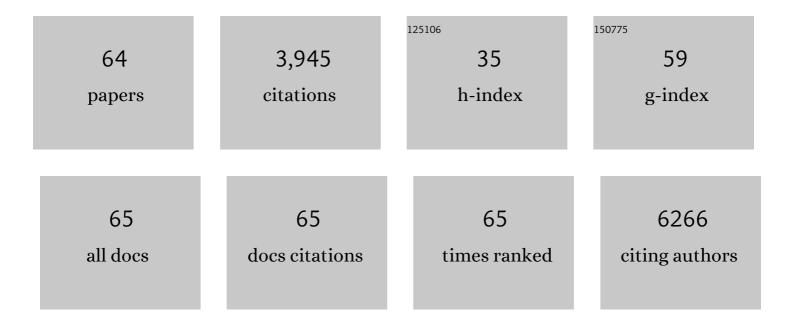
Bernard W Futscher

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Liquid biopsy, using a novel DNA methylation signature, distinguishes pancreatic adenocarcinoma from benign pancreatic disease. Clinical Epigenetics, 2022, 14, 28.	1.8	9
2	DNA methylation biomarkers discovered <i>in silico</i> detect cancer in liquid biopsies from non-small cell lung cancer patients. Epigenetics, 2020, 15, 419-430.	1.3	23
3	DNA methylation changes in biomarker loci occur early in cancer progression. F1000Research, 2019, 8, 2106.	0.8	7
4	A suite of DNA methylation markers that can detect most common human cancers. Epigenetics, 2018, 13, 61-72.	1.3	48
5	Epigenetic silencing of IncRNA MORT in 16 TCGA cancer types. F1000Research, 2018, 7, 211.	0.8	31
6	Age and the means of bypassing stasis influence the intrinsic subtype of immortalized human mammary epithelial cells. Frontiers in Cell and Developmental Biology, 2015, 3, 13.	1.8	25
7	A lincRNA connected to cell mortality and epigenetically-silenced in most common human cancers. Epigenetics, 2015, 10, 1074-1083.	1.3	28
8	Differentially Expressed MicroRNAs in Postpartum Breast Cancer in Hispanic Women. PLoS ONE, 2015, 10, e0124340.	1.1	23
9	Exome-wide mutation profile in benzo[a]pyrene-derived post-stasis and immortal human mammary epithelial cells. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2014, 775-776, 48-54.	0.9	29
10	Immortalization of normal human mammary epithelial cells in two steps by direct targeting of senescence barriers does not require gross genomic alterations. Cell Cycle, 2014, 13, 3423-3435.	1.3	60
11	Hypoxia perturbs aryl hydrocarbon receptor signaling and CYP1A1 expression induced by PCB 126 in human skin and liver-derived cell lines. Toxicology and Applied Pharmacology, 2014, 274, 408-416.	1.3	71
12	Characterization of Hepatocellular Carcinoma Related Genes and Metabolites in Human Nonalcoholic Fatty Liver Disease. Digestive Diseases and Sciences, 2014, 59, 365-374.	1.1	39
13	Maintenance of mitochondrial genomic integrity in the absence of manganese superoxide dismutase in mouse liver hepatocytes. Redox Biology, 2013, 1, 172-177.	3.9	16
14	Arsenic exposure induces the Warburg effect in cultured human cells. Toxicology and Applied Pharmacology, 2013, 271, 72-77.	1.3	61
15	Coordinate H3K9 and DNA methylation silencing of ZNFs in toxicant-induced malignant transformation. Epigenetics, 2013, 8, 1080-1088.	1.3	40
16	miRNA Gene Promoters Are Frequent Targets of Aberrant DNA Methylation in Human Breast Cancer. PLoS ONE, 2013, 8, e54398.	1.1	110
17	In Vitro Assessment of the Inflammatory Breast Cancer Cell Line SUM 149: Discovery of 2 Single Nucleotide Polymorphisms in the RNase L Gene. Journal of Cancer, 2013, 4, 104-116.	1.2	7
18	Epigenetic Changes During Cell Transformation. Advances in Experimental Medicine and Biology, 2013, 754, 179-194.	0.8	22

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19	Genetic and Epigenetic Inactivation of Extracellular Superoxide Dismutase Promotes an Invasive Phenotype in Human Lung Cancer by Disrupting ECM Homeostasis. Molecular Cancer Research, 2012, 10, 40-51.	1.5	69
20	Agglomerates of aberrant DNA methylation are associated with toxicant-induced malignant transformation. Epigenetics, 2012, 7, 1238-1248.	1.3	30
21	Cell-Type Specific DNA Methylation Patterns Define Human Breast Cellular Identity. PLoS ONE, 2012, 7, e52299.	1.1	22
22	The Epigenetic Basis of Cell Type Specificity. FASEB Journal, 2012, 26, 83.1.	0.2	0
23	Hypomethylation of the 14â€3â€3σ promoter leads to increased expression in nonâ€small cell lung cancer. Genes Chromosomes and Cancer, 2011, 50, 830-836.	1.5	22
24	Epigenetic regulation of normal human mammary cell type–specific miRNAs. Genome Research, 2011, 21, 2026-2037.	2.4	68
25	Arsenic Toxicology: Translating between Experimental Models and Human Pathology. Environmental Health Perspectives, 2011, 119, 1356-1363.	2.8	98
26	Role for DNA Methylation in the Regulation of miR-200c and miR-141 Expression in Normal and Cancer Cells. PLoS ONE, 2010, 5, e8697.	1.1	268
27	Monomethylarsonous Acid Produces Irreversible Events Resulting in Malignant Transformation of a Human Bladder Cell Line Following 12 Weeks of Low-Level Exposure. Toxicological Sciences, 2010, 116, 44-57.	1.4	47
28	Stepwise DNA Methylation Changes Are Linked to Escape from Defined Proliferation Barriers and Mammary Epithelial Cell Immortalization. Cancer Research, 2009, 69, 5251-5258.	0.4	113
29	Epigenetic mediated transcriptional activation of WNT5A participates in arsenical-associated malignant transformation. Toxicology and Applied Pharmacology, 2009, 235, 39-46.	1.3	78
30	Arsenicals produce stable progressive changes in DNA methylation patterns that are linked to malignant transformation of immortalized urothelial cells. Toxicology and Applied Pharmacology, 2009, 241, 221-229.	1.3	44
31	p53 induces distinct epigenetic states at its direct target promoters. BMC Genomics, 2008, 9, 486.	1.2	49
32	Different Mutant/Wild-Type p53 Combinations Cause a Spectrum of Increased Invasive Potential in Nonmalignant Immortalized Human Mammary Epithelial Cells. Neoplasia, 2008, 10, 450-461.	2.3	60
33	Epigenetic remodeling during arsenical-induced malignant transformation. Carcinogenesis, 2008, 29, 1500-1508.	1.3	113
34	Agglomerative Epigenetic Aberrations Are a Common Event in Human Breast Cancer. Cancer Research, 2008, 68, 8616-8625.	0.4	146
35	Optimal Search-Based Gene Subset Selection for Gene Array Cancer Classification. IEEE Transactions on Information Technology in Biomedicine, 2007, 11, 398-405.	3.6	40
36	Epigenetic regulation of maspin expression in human ovarian carcinoma cells. Gynecologic Oncology, 2006, 102, 319-324.	0.6	48

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37	Comparisons of PCR-based genome amplification systems using CpG island microarrays. Human Mutation, 2006, 27, 589-596.	1.1	5
38	Pharmacogenomics of the Polyamine Analog 3,8,13,18-tetraaza-10,11-[(E)-1,2-cyclopropyl] eicosane Tetrahydrochloride, CGC-11093, in the Colon Adenocarcinoma Cell Line HCT1161. Technology in Cancer Research and Treatment, 2006, 5, 553-564.	0.8	7
39	Epigenetic Inactivation of the HOXA Gene Cluster in Breast Cancer. Cancer Research, 2006, 66, 10664-10670.	0.4	109
40	Epigenetic Regulation of the Cell Type-Specific Gene 14-3-3Ïf. Neoplasia, 2005, 7, 799-808.	2.3	22
41	Flipping the Epigenetic Switch. American Journal of Pathology, 2004, 164, 1883-1886.	1.9	18
42	Aberrant Methylation of the Maspin Promoter Is an Early Event in Human Breast Cancer. Neoplasia, 2004, 6, 380-389.	2.3	61
43	The acetyltransferase p300/CBP-associated factor is a p53 target gene in breast tumor cells. Neoplasia, 2004, 6, 187-94.	2.3	14
44	Mutant p53 and aberrant cytosine methylation cooperate to silence gene expression. Oncogene, 2003, 22, 3624-3634.	2.6	88
45	Human Pancreatic Carcinoma Cells Activate Maspin Expression Through Loss of Epigenetic Control. Neoplasia, 2003, 5, 427-436.	2.3	43
46	MnSOD Up-Regulates Maspin Tumor Suppressor Gene Expression in Human Breast and Prostate Cancer Cells. Antioxidants and Redox Signaling, 2003, 5, 677-688.	2.5	38
47	Development and molecular characterization of HCT-116 cell lines resistant to the tumor promoter and multiple stress-inducer, deoxycholate. Carcinogenesis, 2002, 23, 2063-2080.	1.3	74
48	Role for DNA methylation in the control of cell type–specific maspin expression. Nature Genetics, 2002, 31, 175-179.	9.4	403
49	5-Azacytidine Modulates the Response of Sensitive and Multidrug-Resistant K562 Leukemic Cells to Cytostatic Drugs. Blood Cells, Molecules, and Diseases, 2001, 27, 637-648.	0.6	24
50	Identification of a Novel Structural Variant of the α6 Integrin. Journal of Biological Chemistry, 2001, 276, 26099-26106.	1.6	53
51	Epigenetic silencing of maspin gene expression in human breast cancers. , 2000, 85, 805-810.		157
52	Methylation of the BRCA1 promoter is associated with decreased BRCA1 mRNA levels in clinical breast cancer specimens. Carcinogenesis, 2000, 21, 1761-1765.	1.3	211
53	Transcriptional repression of BRCA1 by aberrant cytosine methylation, histone hypoacetylation and chromatin condensation of the BRCA1 promoter. Nucleic Acids Research, 2000, 28, 3233-3239.	6.5	83
54	Aberrant methylation of the BRCA1 CpG island promoter is associated with decreased BRCA1 mRNA in sporadic breast cancer cells. Oncogene, 1998, 17, 1807-1812.	2.6	221

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55	Selective variegated methylation of thep15 CpG island in acute myeloid leukemia. , 1998, 78, 561-567.		63
56	Decreased CP-1 (NF-Y) Activity Results in Transcriptional Down-Regulation of Topoisomerase Ilα in a Doxorubicin-Resistant Variant of Human Multiple Myeloma RPMI 8226. Biochemical and Biophysical Research Communications, 1997, 237, 217-224.	1.0	22
57	Methylation of CpG Island Transcription Factor Binding Sites Is Unnecessary for Aberrant Silencing of the Human MGMT Gene. Journal of Biological Chemistry, 1996, 271, 13916-13924.	1.6	72
58	Verapamil suppresses the emergence of P-glycoprotein-mediated multi-drug resistance. , 1996, 66, 520-525.		46
59	Detecting differences in 5-methylcytosine using restriction enzyme isoschizomers: an endogenous control for complete digestion. Nucleic Acids Research, 1995, 23, 4740-4741.	6.5	3
60	Analysis of MRP mRNA in mitoxantrone-selected, multidrug-resistant human tumor cells. Biochemical Pharmacology, 1994, 47, 1601-1606.	2.0	61
61	DNA?Damaging and Transcription-Terminating Lesions Induced by AF64A In Vitro. Journal of Neurochemistry, 1992, 58, 1504-1509.	2.1	21
62	Gene amplification affecting O6-alkylguanine-DNA alkyltransferase activity is not detected in nitrosourea resistant or sensitive human cell lines. Carcinogenesis, 1990, 11, 479-483.	1.3	4
63	Transcription-terminating lesions induced by bifunctional alkylating agents in vitro. Carcinogenesis, 1989, 10, 1307-1314.	1.3	53
64	DNA methylation changes in biomarker loci occur early in cancer progression. F1000Research, 0, 8, 2106.	0.8	5