

Thomas Mikeska

List of Publications by Year in descending order

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47
papers

3,068
citations

257450

24
h-index

243625

44
g-index

47
all docs

47
docs citations

47
times ranked

6371
citing authors

#	ARTICLE	IF	CITATIONS
1	Homologous Recombination DNA Repair Pathway Disruption and Retinoblastoma Protein Loss Are Associated with Exceptional Survival in High-Grade Serous Ovarian Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 569-580.	7.0	79
2	Assessing alternative base substitutions at primer CpG sites to optimise unbiased PCR amplification of methylated sequences. <i>Clinical Epigenetics</i> , 2017, 9, 31.	4.1	10
3	Epigenetic Basis of Human Cancer. , 2017, , 83-102.		1
4	LRH-1 expression patterns in breast cancer tissues are associated with tumour aggressiveness. <i>Oncotarget</i> , 2017, 8, 83626-83636.	1.8	13
5	Fc- γ 3 Receptor Polymorphisms, Cetuximab Therapy, and Survival in the NCIC CTG CO.17 Trial of Colorectal Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 2435-2444.	7.0	33
6	MethPat: a tool for the analysis and visualisation of complex methylation patterns obtained by massively parallel sequencing. <i>BMC Bioinformatics</i> , 2016, 17, 98.	2.6	22
7	Assessment of DNA methylation profiling and copy number variation as indications of clonal relationship in ipsilateral and contralateral breast cancers to distinguish recurrent breast cancer from a second primary tumour. <i>BMC Cancer</i> , 2015, 15, 669.	2.6	14
8	Exemplary multiplex bisulfite amplicon data used to demonstrate the utility of Methpat. <i>GigaScience</i> , 2015, 4, 55.	6.4	3
9	DNA Methylation Biomarkers: Cancer and Beyond. <i>Genes</i> , 2014, 5, 821-864.	2.4	236
10	No evidence for PALB2 methylation in high-grade serous ovarian cancer. <i>Journal of Ovarian Research</i> , 2013, 6, 26.	3.0	8
11	Nonequivalent Gene Expression and Copy Number Alterations in High-Grade Serous Ovarian Cancers with <i>BRCA1</i> and <i>BRCA2</i> Mutations. <i>Clinical Cancer Research</i> , 2013, 19, 3474-3484.	7.0	76
12	No evidence for DNA methylation of the ATM promoter CpG island in chronic lymphocytic leukemia. <i>Leukemia and Lymphoma</i> , 2012, 53, 1420-1422.	1.3	4
13	Silencing of Irf7 pathways in breast cancer cells promotes bone metastasis through immune escape. <i>Nature Medicine</i> , 2012, 18, 1224-1231.	30.7	406
14	RANK (TNFRSF11A) Is Epigenetically Inactivated and Induces Apoptosis in Gliomas. <i>Neoplasia</i> , 2012, 14, 526-532.	5.3	25
15	DNA methylation biomarkers in cancer: progress towards clinical implementation. <i>Expert Review of Molecular Diagnostics</i> , 2012, 12, 473-487.	3.1	146
16	1.31 Investigating Methylation of the Pro-Apoptotic CLL Tumour Suppressor Gene, Death Associated Protein Kinase 1 (DAPK1). <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2011, 11, S159.	0.4	0
17	Analysing DNA Methylation Using Bisulphite Pyrosequencing. <i>Methods in Molecular Biology</i> , 2011, 791, 33-53.	0.9	61
18	Closed-Tube PCR Methods for Locus-Specific DNA Methylation Analysis. <i>Methods in Molecular Biology</i> , 2011, 791, 55-71.	0.9	12

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19	Aberrant DNA methylation but not mutation of CITED4 is associated with alteration of HIF-regulated genes in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 130, 319-329.	2.5	16
20	p75 ^{NTR} induces apoptosis in medulloblastoma cells. <i>International Journal of Cancer</i> , 2011, 128, 1804-1812.	5.1	22
21	Assessing combined methylation-sensitive high resolution melting and pyrosequencing for the analysis of heterogeneous DNA methylation. <i>Epigenetics</i> , 2011, 6, 500-507.	2.7	61
22	A multiplex endpoint RT-PCR assay for quality assessment of RNA extracted from formalin-fixed paraffin-embedded tissues. <i>BMC Biotechnology</i> , 2010, 10, 89.	3.3	17
23	DNA methylation analysis of the HIF-1 α prolyl hydroxylase domain genes <i>PHD1</i> , <i>PHD2</i> , <i>PHD3</i> and the factor inhibiting HIF gene <i>FIH</i> in invasive breast carcinomas. <i>Histopathology</i> , 2010, 57, 451-460.	2.9	15
24	The implications of heterogeneous DNA methylation for the accurate quantification of methylation. <i>Epigenomics</i> , 2010, 2, 561-573.	2.1	126
25	Epigenetic Downregulation of Mitogen-Activated Protein Kinase Phosphatase MKP-2 Relieves Its Growth Suppressive Activity in Glioma Cells. <i>Cancer Research</i> , 2010, 70, 1689-1699.	0.9	66
26	A systematic search for DNA methyltransferase polymorphisms reveals a rare DNMT3L variant associated with subtelomeric hypomethylation. <i>Human Molecular Genetics</i> , 2009, 18, 1755-1768.	2.9	55
27	Validation of a primer optimisation matrix to improve the performance of reverse transcription quantitative real-time PCR assays. <i>BMC Research Notes</i> , 2009, 2, 112.	1.4	31
28	Quality control of astrocyte-directed Cre transgenic mice: The benefits of a direct link between loss of gene expression and reporter activation. <i>Glia</i> , 2009, 57, 680-692.	4.9	22
29	Selective inhibition of proliferation in colorectal carcinoma cell lines expressing mutant APC or activated <i>Raf</i> . <i>International Journal of Cancer</i> , 2009, 125, 297-307.	5.1	36
30	MethMarker: user-friendly design and optimization of gene-specific DNA methylation assays. <i>Genome Biology</i> , 2009, 10, R105.	9.6	25
31	Aberrant Methylation and Reduced Expression of LHX9 in Malignant Gliomas of Childhood. <i>Neoplasia</i> , 2009, 11, 700-711.	5.3	36
32	Rapid analysis of heterogeneously methylated DNA using digital methylation-sensitive high resolution melting: application to the <i>CDKN2B</i> (p15) gene. <i>Epigenetics and Chromatin</i> , 2008, 1, 7.	3.9	65
33	In vitro sensitivity testing of minimally passaged and uncultured gliomas with TRAIL and/or chemotherapy drugs. <i>British Journal of Cancer</i> , 2008, 99, 294-304.	6.4	17
34	Sensitive Melting Analysis after Real Time- Methylation Specific PCR (SMART-MSP): high-throughput and probe-free quantitative DNA methylation detection. <i>Nucleic Acids Research</i> , 2008, 36, e42-e42.	14.5	159
35	Optimization of Quantitative MGMT Promoter Methylation Analysis Using Pyrosequencing and Combined Bisulfite Restriction Analysis. <i>Journal of Molecular Diagnostics</i> , 2007, 9, 368-381.	2.8	194
36	Mutations of the Wnt antagonist AXIN2 (Conductin) result in TCF-dependent transcription in medulloblastomas. <i>International Journal of Cancer</i> , 2007, 121, 284-291.	5.1	60

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37	Epigenetic silencing of the candidate tumor suppressor gene PROX1 in sporadic breast cancer. <i>International Journal of Cancer</i> , 2007, 121, 547-554.	5.1	65
38	SGNE1/7B2 is epigenetically altered and transcriptionally downregulated in human medulloblastomas. <i>Oncogene</i> , 2007, 26, 5662-5668.	5.9	25
39	Oncogenic HRAS suppresses clusterin expression through promoter hypermethylation. <i>Oncogene</i> , 2006, 25, 4890-4903.	5.9	61
40	CpG Island Methylation in Human Lymphocytes Is Highly Correlated with DNA Sequence, Repeats, and Predicted DNA Structure. <i>PLoS Genetics</i> , 2006, 2, e26.	3.5	183
41	BiQ Analyzer: visualization and quality control for DNA methylation data from bisulfite sequencing. <i>Bioinformatics</i> , 2005, 21, 4067-4068.	4.1	554
42	Crystal structures of O-acetylated 2-acylamino-2-deoxy-d-galactose derivatives. <i>Carbohydrate Research</i> , 2003, 338, 2119-2128.	2.3	2
43	(4S,5S)-4-[(1R)-1,2-Dihydroxyethyl]-5-tridecyl-1,3-oxazolidin-2-one. <i>Acta Crystallographica Section C: Crystal Structure Communications</i> , 2003, 59, o225-o227.	0.4	2
44	6(S)-Methyl-3(S)-(1-methylethyl)piperazin-2-one. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2003, 59, o171-o173.	0.2	0
45	1,1-DimethylethylN-propanoylcarbamate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2003, 59, o1359-o1361.	0.2	2
46	tert-Butyl 4-acetyl-2,2-dimethyl-1,3-oxazolidine-3-carboxylate. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2002, 58, o359-o361.	0.2	1
47	2(S)-N-tert-Butoxycarbonylamino-N-methoxy-N-methylbutanamide. <i>Acta Crystallographica Section E: Structure Reports Online</i> , 2002, 58, o1415-o1417.	0.2	1