Rongxi Yang

List of Publications by Year
in descending order

33 papers	1,497 citations	471509 17 h-index	501196 28 g-index
34 all docs	34 docs citations	34 times ranked	3870 citing authors

#	Article	IF	Citations
1	Novel blood-based hypomethylation of SH3BP5 is associated with very early-stage lung adenocarcinoma. Genes and Genomics, 2022, 44, 445-453.	1.4	5
2	F2RL3 Methylation in the Peripheral Blood as a Potential Marker for the Detection of Coronary Heart Disease: A Case-Control Study. Frontiers in Genetics, 2022, 13, 833923.	2.3	5
3	FYB methylation in peripheral blood as a potential marker for the early-stage lung cancer: a case-control study in Chinese population. Biomarkers, 2022, 27, 79-85.	1.9	0
4	The association between RAPSN methylation in peripheral blood and breast cancer in the Chinese population. Journal of Human Genetics, 2021, 66, 1069-1078.	2.3	3
5	ACTB Methylation in Blood as a Potential Marker for the Pre-clinical Detection of Stroke: A Prospective Nested Case-Control Study. Frontiers in Neuroscience, 2021, 15, 644943.	2.8	8
6	The Association Between PNPLA2 Methylation in Peripheral Blood and Early-Stage Lung Cancer in a Caseâ€“Control Study. Cancer Management and Research, 2021, Volume 13, 7919-7927.	1.9	2
7	RPTOR methylation in the peripheral blood and breast cancer in the Chinese population. Genes and Genomics, 2021, , 1.	1.4	3
8	The Association Between RAPSN Methylation in Peripheral Blood and Early Stage Lung Cancer Detected in Caseâ€“Control Cohort . Cancer Management and Research, 2020, Volume 12, 11063-11075.	1.9	9
9	The Association Between Breast Cancer and Blood-Based Methylation of S100P and HYAL2 in the Chinese Population. Frontiers in Genetics, 2020, 11, 977.	2.3	9
10	The association between breast cancer and S100P methylation in peripheral blood by multicenter caseâ€“control studies. Carcinogenesis, 2017, 38, 312-320.	2.8	41
11	HYAL2 methylation in peripheral blood as a potential marker for the detection of pancreatic cancer: a case control study. Oncotarget, 2017, 8, 67614-67625.	1.8	10
12	DNA methylation array analysis identifies breast cancer associated RPTOR, MGRN1 and RAPSN hypomethylation in peripheral blood DNA. Oncotarget, 2016, 7, 64191-64202.	1.8	33
13	Plasma hyaluronic acid level as a prognostic and monitoring marker of metastatic breast cancer. International Journal of Cancer, 2016, 138, 2499-2509.	5.1	31
14	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
15	Plasma S100P level as a novel prognostic marker of metastatic breast cancer. Breast Cancer Research and Treatment, 2016, 157, 329-338.	2.5	18
16	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
17	F2RL3 methylation, lung cancer incidence and mortality. International Journal of Cancer, 2015, 137, 1739-1748.	5.1	65
18	Methylation status at HYAL2 predicts overall and progression-free survival of colon cancer patients under 5-FU chemotherapy. Genomics, 2015, 106, 348-354.	2.9	17

#	Article	IF	Citations
19	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	6.2	76
20	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	2.8	14
21	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
22	S100P and HYAL2 as prognostic markers for patients with triple-negative breast cancer. Experimental and Molecular Pathology, 2015, 99, 180-187.	2.1	21
23	<scp>DNA</scp> methylation array analyses identified breast cancerâ€associated <scp>HYAL2</scp> methylation in peripheral blood. International Journal of Cancer, 2015, 136, 1845-1855.	5.1	53
24	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
25	Genome-wide analysis associates familial colorectal cancer with increases in copy number variations and a rare structural variation at 12p12.3. Carcinogenesis, 2014, 35, 315-323.	2.8	31
26	F2RL3methylation in blood DNA is a strong predictor of mortality. International Journal of Epidemiology, 2014, 43, 1215-1225.	1.9	84
27	Diagnostic, prognostic, and treatment monitoring value of plasma X in patients with metastatic breast cancer.. Journal of Clinical Oncology, 2014, 32, 37-37.	1.6	0
28	DNA methylation array analyses to identify HYAL2 methylation in peripheral blood as a marker for the detection of early breast cancer.. Journal of Clinical Oncology, 2014, 32, 26-26.	1.6	0
29	Genetic variants within miR-126 and miR-335 are not associated with breast cancer risk. Breast Cancer Research and Treatment, 2011, 127, 549-554.	2.5	18
30	A genetic variant in the pre-miR-27a oncogene is associated with a reduced familial breast cancer risk. Breast Cancer Research and Treatment, 2010, 121, 693-702.	2.5	115
31	Polymorphisms in BRCA2 resulting in aberrant codon-usage and their analysis on familial breast cancer risk. Breast Cancer Research and Treatment, 2009, 118, 407-413.	2.5	6
32	SNPs in ultraconserved elements and familial breast cancer risk. Carcinogenesis, 2008, 29, 351-355.	2.8	53
33	The Association Between Breast Cancer and Blood-Based Methylation of CD160, ISYNA1 and RAD51B in the Chinese Population. Frontiers in Genetics, 0, 13, .	2.3	1