

# Lukas Vrba

## List of Publications by Year in descending order

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36  
papers

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citations

394421  
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526287  
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all docs

37  
docs citations

37  
times ranked

2037  
citing authors

#	ARTICLE	IF	CITATIONS
1	Liquid biopsy, using a novel DNA methylation signature, distinguishes pancreatic adenocarcinoma from benign pancreatic disease. Clinical Epigenetics, 2022, 14, 28.	4.1	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.	2.7	23
3	DNA methylation changes in biomarker loci occur early in cancer progression. F1000Research, 2019, 8, 2106.	1.6	7
4	A suite of DNA methylation markers that can detect most common human cancers. Epigenetics, 2018, 13, 61-72.	2.7	48
5	Epigenetic silencing of lncRNA MORT in 16 TCGA cancer types. F1000Research, 2018, 7, 211.	1.6	31
6	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
7	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
8	A lincRNA connected to cell mortality and epigenetically-silenced in most common human cancers. Epigenetics, 2015, 10, 1074-1083.	2.7	28
9	Differentially Expressed MicroRNAs in Postpartum Breast Cancer in Hispanic Women. PLoS ONE, 2015, 10, e0124340.	2.5	23
10	Abstract A79: Post-transcriptional regulatory networks of pancreatic tumor invasion. , 2015, , .		0
11	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
12	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
13	Abstract 127: Alternative transcription of the SLIT2/mir-218-1 signaling axis mediates pancreatic cancer invasion through the regulation of invadopodia. , 2014, , .		0
14	Abstract C74: Epigenetic changes in postpartum breast cancer amongst Hispanic women. , 2014, , .		0
15	Coordinate H3K9 and DNA methylation silencing of ZNFs in toxicant-induced malignant transformation. Epigenetics, 2013, 8, 1080-1088.	2.7	40
16	miRNA Gene Promoters Are Frequent Targets of Aberrant DNA Methylation in Human Breast Cancer. PLoS ONE, 2013, 8, e54398.	2.5	110
17	Abstract B008: Efficient immortalization of normal human mammary epithelial cells using two pathologically relevant agents does not require gross genomic alterations. , 2013, , .		1
18	Abstract B13: Epigenetic silencing alters the SLIT2/ROBO1/miR-218-1 signaling axis in pancreatic cancer. , 2013, , .		1

#	ARTICLE	IF	CITATIONS
19	Agglomerates of aberrant DNA methylation are associated with toxicant-induced malignant transformation. <i>Epigenetics</i> , 2012, 7, 1238-1248.	2.7	30
20	Abstract 5448: Common targets of epigenetic dysfunction in distinct target tissues of arsenic and cadmium induced malignant transformation. , 2012, , .		1
21	Abstract 123: DNA methylation of miRNA promoters in breast cancer. , 2012, , .		0
22	Epigenetic regulation of normal human mammary cell type-specific miRNAs. <i>Genome Research</i> , 2011, 21, 2026-2037.	5.5	68
23	Abstract A41: Vulnerability of human mammary epithelial cells to oncogenic transformation. , 2011, , .		0
24	Role for DNA Methylation in the Regulation of miR-200c and miR-141 Expression in Normal and Cancer Cells. <i>PLoS ONE</i> , 2010, 5, e8697.	2.5	268
25	p53 induces distinct epigenetic states at its direct target promoters. <i>BMC Genomics</i> , 2008, 9, 486.	2.8	49
26	Different Mutant/Wild-Type p53 Combinations Cause a Spectrum of Increased Invasive Potential in Nonmalignant Immortalized Human Mammary Epithelial Cells. <i>Neoplasia</i> , 2008, 10, 450-461.	5.3	60
27	New STS molecular markers for assessment of genetic diversity and DNA fingerprinting in hop ( <i>Humulus lupulus</i> L.). <i>Genome</i> , 2007, 50, 15-25.	2.0	27
28	Sequence Analysis of a <i>TrueChalcone Synthase (chs_H1)</i> Oligofamily from hop ( <i>Humulus lupulus</i> L.) and PAP1 Activation of <i>chs_H1</i> in Heterologous Systems. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 7606-7615.	5.2	37
29	Isolation and characterization of a novel semi-lethal <i>Arabidopsis thaliana</i> mutant of gene for pentatricopeptide (PPR) repeat-containing protein. <i>Genetica</i> , 2006, 128, 395-407.	1.1	16
30	Expression of modified 7SL RNA gene in transgenic <i>Solanum tuberosum</i> plants. <i>Biologia Plantarum</i> , 2005, 49, 371-380.	1.9	7
31	Cloning and Molecular Analysis of the Regulatory Factor <i>HMylb1</i> in Hop ( <i>Humulus lupulus</i> L.) and the Potential of Hop To Produce Bioactive Prenylated Flavonoids. <i>Journal of Agricultural and Food Chemistry</i> , 2005, 53, 4793-4798.	5.2	26
32	The promiscuity of heterospecific lox sites increases dramatically in the presence of palindromic DNA. <i>Gene</i> , 2002, 296, 129-137.	2.2	17
33	Plant 7SL RNA and tRNA(Tyr) genes with inserted antisense sequences are efficiently expressed in an in vitro transcription system from <i>Nicotiana tabacum</i> cells. <i>Plant Molecular Biology</i> , 2002, 50, 713-723.	3.9	7
34	The Variability of Hop Latent Viroid as Induced upon Heat Treatment. <i>Virology</i> , 2001, 287, 349-358.	2.4	35
35	Molecular characterization and genome organization of 7SL RNA genes from hop ( <i>Humulus lupulus</i> ) Tj ETQq1 1 0.784314 rgBT /Over	2.2	25
36	DNA methylation changes in biomarker loci occur early in cancer progression. <i>F1000Research</i> , 0, 8, 2106.	1.6	5