## Rongxi Yang

## List of Publications by Year in descending order

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

#	Article	IF	CITATIONS
1	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
2	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
3	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
4	<i>F2RL3</i> methylation in blood DNA is a strong predictor of mortality. International Journal of Epidemiology, 2014, 43, 1215-1225.	1.9	84
5	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
6	<i>F2RL3</i> methylation, lung cancer incidence and mortality. International Journal of Cancer, 2015, 137, 1739-1748.	5.1	65
7	SNPs in ultraconserved elements and familial breast cancer risk. Carcinogenesis, 2008, 29, 351-355.	2.8	53
8	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
9	<scp>DNA</scp> methylation array analyses identified breast cancerâ€associated <scp><i>HYAL2</i></scp> methylation in peripheral blood. International Journal of Cancer, 2015, 136, 1845-1855.	5.1	53
10	The association between breast cancer and \$100P methylation in peripheral blood by multicenter caseâ€"control studies. Carcinogenesis, 2017, 38, 312-320.	2.8	41
11	DNA methylation array analysis identifies breast cancer associated <i>RPTOR</i> , <i>MGRN1</i> and <i>RAPSN</i> hypomethylation in peripheral blood DNA. Oncotarget, 2016, 7, 64191-64202.	1.8	33
12	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
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	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
15	S100P and HYAL2 as prognostic markers for patients with triple-negative breast cancer. Experimental and Molecular Pathology, 2015, 99, 180-187.	2.1	21
16	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
17	Plasma S100P level as a novel prognostic marker of metastatic breast cancer. Breast Cancer Research and Treatment, 2016, 157, 329-338.	2.5	18
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	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
20	<i>HYAL2</i> 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
21	<p>The Association Between RAPSN Methylation in Peripheral Blood and Early Stage Lung Cancer Detected in Case–Control Cohort</p> . Cancer Management and Research, 2020, Volume 12, 11063-11075.	1.9	9
22	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
23	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
24	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
25	Novel blood-based hypomethylation of SH3BP5 is associated with very early-stage lung adenocarcinoma. Genes and Genomics, 2022, 44, 445-453.	1.4	5
26	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
27	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
28	RPTOR methylation in the peripheral blood and breast cancer in the Chinese population. Genes and Genomics, 2021, , 1.	1.4	3
29	The Association Between PNPLA2 Methylation in Peripheral Blood and Early-Stage Lung Cancer in a Case–Control Study. Cancer Management and Research, 2021, Volume 13, 7919-7927.	1.9	2
30	The Association Between Breast Cancer and Blood-Based Methylation of CD160, ISYNA1 and RAD51B in the Chinese Population. Frontiers in Genetics, $0, 13, \ldots$	2.3	1
31	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
32	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
33	<i>FYB</i> 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