

Geert Trooskens

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

688
citations

759233

12
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940533

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16
all docs

16
docs citations

16
times ranked

1373
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploratory analysis of the human breast DNA methylation profile upon soymilk exposure. <i>Scientific Reports</i> , 2018, 8, 13617.	3.3	3
2	Genome-wide DNA Methylation Profiling Reveals Methylation Markers Associated with 3q Gain for Detection of Cervical Precancer and Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 3813-3822.	7.0	68
3	Decoy receptor 1 (DCR1) promoter hypermethylation and response to irinotecan in metastatic colorectal cancer. <i>Oncotarget</i> , 2017, 8, 63140-63154.	1.8	19
4	<i>WRN</i> Promoter CpG Island Hypermethylation Does Not Predict More Favorable Outcomes for Patients with Metastatic Colorectal Cancer Treated with Irinotecan-Based Therapy. <i>Clinical Cancer Research</i> , 2016, 22, 4612-4622.	7.0	9
5	Dynamic epigenetic changes to <i>VHL</i> occur with sunitinib in metastatic clear cell renal cancer. <i>Oncotarget</i> , 2016, 7, 25241-25250.	1.8	14
6	Genome-wide DNA methylation detection by MethylCap-seq and Infinium HumanMethylation450 BeadChips: an independent large-scale comparison. <i>Scientific Reports</i> , 2015, 5, 15375.	3.3	17
7	Epigenetic effects of casein-derived opioid peptides in SH-SY5Y human neuroblastoma cells. <i>Nutrition and Metabolism</i> , 2015, 12, 54.	3.0	26
8	ViVar: A Comprehensive Platform for the Analysis and Visualization of Structural Genomic Variation. <i>PLoS ONE</i> , 2014, 9, e113800.	2.5	45
9	SNP-guided identification of monoallelic DNA-methylation events from enrichment-based sequencing data. <i>Nucleic Acids Research</i> , 2014, 42, e157-e157.	14.5	6
10	Next-generation technologies and data analytical approaches for epigenomics. <i>Environmental and Molecular Mutagenesis</i> , 2014, 55, 155-170.	2.2	55
11	Staphylococcal enterotoxin B influences the DNA methylation pattern in nasal polyp tissue: a preliminary study. <i>Allergy, Asthma and Clinical Immunology</i> , 2013, 9, 48.	2.0	13
12	Transcriptional analysis through RNA sequencing of giant cells induced by <i>Meloidogyne graminicola</i> in rice roots. <i>Journal of Experimental Botany</i> , 2013, 64, 3885-3898.	4.8	128
13	Quality Evaluation of Methyl Binding Domain Based Kits for Enrichment DNA-Methylation Sequencing. <i>PLoS ONE</i> , 2013, 8, e59068.	2.5	50
14	Transcriptome analysis of rice mature root tissue and root tips in early development by massive parallel sequencing. <i>Journal of Experimental Botany</i> , 2012, 63, 2141-2157.	4.8	41
15	Transcriptional reprogramming by root knot and migratory nematode infection in rice. <i>New Phytologist</i> , 2012, 196, 887-900.	7.3	157
16	Phylogenetic trees: visualizing, customizing and detecting incongruence. <i>Bioinformatics</i> , 2005, 21, 3801-3802.	4.1	37