

Michael J Higgins

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,229
citations

687363

13
h-index

713466

21
g-index

22
all docs

22
docs citations

22
times ranked

2302
citing authors

#	ARTICLE	IF	CITATIONS
1	mTOR pathway gene expression in association with race and clinicopathological characteristics in Black and White breast cancer patients. <i>Discover Oncology</i> , 2022, 13, .	2.1	4
2	Gene expression of adipokines and adipokine receptors in the tumor microenvironment: associations of lower expression with more aggressive breast tumor features. <i>Breast Cancer Research and Treatment</i> , 2021, 185, 785-798.	2.5	10
3	Differential methylation and expression patterns of microRNAs in relation to breast cancer subtypes among American women of African and European ancestry. <i>PLoS ONE</i> , 2021, 16, e0249229.	2.5	8
4	Deletion of in the mouse mammary gland results in abnormal accumulation of luminal progenitor cells: a link between reproductive factors and ER-/TNBC breast cancer?. <i>American Journal of Cancer Research</i> , 2021, 11, 3263-3270.	1.4	0
5	Relationships between Breast Feeding and Breast Cancer Subtypes: Lessons Learned from Studies in Humans and in Mice. <i>Cancer Research</i> , 2020, 80, 4871-4877.	0.9	20
6	FOXA1 Protein Expression in ER+ and ER ⁺ Breast Cancer in Relation to Parity and Breastfeeding in Black and White Women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 379-385.	2.5	8
7	Immunohistochemical analysis of adipokine and adipokine receptor expression in the breast tumor microenvironment: associations of lower leptin receptor expression with estrogen receptor-negative status and triple-negative subtype. <i>Breast Cancer Research</i> , 2020, 22, 18.	5.0	8
8	<i>BORIS</i> Expression in Ovarian Cancer Precursor Cells Alters the CTCF Cistrome and Enhances Invasiveness through <i>GALNT14</i> . <i>Molecular Cancer Research</i> , 2019, 17, 2051-2062.	3.4	25
9	Differences in microRNA expression in breast cancer between women of African and European ancestry. <i>Carcinogenesis</i> , 2019, 40, 61-69.	2.8	21
10	Uncovering the fine print of the CreERT2-LoxP system while generating a conditional knockout mouse model of <i>Ssrp1</i> gene. <i>PLoS ONE</i> , 2018, 13, e0199785.	2.5	26
11	Blocked transcription through <i>KvDMR1</i> results in absence of methylation and gene silencing resembling Beckwith-Wiedemann syndrome. <i>Development (Cambridge)</i> , 2017, 144, 1820-1830.	2.5	30
12	FOXA1 hypermethylation: link between parity and ER-negative breast cancer in African American women?. <i>Breast Cancer Research and Treatment</i> , 2017, 166, 559-568.	2.5	24
13	Single nucleotide variants in metastasis-related genes are associated with breast cancer risk, by lymph node involvement and estrogen receptor status, in women with European and African ancestry. <i>Molecular Carcinogenesis</i> , 2017, 56, 1000-1009.	2.7	12
14	A methodological study of genome-wide DNA methylation analyses using matched archival formalin-fixed paraffin embedded and fresh frozen breast tumors. <i>Oncotarget</i> , 2017, 8, 14821-14829.	1.8	8
15	Landscape of genome-wide age-related DNA methylation in breast tissue. <i>Oncotarget</i> , 2017, 8, 114648-114662.	1.8	27
16	Paternal allelic mutation at the <i>Kcnq1</i> locus reduces pancreatic β -cell mass by epigenetic modification of <i>Cdkn1c</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8332-8337.	7.1	49
17	Genetic determinants of FOXM1 overexpression in epithelial ovarian cancer and functional contribution to cell cycle progression. <i>Oncotarget</i> , 2015, 6, 27613-27627.	1.8	54
18	Genome-wide methylation patterns provide insight into differences in breast tumor biology between American women of African and European ancestry. <i>Oncotarget</i> , 2014, 5, 237-248.	1.8	57

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19	Case-only analyses of the associations between polymorphisms in the metastasis-modifying genes BRMS1 and SIPA1 and breast tumor characteristics, lymph node metastasis, and survival. <i>Breast Cancer Research and Treatment</i> , 2013, 139, 873-885.	2.5	9
20	IMA: an R package for high-throughput analysis of Illumina's 450K Infinium methylation data. <i>Bioinformatics</i> , 2012, 28, 729-730.	4.1	275
21	Two distinct mechanisms of silencing by the KvDMR1 imprinting control region. <i>EMBO Journal</i> , 2008, 27, 168-178.	7.8	126
22	Regional loss of imprinting and growth deficiency in mice with a targeted deletion of KvDMR1. <i>Nature Genetics</i> , 2002, 32, 426-431.	21.4	428