Yonglan Zheng

List of Publications by Year
in descending order

74	4,014	168829	134545
papers	citations	31 h-index	62 g-index

77	77	77	9133
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mutational spectrum of breast cancer susceptibility genes among women ascertained in a cancer risk clinic in Northeast Brazil. Breast Cancer Research and Treatment, 2022, 193, 485-494.	1.1	5
2	Detection of germline variants in Brazilian breast cancer patients using multigene panel testing. Scientific Reports, 2022, 12, 4190.	1.6	21
3	Subtype-specific expression of MELK is partly due to copy number alterations in breast cancer. PLoS ONE, 2022, 17, e0268693.	1.1	6
4	Racial disparities in survival outcomes among breast cancer patients by molecular subtypes. Breast Cancer Research and Treatment, 2021, 185, 841-849.	1.1	25
5	Abstract PS18-12: Comparative analysis of differential gene expression by ancestry using primary breast cancers from Nigeria and the cancer genome atlas (TCGA). , 2021, , .		0
6	Whole-genome analysis of Nigerian patients with breast cancer reveals ethnic-driven somatic evolution and distinct genomic subtypes. Nature Communications, 2021, 12, 6946.	5.8	22
7	Prevalence of Inherited Mutations in Breast Cancer Predisposition Genes among Women in Uganda and Cameroon. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 359-367.	1.1	36
8	Radiogenomics of breast cancer using dynamic contrast enhanced MRI and gene expression profiling. Cancer Imaging, 2019, 19, 48.	1.2	48
9	Germline variants and somatic mutation signatures of breast cancer across populations of African and European ancestry in the US and Nigeria. International Journal of Cancer, 2019, 145, 3321-3333.	2.3	16
10	Intensive Surveillance with Biannual Dynamic Contrast-Enhanced Magnetic Resonance Imaging Downstages Breast Cancer in BRCA1 Mutation Carriers. Clinical Cancer Research, 2019, 25, 1786-1794.	3.2	44
11	Genomic profiling of residual tumor after neoadjuvant chemotherapy for breast cancer.. Journal of Clinical Oncology, 2019, 37, e12106-e12106.	0.8	0
12	Determining clinical relevance of genomic heterogeneity in an ethnically diverse cohort of newly diagnosed patients with breast cancer.. Journal of Clinical Oncology, 2019, 37, 3084-3084.	0.8	0
13	Association of Pancreatic Cancer Susceptibility Variants with Risk of Breast Cancer in Women of European and African Ancestry. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 116-118.	1.1	5
14	Population-dependent Intron Retention and DNA Methylation in Breast Cancer. Molecular Cancer Research, 2018, 16, 461-469.	1.5	23
15	Genetic variants demonstrating flip-flop phenomenon and breast cancer risk prediction among women of African ancestry. Breast Cancer Research and Treatment, 2018, 168, 703-712.	1.1	42
16	Mutations in context: implications of BRCA testing in diverse populations. Familial Cancer, 2018, 17, 471-483.	0.9	23
17	Genetic variation in the vitamin D related pathway and breast cancer risk in women of African ancestry in the root consortium. International Journal of Cancer, 2018, 142, 36-43.	2.3	11
18	Inherited Breast Cancer in Nigerian Women. Journal of Clinical Oncology, 2018, 36, 2820-2825.	0.8	80

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19	Genetic Ancestry May Influence the Evolutionary Trajectory of Cancers. Cancer Cell, 2018, 34, 529-530.	7.7	4
20	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. Nature Communications, 2018, 9, 4181.	5.8	77
21	LncRNA BLAT1 is Upregulated in Basal-like Breast Cancer through Epigenetic Modifications. Scientific Reports, 2018, 8, 15572.	1.6	26
22	Genetic variation in the Hippo pathway and breast cancer risk in women of African ancestry. Molecular Carcinogenesis, 2018, 57, 1311-1318.	1.3	6
23	Characterizing Genetic Susceptibility to Breast Cancer in Women of African Ancestry. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1016-1026.	1.1	24
24	Association between MGMT Promoter Methylation and Risk of Breast and Gynecologic Cancers: A Systematic Review and Meta-Analysis. Scientific Reports, 2017, 7, 12783.	1.6	7
25	Association of breast cancer risk and the mTOR pathway in women of African ancestry in â€˜The Rootâ€™ Consortium. Carcinogenesis, 2017, 38, 789-796.	1.3	6
26	The association between miR-423 rs6505162 polymorphism and cancer susceptibility: a systematic review and meta-analysis. Oncotarget, 2017, 8, 40204-40213.	0.8	16
27	Association of breast cancer risk in women of African ancestry with genetic variants in the TET-related DNA demethylation pathway.. Journal of Clinical Oncology, 2017, 35, e13015-e13015.	0.8	0
28	Genetic variants in microRNA and microRNA biogenesis pathway genes and breast cancer risk among women of African ancestry. Human Genetics, 2016, 135, 1145-1159.	1.8	32
29	Genome-wide association studies in women of African ancestry identified 3q26.21 as a novel susceptibility locus for oestrogen receptor negative breast cancer. Human Molecular Genetics, 2016, 25, ddw305.	1.4	50
30	Genetic and Epigenetic Regulation of TOX3 Expression in Breast Cancer. PLoS ONE, 2016, 11, e0165559.	1.1	23
31	Inherited predisposition to breast cancer among African American women. Breast Cancer Research and Treatment, 2015, 149, 31-39.	1.1	116
32	TERT Polymorphism rs2736100-C Is Associated with EGFR Mutationâ€“Positive Nonâ€“Small Cell Lung Cancer. Clinical Cancer Research, 2015, 21, 5173-5180.	3.2	47
33	Molecular Subtype-Specific Expression of MicroRNA-29c in Breast Cancer Is Associated with CpG Dinucleotide Methylation of the Promoter. PLoS ONE, 2015, 10, e0142224.	1.1	20
34	Identification of Duplication Downstream of BMP2 in a Chinese Family with Brachydactyly Type A2 (BDA2). PLoS ONE, 2014, 9, e94201.	1.1	9
35	Hypermethylation of the CpG-island near the C9orf72 G4C2-repeat expansion in FTLD patients. Human Molecular Genetics, 2014, 23, 5630-5637.	1.4	74
36	Whole-exome and targeted gene sequencing of gallbladder carcinoma identifies recurrent mutations in the ErbB pathway. Nature Genetics, 2014, 46, 872-876.	9.4	343

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37	Risk factors for pregnancy-associated breast cancer: a report from the Nigerian Breast Cancer Study. Annals of Epidemiology, 2013, 23, 551-557.	0.9	31
38	A genome-wide association study of breast cancer in women of African ancestry. Human Genetics, 2013, 132, 39-48.	1.8	70
39	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
40	Hypermethylation of the CpG Island Near the G4C2 Repeat in ALS with a C9orf72 Expansion. American Journal of Human Genetics, 2013, 92, 981-989.	2.6	241
41	Fine mapping of breast cancer genome-wide association studies loci in women of African ancestry identifies novel susceptibility markers. Carcinogenesis, 2013, 34, 1520-1528.	1.3	26
42	Opportunities in Genetic Epidemiology in Developing Countries. , 2013, , 57-77.		0
43	Genetic Susceptibility to Type 2 Diabetes and Breast Cancer Risk in Women of European and African Ancestry. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 552-556.	1.1	10
44	GPC5rs2352028 Polymorphism and Risk of Lung Cancer in Han Chinese. Cancer Investigation, 2012, 30, 13-19.	0.6	6
45	Microsatellites in the Estrogen Receptor (ESR1, ESR2) and Androgen Receptor (AR) Genes and Breast Cancer Risk in African American and Nigerian Women. PLoS ONE, 2012, 7, e40494.	1.1	10
46	Evaluation of 19 susceptibility loci of breast cancer in women of African ancestry. Carcinogenesis, 2012, 33, 835-840.	1.3	64
47	High prevalence of BRCA1 and BRCA2 mutations in unselected Nigerian breast cancer patients. International Journal of Cancer, 2012, 131, 1114-1123.	2.3	81
48	Recurrent BRCA1 and BRCA2 mutations in breast cancer patients of African ancestry. Breast Cancer Research and Treatment, 2012, 134, 889-894.	1.1	42
49	Novel germline PALB2 truncating mutations in African American breast cancer patients. Cancer, 2012, 118, 1362-1370.	2.0	32
50	Lack of association between common single nucleotide polymorphisms in the TERT-CLPTM1L locus and breast cancer in women of African ancestry. Breast Cancer Research and Treatment, 2012, 132, 341-345.	1.1	12
51	. Familial Cancer Syndromes in Africa. , 2012, , 500-530.		0
52	Germline mutational analysis of the C19orf62 gene in African-American women with breast cancer. Breast Cancer Research and Treatment, 2011, 127, 871-877.	1.1	0
53	Searching for large genomic rearrangements of the BRCA1 gene in a Nigerian population. Breast Cancer Research and Treatment, 2010, 124, 573-577.	1.1	25
54	Screening RAD51C nucleotide alterations in patients with a family history of breast and ovarian cancer. Breast Cancer Research and Treatment, 2010, 124, 857-861.	1.1	46

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55	Pharacogenetic effects of dopamine transporter gene polymorphisms on response to chlorpromazine and clozapine and on extrapyramidal syndrome in schizophrenia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2010, 34, 1026-1032.	2.5	46
56	Common variants on chromosome 6p22.1 are associated with schizophrenia. Nature, 2009, 460, 753-757.	13.7	1,063
57	No significant association between the genetic polymorphisms in the GSK-3Î² gene and schizophrenia in the Chinese population. Journal of Psychiatric Research, 2008, 42, 365-370.	1.5	15
58	Positive association between PDLIM5 and schizophrenia in the Chinese Han population. International Journal of Neuropsychopharmacology, 2008, 11, 27-34.	1.0	19
59	Poly A- Transcripts Expressed in HeLa Cells. PLoS ONE, 2008, 3, e2803.	1.1	78
60	Positive association between SIAT8B and schizophrenia in the Chinese Han population. Schizophrenia Research, 2007, 90, 108-114.	1.1	87
61	No association between PPP3CC and schizophrenia in the Chinese population. Schizophrenia Research, 2007, 90, 357-359.	1.1	15
62	No association between the genetic polymorphisms in the RTN4R gene and schizophrenia in the Chinese population. Journal of Neural Transmission, 2007, 114, 249-254.	1.4	21
63	Association of AKT1 Gene Polymorphisms With Risk of Schizophrenia and With Response to Antipsychotics in the Chinese Population. Journal of Clinical Psychiatry, 2007, 68, 1358-1367.	1.1	74
64	A two-stage linkage analysis of Chinese schizophrenia pedigrees in 10 target chromosomes. Biochemical and Biophysical Research Communications, 2006, 342, 1049-1057.	1.0	17
65	Variants in the RAB3A gene are not associated with mental retardation in the Chinese population. Neuroscience Letters, 2006, 401, 114-118.	1.0	1
66	A family-based association study of kinesin heavy chain member 2 gene (KIF2) and schizophrenia. Neuroscience Letters, 2006, 407, 151-155.	1.0	16
67	Positive association between POU1F1 and mental retardation in young females in the Chinese Han population. Human Molecular Genetics, 2006, 15, 1237-1243.	1.4	6
68	Association of the carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase gene with schizophrenia in the Chinese Han population. Biochemical and Biophysical Research Communications, 2005, 328, 809-815.	1.0	68
69	A family-based study of the association between the G72/G30 genes and schizophrenia in the Chinese population. Schizophrenia Research, 2005, 73, 257-261.	1.1	59
70	Caseâ€“control study and transmission disequilibrium test provide consistent evidence for association between schizophrenia and genetic variation in the 22q11 gene ZDHHC8. Human Molecular Genetics, 2004, 13, 2991-2995.	1.4	79
71	A caseâ€“control study provides evidence of association for a functional polymorphism â^'197C/G in XBP1 to schizophrenia and suggests a sex-dependent effect. Biochemical and Biophysical Research Communications, 2004, 319, 866-870.	1.0	39
72	No association between the genetic polymorphisms within RTN4 and schizophrenia in the Chinese population. Neuroscience Letters, 2004, 365, 23-27.	1.0	12

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73	No association between the promoter variants of tumor necrosis factor alpha (TNF-Î±) and schizophrenia in Chinese Han population. Neuroscience Letters, 2004, 366, 139-143.	1.0	39
74	A family-based and case-control association study of the NOTCH4 gene and schizophrenia. Molecular Psychiatry, 2002, 7, 100-103.	4.1	44