

Lukas Vrba

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,132
citations

393982

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525886

27
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all docs

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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 α -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 |