BogumiÅ, Kaczkowski

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
2	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
3	MicroRNAs and potential target interactions in psoriasis. Journal of Dermatological Science, 2010, 58, 177-185.	1.9	193
4	The Rectal Cancer microRNAome – microRNA Expression in Rectal Cancer and Matched Normal Mucosa. Clinical Cancer Research, 2012, 18, 4919-4930.	7.0	174
5	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
6	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. Scientific Reports, 2018, 8, 6758.	3.3	92
7	Batf2/Irf1 Induces Inflammatory Responses in Classically Activated Macrophages, Lipopolysaccharides, and Mycobacterial Infection. Journal of Immunology, 2015, 194, 6035-6044.	0.8	83
8	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. Cancer Research, 2016, 76, 216-226.	0.9	80
9	Global microRNA Analysis of the NCI-60 Cancer Cell Panel. Molecular Cancer Therapeutics, 2011, 10, 375-384.	4.1	74
10	HemaExplorer: a database of mRNA expression profiles in normal and malignant haematopoiesis. Nucleic Acids Research, 2013, 41, D1034-D1039.	14.5	65
11	Structural profiles of human miRNA families from pairwise clustering. Bioinformatics, 2009, 25, 291-294.	4.1	62
12	Down-Regulation of miR-129-5p and the let-7 Family in Neuroendocrine Tumors and Metastases Leads to Up-Regulation of Their Targets Egr1, G3bp1, Hmga2 and Bach1. Genes, 2015, 6, 1-21.	2.4	53
13	MicroRNA Expression Profiling of the Porcine Developing Brain. PLoS ONE, 2011, 6, e14494.	2.5	52
14	CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. Genome Research, 2015, 25, 1812-1824.	5.5	49
15	Integrative analyses reveal novel strategies in HPV11,-16 and -45 early infection. Scientific Reports, 2012, 2, 515.	3.3	45
16	Cancers of unknown primary origin (CUP) are characterized by chromosomal instability (CIN) compared to metastasis of know origin. BMC Cancer, 2015, 15, 151.	2.6	36
17	HemaExplorer: a Web server for easy and fast visualization of gene expression in normal and malignant hematopoiesis. Blood, 2012, 119, 6394-6395.	1.4	32
18	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. Epigenetics, 2018, 13, 410-431.	2.7	32

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19	Micro <scp>RNA</scp> expression analysis and <scp>M</scp> ultiplex ligationâ€dependent probe amplification in metastatic and nonâ€metastatic uveal melanoma. Acta Ophthalmologica, 2014, 92, 541-549.	1.1	29
20	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. Molecular Cancer Research, 2017, 15, 1354-1365.	3.4	25
21	The microRNA molecular signature of atypic and common acquired melanocytic nevi: differential expression of miR-125b and let-7c. Experimental Dermatology, 2011, 20, 278-280.	2.9	23
22	A Decade of Global mRNA and miRNA Profiling of HPV-Positive Cell Lines and Clinical Specimens. The Open Virology Journal, 2012, 6, 216-231.	1.8	23
23	Differential expression of cellular microRNAs in HPV 11, -16, and -45 transfected cells. Biochemical and Biophysical Research Communications, 2011, 412, 20-25.	2.1	22
24	Reproducible pattern of microRNA in normal human skin. Experimental Dermatology, 2010, 19, e201-5.	2.9	20
25	Differential expression of cellular microRNAs in HPV-11 transfected cells. An analysis by three different array platforms and qRT-PCR. Biochemical and Biophysical Research Communications, 2010, 403, 357-362.	2.1	12
26	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
27	Inhibition of BCL2A1 by STAT5 inactivation overcomes resistance to targeted therapies of FLT3-ITD/D835 mutant AML. Translational Oncology, 2022, 18, 101354.	3.7	9
28	Changes in oncomiR expression in CTCL cell lines during apoptosis induced by Notch inhibition. Leukemia Research, 2010, 34, e235-e236.	0.8	8
29	A simple procedure for routine RNA extraction and miRNA array analyses from a single thyroid <i>in vivo</i> fine needle aspirate. Scandinavian Journal of Clinical and Laboratory Investigation, 2010, 70, 529-534.	1.2	8
30	MICRORNA EXPRESSION ANALYSIS BY LNA ENHANCED MICROARRAYS. , 0, , 23-46.		1
31	Epi-drivers and cancer-testis genes. Translational Cancer Research, 2016, 5, 334-336.	1.0	1
32	Development of p53 knockout U87MG cell line for unbiased drug delivery testing system using CRISPR-Cas9 and transcriptomic analysis. Journal of Biotechnology, 2021, 332, 72-82.	3.8	0