

Jaroslav Jelinek

List of Publications by Year in descending order

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116
papers

9,696
citations

30070

54
h-index

37204

96
g-index

121
all docs

121
docs citations

121
times ranked

14188
citing authors

#	ARTICLE	IF	CITATIONS
1	Dnmt3a is essential for hematopoietic stem cell differentiation. <i>Nature Genetics</i> , 2012, 44, 23-31.	21.4	916
2	Disruption of oxygen homeostasis underlies congenital Chuvash polycythemia. <i>Nature Genetics</i> , 2002, 32, 614-621.	21.4	469
3	<i>Fusobacterium</i> in Colonic Flora and Molecular Features of Colorectal Carcinoma. <i>Cancer Research</i> , 2014, 74, 1311-1318.	0.9	389
4	JAK2 mutation 1849G>T is rare in acute leukemias but can be found in CMML, Philadelphia chromosome-negative CML, and megakaryocytic leukemia. <i>Blood</i> , 2005, 106, 3370-3373.	1.4	356
5	Epidermal Growth Factor Receptor Copy Number Alterations Correlate With Poor Clinical Outcome in Patients With Head and Neck Squamous Cancer. <i>Journal of Clinical Oncology</i> , 2007, 25, 2164-2170.	1.6	356
6	DNA Methylation Predicts Survival and Response to Therapy in Patients With Myelodysplastic Syndromes. <i>Journal of Clinical Oncology</i> , 2010, 28, 605-613.	1.6	327
7	Phase II Study of Low-Dose Decitabine in Patients With Chronic Myelogenous Leukemia Resistant to Imatinib Mesylate. <i>Journal of Clinical Oncology</i> , 2005, 23, 3948-3956.	1.6	290
8	LINE-1 Hypomethylation in Cancer Is Highly Variable and Inversely Correlated with Microsatellite Instability. <i>PLoS ONE</i> , 2007, 2, e399.	2.5	221
9	Mechanisms of resistance to 5-aza-2-deoxycytidine in human cancer cell lines. <i>Blood</i> , 2009, 113, 659-667.	1.4	217
10	Caloric restriction delays age-related methylation drift. <i>Nature Communications</i> , 2017, 8, 539.	12.8	204
11	Age-Related DNA Methylation Changes in Normal Human Prostate Tissues. <i>Clinical Cancer Research</i> , 2007, 13, 3796-3802.	7.0	192
12	Chromosome 5q deletion and epigenetic suppression of the gene encoding β -catenin (CTNNA1) in myeloid cell transformation. <i>Nature Medicine</i> , 2007, 13, 78-83.	30.7	191
13	Targeting CDK9 Reactivates Epigenetically Silenced Genes in Cancer. <i>Cell</i> , 2018, 175, 1244-1258.e26.	28.9	182
14	Polycythemia vera is not initiated by JAK2V617F mutation. <i>Experimental Hematology</i> , 2007, 35, 32.e1-32.e9.	0.4	178
15	Epigenetic changes in estrogen receptor β gene in atherosclerotic cardiovascular tissues and in-vitro vascular senescence. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2007, 1772, 72-80.	3.8	159
16	G9a is essential for epigenetic silencing of K ⁺ channel genes in acute-to-chronic pain transition. <i>Nature Neuroscience</i> , 2015, 18, 1746-1755.	14.8	159
17	Genome-wide identification of aberrantly methylated promoter associated CpG islands in acute lymphocytic leukemia. <i>Leukemia</i> , 2008, 22, 1529-1538.	7.2	144
18	Discrimination of polycythemias and thrombocytoses by novel, simple, accurate clonality assays and comparison with PRV-1 expression and BFU-E response to erythropoietin. <i>Blood</i> , 2003, 101, 3294-3301.	1.4	140

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19	Aberrant CpG island methylation in acute myeloid leukemia is accentuated at relapse. <i>Blood</i> , 2008, 112, 1366-1373.	1.4	138
20	Mutations in the VHL gene in sporadic apparently congenital polycythemia. <i>Blood</i> , 2003, 101, 1591-1595.	1.4	133
21	Detection of Bladder Cancer Using Novel DNA Methylation Biomarkers in Urine Sediments. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1483-1491.	2.5	133
22	Phase I Trial of Sequential Low-Dose 5-Aza-2-Deoxycytidine Plus High-Dose Intravenous Bolus Interleukin-2 in Patients with Melanoma or Renal Cell Carcinoma. <i>Clinical Cancer Research</i> , 2006, 12, 4619-4627.	7.0	132
23	Correlation between CpG methylation profiles and hormone receptor status in breast cancers. <i>Breast Cancer Research</i> , 2007, 9, R57.	5.0	130
24	Sensitive and Specific Detection of Early Gastric Cancer with DNA Methylation Analysis of Gastric Washes. <i>Gastroenterology</i> , 2009, 136, 2149-2158.	1.3	126
25	Decitabine Effect on Tumor Global DNA Methylation and Other Parameters in a Phase I Trial in Refractory Solid Tumors and Lymphomas. <i>Clinical Cancer Research</i> , 2009, 15, 3881-3888.	7.0	122
26	Identification of Differentially Methylated Genes in Normal Prostate Tissues from African American and Caucasian Men. <i>Clinical Cancer Research</i> , 2010, 16, 3539-3547.	7.0	120
27	Effect of Cytarabine and Decitabine in Combination in Human Leukemic Cell Lines. <i>Clinical Cancer Research</i> , 2007, 13, 4225-4232.	7.0	119
28	Mechanisms of Resistance to Decitabine in the Myelodysplastic Syndrome. <i>PLoS ONE</i> , 2011, 6, e23372.	2.5	119
29	DNA Methylation Does Not Stably Lock Gene Expression but Instead Serves as a Molecular Mark for Gene Silencing Memory. <i>Cancer Research</i> , 2012, 72, 1170-1181.	0.9	118
30	Effects of TET2 mutations on DNA methylation in chronic myelomonocytic leukemia. <i>Epigenetics</i> , 2012, 7, 201-207.	2.7	110
31	Identification of Novel Tumor Markers in Prostate, Colon and Breast Cancer by Unbiased Methylation Profiling. <i>PLoS ONE</i> , 2008, 3, e2079.	2.5	110
32	TET1-Mediated Hypomethylation Activates Oncogenic Signaling in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2018, 78, 4126-4137.	0.9	109
33	TRAIL (Apo2L) suppresses growth of primary human leukemia and myelodysplasia progenitors. <i>Leukemia</i> , 2002, 16, 67-73.	7.2	108
34	TET1 is a maintenance DNA demethylase that prevents methylation spreading in differentiated cells. <i>Nucleic Acids Research</i> , 2014, 42, 6956-6971.	14.5	108
35	Silencing of Bidirectional Promoters by DNA Methylation in Tumorigenesis. <i>Cancer Research</i> , 2006, 66, 5077-5084.	0.9	104
36	Aberrant DNA Methylation Is Associated with Disease Progression, Resistance to Imatinib and Shortened Survival in Chronic Myelogenous Leukemia. <i>PLoS ONE</i> , 2011, 6, e22110.	2.5	97

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37	CpG island methylation profiling in human melanoma cell lines. <i>Melanoma Research</i> , 2009, 19, 146-155.	1.2	91
38	Targeting Calcium Signaling Induces Epigenetic Reactivation of Tumor Suppressor Genes in Cancer. <i>Cancer Research</i> , 2016, 76, 1494-1505.	0.9	88
39	Concordance of assays designed for the quantification of JAK2V617F: a multicenter study. <i>Haematologica</i> , 2009, 94, 38-45.	3.5	82
40	Chromatin Remodeling Is Required for Gene Reactivation after Decitabine-Mediated DNA Hypomethylation. <i>Cancer Research</i> , 2010, 70, 6968-6977.	0.9	81
41	<i>TET2</i> Mutations Affect Non-CpG Island DNA Methylation at Enhancers and Transcription Factor Binding Sites in Chronic Myelomonocytic Leukemia. <i>Cancer Research</i> , 2015, 75, 2833-2843.	0.9	80
42	Genome architecture marked by retrotransposons modulates predisposition to DNA methylation in cancer. <i>Genome Research</i> , 2010, 20, 1369-1382.	5.5	78
43	Colorectal Carcinomas With CpG Island Methylator Phenotype 1 Frequently Contain Mutations in Chromatin Regulators. <i>Gastroenterology</i> , 2014, 146, 530-538.e5.	1.3	76
44	Age-related epigenetic drift in the pathogenesis of MDS and AML. <i>Genome Research</i> , 2014, 24, 580-591.	5.5	76
45	Architecture of epigenetic reprogramming following Twist1-mediated epithelial-mesenchymal transition. <i>Genome Biology</i> , 2013, 14, R144.	9.6	74
46	Induction of hypomethylation and molecular response after decitabine therapy in patients with chronic myelomonocytic leukemia. <i>Blood</i> , 2008, 111, 2382-2384.	1.4	68
47	Conserved DNA methylation patterns in healthy blood cells and extensive changes in leukemia measured by a new quantitative technique. <i>Epigenetics</i> , 2012, 7, 1368-1378.	2.7	66
48	Nerve Injury-Induced Chronic Pain Is Associated with Persistent DNA Methylation Reprogramming in Dorsal Root Ganglion. <i>Journal of Neuroscience</i> , 2018, 38, 6090-6101.	3.6	66
49	Frequent Alteration of MLL3 Frameshift Mutations in Microsatellite Deficient Colorectal Cancer. <i>PLoS ONE</i> , 2011, 6, e23320.	2.5	63
50	Disruption of ferroportin 1 regulation causes dynamic alterations in iron homeostasis and erythropoiesis in polycythaemia mice. <i>Development (Cambridge)</i> , 2004, 131, 1859-1868.	2.5	62
51	Prognostic factors and risk assessment in chronic myelomonocytic leukemia: Validation study of the M.D. Anderson Prognostic Scoring System. <i>Leukemia and Lymphoma</i> , 2007, 48, 1150-1160.	1.3	60
52	New DNA Methylation Markers and Global DNA Hypomethylation Are Associated with Oral Cancer Development. <i>Cancer Prevention Research</i> , 2015, 8, 1027-1035.	1.5	60
53	Zebrafish embryos as a screen for DNA methylation modifications after compound exposure. <i>Toxicology and Applied Pharmacology</i> , 2016, 291, 84-96.	2.8	59
54	Transfection of murine multi-potent haemopoietic stem cells with an E.coli DNA alkyltransferase gene confers resistance to the toxic effects of alkylating agents. <i>Carcinogenesis</i> , 1988, 9, 81-87.	2.8	54

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55	<i>DNMT3B</i> Variants Regulate DNA Methylation in a Promoter-Specific Manner. <i>Cancer Research</i> , 2007, 67, 10647-10652.	0.9	53
56	Transcriptional Selectivity of Epigenetic Therapy in Cancer. <i>Cancer Research</i> , 2017, 77, 470-481.	0.9	53
57	Sex chromosomes drive gene expression and regulatory dimorphisms in mouse embryonic stem cells. <i>Biology of Sex Differences</i> , 2017, 8, 28.	4.1	53
58	Differentially methylated genes and androgen receptor re-expression in small cell prostate carcinomas. <i>Epigenetics</i> , 2016, 11, 184-193.	2.7	52
59	Mixed myelodysplastic and myeloproliferative syndromes. <i>Leukemia Research</i> , 1996, 20, 717-726.	0.8	48
60	Progesterone Receptor Isoform-Specific Promoter Methylation: Association of <i>PRA</i> Promoter Methylation with Worse Outcome in Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2011, 17, 4177-4186.	7.0	47
61	DNA Methylation Signature Reveals Cell Ontogeny of Renal Cell Carcinomas. <i>Clinical Cancer Research</i> , 2016, 22, 6236-6246.	7.0	47
62	A novel isoform of TET1 that lacks a CXXC domain is overexpressed in cancer. <i>Nucleic Acids Research</i> , 2017, 45, 8269-8281.	14.5	46
63	Chromatin remodeling gene SMARCA5 is dysregulated in primitive hematopoietic cells of acute leukemia. <i>Leukemia</i> , 2000, 14, 1247-1252.	7.2	45
64	Ribosomal Protein S19 Gene Mutations in Patients with Diamond-Blackfan Anemia and Identification of Ribosomal Protein S19 Pseudogenes. <i>Blood Cells, Molecules, and Diseases</i> , 2000, 26, 124-132.	1.4	44
65	Methylation of AR locus does not always reflect X chromosome inactivation state. <i>Blood</i> , 2012, 119, e100-e109.	1.4	44
66	Search for genetic determinants of individual variability of the erythropoietin response to high altitude. <i>Blood Cells, Molecules, and Diseases</i> , 2003, 31, 175-182.	1.4	39
67	Concordant DNA Methylation in Synchronous Colorectal Carcinomas. <i>Cancer Prevention Research</i> , 2009, 2, 814-822.	1.5	39
68	The epigenome of AML stem and progenitor cells. <i>Epigenetics</i> , 2013, 8, 92-104.	2.7	38
69	Examination of Whole Blood DNA Methylation as a Potential Risk Marker for Gastric Cancer. <i>Cancer Prevention Research</i> , 2013, 6, 1093-1100.	1.5	35
70	A novel dual function retrovirus expressing multidrug resistance 1 and O ⁶ -alkylguanine-DNA-alkyltransferase for engineering resistance of haemopoietic progenitor cells to multiple chemotherapeutic agents. <i>Gene Therapy</i> , 1999, 6, 1489-1493.	4.5	34
71	DNA Methylation Profiles of Primary Colorectal Carcinoma and Matched Liver Metastasis. <i>PLoS ONE</i> , 2011, 6, e27889.	2.5	33
72	Epigenetic synergy between decitabine and platinum derivatives. <i>Clinical Epigenetics</i> , 2015, 7, 97.	4.1	33

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73	Thymine DNA glycosylase as a novel target for melanoma. <i>Oncogene</i> , 2019, 38, 3710-3728.	5.9	28
74	JAK2 mutation and disease phenotype: a double L611V/V617F in cis mutation of JAK2 is associated with isolated erythrocytosis and increased activation of AKT and ERK1/2 rather than STAT5. <i>Leukemia</i> , 2010, 24, 1069-1073.	7.2	26
75	Mutations and promoter methylation status of NPM1 in myeloproliferative disorders. <i>Haematologica</i> , 2006, 91, 1147-8.	3.5	25
76	Genomic and epigenomic predictors of response to guadecitabine in relapsed/refractory acute myelogenous leukemia. <i>Clinical Epigenetics</i> , 2019, 11, 106.	4.1	21
77	Minimal role of base excision repair in TET-induced global DNA demethylation in HEK293T cells. <i>Epigenetics</i> , 2015, 10, 1006-1013.	2.7	20
78	Single cell transcriptomic analysis reveals cellular diversity of murine esophageal epithelium. <i>Nature Communications</i> , 2022, 13, 2167.	12.8	20
79	Near-tetraploid poorly differentiated acute myeloid leukemia M0 diagnosed by short-term cultures with a Phorbol ester TPA. <i>Leukemia Research</i> , 1994, 18, 493-497.	0.8	17
80	Methylome sequencing for fibrolamellar hepatocellular carcinoma depicts distinctive features. <i>Epigenetics</i> , 2015, 10, 872-881.	2.7	17
81	DREAM: A Simple Method for DNA Methylation Profiling by High-throughput Sequencing. <i>Methods in Molecular Biology</i> , 2016, 1465, 111-127.	0.9	15
82	Phase I study of azacitidine and oxaliplatin in patients with advanced cancers that have relapsed or are refractory to any platinum therapy. <i>Clinical Epigenetics</i> , 2015, 7, 29.	4.1	13
83	Hypomethylation of TET2 Target Genes Identifies a Curable Subset of Acute Myeloid Leukemia. <i>Journal of the National Cancer Institute</i> , 2016, 108, .	6.3	13
84	Promoter methylation changes in ALOX12 and AIRE1: novel epigenetic markers for atherosclerosis. <i>Clinical Epigenetics</i> , 2020, 12, 66.	4.1	13
85	High folic acid intake increases methylation-dependent expression of Lsr and dysregulates hepatic cholesterol homeostasis. <i>Journal of Nutritional Biochemistry</i> , 2021, 88, 108554.	4.2	13
86	Epigenetic control of PRV-1 expression on neutrophils. <i>Experimental Hematology</i> , 2007, 35, 1677.e1-1677.e8.	0.4	12
87	Digital Restriction Enzyme Analysis of Methylation (DREAM). <i>Methods in Molecular Biology</i> , 2018, 1708, 247-265.	0.9	11
88	Diamond blackfan anemia stem cells fail to repopulate erythropoiesis in NOD/SCID mice. <i>Blood Cells, Molecules, and Diseases</i> , 2003, 31, 93-97.	1.4	10
89	Oxygen-Dependent Regulation of Erythropoiesis. <i>Methods in Enzymology</i> , 2004, 381, 201-210.	1.0	10
90	Concomitant JAK2 V617F positive polycythemia vera and B cell chronic lymphocytic leukemia in three patients originating from two separate hematopoietic stem cells. <i>American Journal of Hematology</i> , 2013, 88, 157-158.	4.1	10

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91	Decreased efficacy of drugs targeting the vascular endothelial growth factor pathway by the epigenetic silencing of FLT1 in renal cancer cells. <i>Clinical Epigenetics</i> , 2015, 7, 99.	4.1	10
92	Partial trisomy of 3q detected by chromosome painting in a case of juvenile chronic myelomonocytic leukemia. <i>Cancer Genetics and Cytogenetics</i> , 1993, 71, 67-70.	1.0	9
93	Decitabine impact on the endocytosis regulator RhoA, the folate carriers RFC1 and FOLR1, and the glucose transporter GLUT4 in human tumors. <i>Clinical Epigenetics</i> , 2014, 6, 2.	4.1	9
94	Impact of decitabine on immunohistochemistry expression of the putative tumor suppressor genes FHIT, WWOX, FUS1 and PTEN in clinical tumor samples. <i>Clinical Epigenetics</i> , 2014, 6, 13.	4.1	9
95	Accelerated aging in normal breast tissue of women with breast cancer. <i>Breast Cancer Research</i> , 2021, 23, 58.	5.0	9
96	Ribosomal proteins S3a, S13, S16, and S24 are not mutated in patients with Diamond-Blackfan anemia. <i>Blood</i> , 2001, 97, 579-580.	1.4	8
97	Impact of splice-site mutations of the human MDR1 cDNA on its stability and expression following retroviral gene transfer. <i>Gene Therapy</i> , 2003, 10, 1061-1065.	4.5	8
98	Unusually Long Survival of a 67-Year-Old Patient with Near-Tetraploid Acute Myeloid Leukemia M0 without Erythroblastic and Megakaryocytic Dysplasia. <i>Acta Haematologica</i> , 2011, 126, 129-134.	1.4	5
99	DNA methylation landscape of 16 canine somatic tissues by methylation-sensitive restriction enzyme-based next generation sequencing. <i>Scientific Reports</i> , 2021, 11, 10005.	3.3	5
100	Obese status is associated with accelerated DNA methylation change in peripheral blood of senior dogs. <i>Research in Veterinary Science</i> , 2021, 139, 193-199.	1.9	5
101	CpG Island Methylation Is a Poor Prognostic Factors in Myelodysplastic Syndrome Patients and Is Reversed by Decitabine Therapy-Results of a Phase III Randomized Study.. <i>Blood</i> , 2005, 106, 790-790.	1.4	5
102	Derivative (6)t(1;6)(q22;p21) revealed in bone marrow cells by FISH 9 months before diagnosis of acute T-lymphoblastic leukemia. <i>Cancer Genetics and Cytogenetics</i> , 1996, 86, 131-135.	1.0	4
103	BRCA1 promoter methylation status does not predict response to tamoxifen in sporadic breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2012, 135, 135-143.	2.5	4
104	Genome-wide DNA methylation analysis in canine gastrointestinal lymphoma. <i>Journal of Veterinary Medical Science</i> , 2020, 82, 632-638.	0.9	4
105	Genome-wide DNA methylation analysis of dogs with high lead exposure living near a lead mining area in Kabwe, Zambia. <i>Environmental Pollution</i> , 2021, 286, 117229.	7.5	4
106	An Adverse Outcome Pathway Analysis Employing DNA Methylation Effects in Arsenic-Exposed Zebrafish Embryos Supports a Role of Epigenetic Events in Arsenic-Induced Chronic Disease. <i>Applied in Vitro Toxicology</i> , 2017, 3, 312-324.	1.1	3
107	Identification of 41 Novel Promoter-Associated CpG Islands Methylated in Leukemias.. <i>Blood</i> , 2004, 104, 1126-1126.	1.4	3
108	RPS19 and JAK2 Genes are not Silenced by DNA Methylation in Diamond Blackfan Anemia. <i>Journal of Pediatric Hematology/Oncology</i> , 2007, 29, 207-208.	0.6	1

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109	Genome-wide DNA methylation profile in feline haematological tumours: A preliminary study. Research in Veterinary Science, 2021, 140, 221-228.	1.9	1
110	Distinct DNA Methylation Patterns of HOX Genes in Leukemia.. Blood, 2006, 108, 2238-2238.	1.4	1
111	Interleukin-3-Specific Modification of Cell Membrane "Fluidity" of Haemopoietic Cells. Growth Factors, 1988, 1, 67-73.	1.7	0
112	Granulocyte colony‐stimulating factor treatment of mice modulates differently the sensitivity of blood and bone marrow hematopoietic progenitors to retroviral vector infection. Stem Cells, 1993, 11, 46-50.	3.2	0
113	Hypermethylation of HOX Genes Is Associated with Longer Survival in Acute Myeloid Leukemia. Blood, 2008, 112, 312-312.	1.4	0
114	Abstract 167: Identification of differentially methylated genes in normal prostate tissues from African American and Caucasian men. , 2010, , .		0
115	DNA methylation signature to define cell ontogeny of renal cell carcinomas.. Journal of Clinical Oncology, 2016, 34, 536-536.	1.6	0
116	DNA methylation profiling of renal cell carcinomas subtypes to identify epi-clusters linked to cell ontogeny.. Journal of Clinical Oncology, 2016, 34, 4512-4512.	1.6	0