, 278, 16454.	1.6	6
104	3′HS1 CTCF binding site in human β-globin locus regulates fetal hemoglobin expression. ELife, 2021, 10, .	2.8	5
105	High-Resolution Analysis of 5-Hydroxymethylcytosine by TET-Assisted Bisulfite Sequencing. Methods in Molecular Biology, 2021, 2198, 321-331.	0.4	4
106	DNA Damage and Mutagenesis Induced by Polycyclic Aromatic Hydrocarbons. , 2005, , 171-210.		3
107	Purification of TET Proteins. Methods in Molecular Biology, 2021, 2272, 225-237.	0.4	2
108	Properly dividing with YAP. Science Signaling, 2016, 9, fs3.	1.6	1

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109	DNA repair in neurons and its possible link to the epigenetic machinery at enhancers. Epigenomics, 2021, 13, 913-917.	1.0	1
110	The ups and downs of DNA methylation: an interview with Gerd Pfeifer. Epigenomics, 2021, , .	1.0	1
111	Methylated-CpG island recovery assay-assisted microarrays for cancer diagnosis. Expert Opinion on Medical Diagnostics, 2007, 1, 99-108.	1.6	0
112	Switching enhancer methylation in metastatic melanoma. Pigment Cell and Melanoma Research, 2016, 29, 491-493.	1.5	0
113	Methods for Assessing DNA Cytosine Modifications Genome-Wide. , 2017, , 125-134.		0
114	5-Methylcytosine and Its Oxidized Derivatives. , 2019, , 65-86.		0
115	Lack of Major Genome-Wide DNA Methylation Changes in Succinate-Treated Human Epithelial Cells. International Journal of Molecular Sciences, 2022, 23, 5663.	1.8	0