Vera N Senchenko

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Tumor suppressor properties of the small C-terminal domain phosphatases in non-small cell lung cancer. Bioscience Reports, 2019, 39, .	2.4	12
2	DNA methylation contributes to deregulation of 12 cancer-associated microRNAs and breast cancer progression. Gene, 2017, 604, 1-8.	2.2	64
3	CrossHub: a tool for multi-way analysis of The Cancer Genome Atlas (TCGA) in the context of gene expression regulation mechanisms. Nucleic Acids Research, 2016, 44, e62-e62.	14.5	41
4	<i>MICAL2</i> is a novel human cancer gene controlling mesenchymal to epithelial transition involved in cancer growth and invasion. Oncotarget, 2016, 7, 1808-1825.	1.8	55
5	Tumor Suppressor Function of the SEMA3B Gene in Human Lung and Renal Cancers. PLoS ONE, 2015, 10, e0123369.	2.5	44
6	ldentification of Novel Epigenetic Markers of Prostate Cancer by Notl-Microarray Analysis. Disease Markers, 2015, 2015, 1-13.	1.3	41
7	Epigenetic Alterations of Chromosome 3 Revealed by NotI-Microarrays in Clear Cell Renal Cell Carcinoma. BioMed Research International, 2014, 2014, 1-9.	1.9	53
8	Differential expression of genes that encode glycolysis enzymes in kidney and lung cancer in humans. Russian Journal of Genetics, 2013, 49, 707-716.	0.6	16
9	Novel tumor suppressor candidates on chromosome 3 revealed by NotI-microarrays in cervical cancer. Epigenetics, 2013, 8, 409-420.	2.7	61
10	Notl Microarrays: Novel Epigenetic Markers for Early Detection and Prognosis of High Grade Serous Ovarian Cancer. International Journal of Molecular Sciences, 2012, 13, 13352-13377.	4.1	30
11	LRRC3B gene is frequently epigenetically inactivated in several epithelial malignancies and inhibits cell growth and replication. Biochimie, 2012, 94, 1151-1157.	2.6	25
12	Genetic and epigenetic analysis of non-small cell lung cancer with Notl-microarrays. Epigenetics, 2012, 7, 502-513.	2.7	88
13	Increase in NETO2 gene expression is a potential molecular genetic marker in renal and lung cancers. Russian Journal of Genetics, 2012, 48, 506-512.	0.6	22
14	Inactivation of the von Hippel–Lindau tumor suppressor leads to selective expression of a human endogenous retrovirus in kidney cancer. Oncogene, 2011, 30, 4697-4706.	5.9	59
15	Differential Expression of CHL1 Gene during Development of Major Human Cancers. PLoS ONE, 2011, 6, e15612.	2.5	84
16	Simultaneous down-regulation of tumor suppressor genes RBSP3/CTDSPL, NPRL2/G21 and RASSF1A in primary non-small cell lung cancer. BMC Cancer, 2010, 10, 75.	2.6	51
17	High Mutability of the Tumor Suppressor Genes RASSF1 and RBSP3 (CTDSPL) in Cancer. PLoS ONE, 2009, 4, e5231.	2.5	39
18	HYAL1 and HYAL2 Inhibit Tumour Growth In Vivo but Not In Vitro. PLoS ONE, 2008, 3, e3031.	2.5	33

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19	RBSP3 (HYA22) is a tumor suppressor gene implicated in major epithelial malignancies. Proceedings of the United States of America, 2004, 101, 4906-4911.	7.1	88
20	Discovery of frequent homozygous deletions in chromosome 3p21.3 LUCA and AP20 regions in renal, lung and breast carcinomas. Oncogene, 2004, 23, 5719-5728.	5.9	102
21	Deletion mapping using quantitative real-time PCR identifies two distinct 3p21.3 regions affected in most cervical carcinomas. Oncogene, 2003, 22, 2984-2992.	5.9	61
22	Notl subtraction and Notl-specific microarrays to detect copy number and methylation changes in whole genomes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10724-10729.	7.1	54
23	Critical tumor-suppressor gene regions on chromosome 3P in major human epithelial malignancies: Allelotyping and quantitative real-time PCR. International Journal of Cancer, 2002, 100, 534-541.	5.1	64
24	Activation of the hTERT expression in squamous cell cervical carcinoma is not associated with gene amplification. Oncology Reports, 1994, 20, 469.	2.6	2
25	Formation and properties of S-protein complex with S-peptide-containing fusion protein. FEBS Letters, 1994, 339, 209-212.	2.8	24