

# Lukas Vrba

## List of Publications by Year in descending order

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36  
papers

1,132  
citations

394286

19  
h-index

526166

27  
g-index

37  
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. <i>Clinical Epigenetics</i> , 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. <i>Epigenetics</i> , 2020, 15, 419-430.	1.3	23
3	DNA methylation changes in biomarker loci occur early in cancer progression. <i>F1000Research</i> , 2019, 8, 2106.	0.8	7
4	A suite of DNA methylation markers that can detect most common human cancers. <i>Epigenetics</i> , 2018, 13, 61-72.	1.3	48
5	Epigenetic silencing of lncRNA MORT in 16 TCGA cancer types. <i>F1000Research</i> , 2018, 7, 211.	0.8	31
6	Epigenetic Silencing of <i>MORT</i> Is an Early Event in Cancer and Is Associated with Luminal, Receptor Positive Breast Tumor Subtypes. <i>Journal of Breast Cancer</i> , 2017, 20, 198.	0.8	19
7	Age and the means of bypassing stasis influence the intrinsic subtype of immortalized human mammary epithelial cells. <i>Frontiers in Cell and Developmental Biology</i> , 2015, 3, 13.	1.8	25
8	A lincRNA connected to cell mortality and epigenetically-silenced in most common human cancers. <i>Epigenetics</i> , 2015, 10, 1074-1083.	1.3	28
9	Differentially Expressed MicroRNAs in Postpartum Breast Cancer in Hispanic Women. <i>PLoS ONE</i> , 2015, 10, e0124340.	1.1	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. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2014, 775-776, 48-54.	0.9	29
12	Immortalization of normal human mammary epithelial cells in two steps by direct targeting of senescence barriers does not require gross genomic alterations. <i>Cell Cycle</i> , 2014, 13, 3423-3435.	1.3	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. <i>Epigenetics</i> , 2013, 8, 1080-1088.	1.3	40
16	miRNA Gene Promoters Are Frequent Targets of Aberrant DNA Methylation in Human Breast Cancer. <i>PLoS ONE</i> , 2013, 8, e54398.	1.1	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.	1.3	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.	2.4	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.	1.1	268
25	p53 induces distinct epigenetic states at its direct target promoters. <i>BMC Genomics</i> , 2008, 9, 486.	1.2	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.	2.3	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.	0.9	27
28	Sequence Analysis of a $\alpha$ -Chalcone Synthase (chs_H1) Oligofamily from hop ( <i>Humulus lupulus</i> L.) and PAP1 Activation of chs_H1 in Heterologous Systems. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 7606-7615.	2.4	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.	0.5	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 HlMyb1 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.	2.4	26
32	The promiscuity of heterospecific lox sites increases dramatically in the presence of palindromic DNA. <i>Gene</i> , 2002, 296, 129-137.	1.0	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.	2.0	7
34	The Variability of Hop Latent Viroid as Induced upon Heat Treatment. <i>Virology</i> , 2001, 287, 349-358.	1.1	35
35	Molecular characterization and genome organization of 7SL RNA genes from hop ( <i>Humulus lupulus</i> ) Tj ETQq1 1 0.784314 rgBT /Over 1.0 25		
36	DNA methylation changes in biomarker loci occur early in cancer progression. <i>F1000Research</i> , 0, 8, 2106.	0.8	5