Lukas Vrba

List of Publications by Year in descending order

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LIIKAS VORA

#	Article	IF	CITATIONS
1	Role for DNA Methylation in the Regulation of miR-200c and miR-141 Expression in Normal and Cancer Cells. PLoS ONE, 2010, 5, e8697.	2.5	268
2	miRNA Gene Promoters Are Frequent Targets of Aberrant DNA Methylation in Human Breast Cancer. PLoS ONE, 2013, 8, e54398.	2.5	110
3	Epigenetic regulation of normal human mammary cell type–specific miRNAs. Genome Research, 2011, 21, 2026-2037.	5.5	68
4	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.	5.3	60
5	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.	2.6	60
6	p53 induces distinct epigenetic states at its direct target promoters. BMC Genomics, 2008, 9, 486.	2.8	49
7	A suite of DNA methylation markers that can detect most common human cancers. Epigenetics, 2018, 13, 61-72.	2.7	48
8	Coordinate H3K9 and DNA methylation silencing of ZNFs in toxicant-induced malignant transformation. Epigenetics, 2013, 8, 1080-1088.	2.7	40
9	Sequence Analysis of a "True―Chalcone Synthase (chs_H1) Oligofamily from hop (Humulus lupulusL.) and PAP1 Activation ofchs_H1 in Heterologous Systems. Journal of Agricultural and Food Chemistry, 2006, 54, 7606-7615.	5.2	37
10	The Variability of Hop Latent Viroid as Induced upon Heat Treatment. Virology, 2001, 287, 349-358.	2.4	35
11	Epigenetic silencing of IncRNA MORT in 16 TCGA cancer types. F1000Research, 2018, 7, 211.	1.6	31
12	Agglomerates of aberrant DNA methylation are associated with toxicant-induced malignant transformation. Epigenetics, 2012, 7, 1238-1248.	2.7	30
13	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.	1.7	29
14	A lincRNA connected to cell mortality and epigenetically-silenced in most common human cancers. Epigenetics, 2015, 10, 1074-1083.	2.7	28
15	New STS molecular markers for assessment of genetic diversity and DNA fingerprinting in hop (Humulus lupulus L.). Genome, 2007, 50, 15-25.	2.0	27
16	Cloning and Molecular Analysis of the Regulatory FactorHlMyb1in Hop (Humulus lupulusL.) and the Potential of Hop To Produce Bioactive Prenylated Flavonoids. Journal of Agricultural and Food Chemistry, 2005, 53, 4793-4798.	5.2	26
17	Molecular characterization and genome organization of 7SL RNA genes from hop (Humulus lupulus) Tj ETQq1 I	l 0.784314 2.2	rgBT /Over o
18	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.	3.7	25

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19	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.	2.7	23
20	Differentially Expressed MicroRNAs in Postpartum Breast Cancer in Hispanic Women. PLoS ONE, 2015, 10, e0124340.	2.5	23
21	Epigenetic Silencing of <i>MORT</i> Is an Early Event in Cancer and Is Associated with Luminal, Receptor Positive Breast Tumor Subtypes. Journal of Breast Cancer, 2017, 20, 198.	1.9	19
22	The promiscuity of heterospecific lox sites increases dramatically in the presence of palindromic DNA. Gene, 2002, 296, 129-137.	2.2	17
23	Isolation and characterization of a novel semi-lethal Arabidopsis thaliana mutant of gene for pentatricopeptide (PPR) repeat-containing protein. Genetica, 2006, 128, 395-407.	1.1	16
24	Liquid biopsy, using a novel DNA methylation signature, distinguishes pancreatic adenocarcinoma from benign pancreatic disease. Clinical Epigenetics, 2022, 14, 28.	4.1	9
25	Plant 7SL RNA and tRNA(Tyr) genes with inserted antisense sequences are efficiently expressed in an in vitro transcription system from Nicotiana tabacum cells. Plant Molecular Biology, 2002, 50, 713-723.	3.9	7
26	Expression of modified 7SL RNA gene in transgenic Solanum tuberosum plants. Biologia Plantarum, 2005, 49, 371-380.	1.9	7
27	DNA methylation changes in biomarker loci occur early in cancer progression. F1000Research, 2019, 8, 2106.	1.6	7
28	DNA methylation changes in biomarker loci occur early in cancer progression. F1000Research, 0, 8, 2106.	1.6	5
29	Abstract 5448: Common targets of epigenetic dysfunction in distinct target tissues of arsenic and cadmium induced malignant transformation. , 2012, , .		1
30	Abstract B008: Efficient immortalization of normal human mammary epithelial cells using two pathologically relevant agents does not require gross genomic alterations. , 2013, , .		1
31	Abstract B13: Epigenetic silencing alters the SLIT2/ROBO1/miR-218-1 signaling axis in pancreatic cancer. , 2013, , .		1
32	Abstract A41: Vulnerability of human mammary epithelial cells to oncogenic transformation. , 2011, , .		0
33	Abstract 123: DNA methylation of miRNA promoters in breast cancer. , 2012, , .		0
34	Abstract 127: Alternative transcription of the SLIT2/mir-218-1 signaling axis mediates pancreatic cancer invasion through the regulation of invadopodia. , 2014, , .		0
35	Abstract C74: Epigenetic changes in postpartum breast cancer amongst Hispanic women. , 2014, , .		0
36	Abstract A79: Post-transcriptional regulatory networks of pancreatic tumor invasion. , 2015, , .		0