Yon-Dschun Ko

List of Publications by Year
in descending order

88 papers	10,224 citations	71102 41 h-index	48315 88 g-index
94 all docs	94 docs citations	94 times ranked	13907 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
2	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
3	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. Journal of the National Cancer Institute, 2011, 103, 250-263.	6.3	596
4	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	27.0	532
5	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
6	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
7	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
8	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	3.5	315
9	First-line selective internal radiotherapy plus chemotherapy versus chemotherapy alone in patients with liver metastases from colorectal cancer (FOXFIRE, SIRFLOX, and FOXFIRE-Global): a combined analysis of three multicentre, randomised, phase 3 trials. Lancet Oncology, The, 2017, 18, 1159-1171.	10.7	293
10	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
11	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
12	K-ras Mutation Subtypes in NSCLC and Associated Co-occuring Mutations in Other Oncogenic Pathways. Journal of Thoracic Oncology, 2019, 14, 606-616.	1.1	178
13	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
14	MET Amplification Status in Therapy-NaÃ¯ve Adeno- and Squamous Cell Carcinomas of the Lung. Clinical Cancer Research, 2015, 21, 907-915.	7.0	155
15	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2011, 20, 3289-3303.	2.9	152
16	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
17	Definition of a fluorescence in-situ hybridization score identifies high- and low-level FGFR1 amplification types in squamous cell lung cancer. Modern Pathology, 2012, 25, 1473-1480.	5.5	118
18	Clinical and Pathological Characteristics of KEAP1- and NFE2L2-Mutated Nonâ€“Small Cell Lung Carcinoma (NSCLC). Clinical Cancer Research, 2018, 24, 3087-3096.	7.0	116

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19	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.9	109
20	PIK3CA mutations in non-small cell lung cancer (NSCLC): Genetic heterogeneity, prognostic impact and incidence of prior malignancies. Oncotarget, 2015, 6, 1315-1326.	1.8	105
21	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
22	Risk of Estrogen Receptorâ€“Positive and â€“Negative Breast Cancer and Singleâ€“Nucleotide Polymorphism 2q35-rs13387042. Journal of the National Cancer Institute, 2009, 101, 1012-1018.	6.3	99
23	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
24	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98
25	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
26	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
27	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
28	Implementation of Amplicon Parallel Sequencing Leads to Improvement of Diagnosis and Therapy of Lung Cancer Patients. Journal of Thoracic Oncology, 2015, 10, 1049-1057.	1.1	85
29	ROS1 rearrangements in lung adenocarcinoma: prognostic impact, therapeutic options and genetic variability. Oncotarget, 2015, 6, 10577-10585.	1.8	85
30	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. Breast Cancer Research, 2010, 12, R110.	5.0	82
31	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
32	Breast cancer: a candidate gene approach across the estrogen metabolic pathway. Breast Cancer Research and Treatment, 2008, 108, 137-149.	2.5	74
33	Head and Neck Squamous-Cell Cancer and its Association with Polymorphic Enzymes of Xenobiotic Metabolism and Repair. Journal of Toxicology and Environmental Health - Part A: Current Issues, 2008, 71, 887-897.	2.3	71
34	CYP2C19*17 is associated with decreased breast cancer risk. Breast Cancer Research and Treatment, 2009, 115, 391-396.	2.5	62
35	Effect of Primary Tumor Side on Survival Outcomes in Untreated Patients With Metastatic Colorectal Cancer When Selective Internal Radiation Therapy Is Added to Chemotherapy: Combined Analysis of Two Randomized Controlled Studies. Clinical Colorectal Cancer, 2018, 17, e617-e629.	2.3	54
36	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

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37	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
38	The CASP8 -652 6N del promoter polymorphism and breast cancer risk: a multicenter study. Breast Cancer Research and Treatment, 2008, 111, 139-144.	2.5	50
39	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
40	ERCC2 genotypes and a corresponding haplotype are linked with breast cancer risk in a German population. Cancer Epidemiology Biomarkers and Prevention, 2004, 13, 2059-64.	2.5	49
41	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	6.3	45
42	Association of a Common AKAP9 Variant With Breast Cancer Risk: A Collaborative Analysis. Journal of the National Cancer Institute, 2008, 100, 437-442.	6.3	44
43	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
44	The CYP1B1_1358_GG genotype is associated with estrogen receptor-negative breast cancer. Breast Cancer Research and Treatment, 2008, 111, 171-177.	2.5	39
45	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
46	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
47	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	2.9	38
48	Adherence management for patients with cancer taking capecitabine: a prospective two-arm cohort study. BMJ Open, 2013, 3, e003139.	1.9	37
49	Common variants in the UBC9 gene encoding the SUMOâ€conjugating enzyme are associated with breast tumor grade. International Journal of Cancer, 2009, 125, 596-602.	5.1	36
50	Investigation of Genetic Variants of Genes of the Hemochromatosis Pathway and Their Role in Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 1102-1107.	2.5	35
51	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35
52	Association of cytochrome P450 2E1 polymorphisms and head and neck squamous cell cancer. Toxicology Letters, 2004, 151, 273-282.	0.8	34
53	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	5.1	34
54	Missense Variants in ATM in 26,101 Breast Cancer Cases and 29,842 Controls. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2143-2151.	2.5	33

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55	No evidence for glutathione S-transferases GSTA2, GSTM2, GSTO1, GSTO2, and GSTZ1 in breast cancer risk. Breast Cancer Research and Treatment, 2010, 121, 497-502.	2.5	32
56	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	2.9	32
57	Long intergenic noncoding RNA 299 methylation in peripheral blood is a biomarker for triple-negative breast cancer. Epigenomics, 2019, 11, 81-93.	2.1	32
58	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28
59	N-acetyltransferase 2, exposure to aromatic and heterocyclic amines, and receptor-defined breast cancer. European Journal of Cancer Prevention, 2010, 19, 100-109.	1.3	25
60	CYP2B6*6 is associated with increased breast cancer risk. International Journal of Cancer, 2014, 134, 426-430.	5.1	24
61	Polymorphisms in the UBC9 and PIAS3 genes of the SUMO-conjugating system and breast cancer risk. Breast Cancer Research and Treatment, 2010, 121, 185-194.	2.5	23
62	Comorbidity Burden and Presence of Multiple Intracranial Lesions Are Associated with Adverse Events after Surgical Treatment of Patients with Brain Metastases. Cancers, 2020, 12, 3209.	3.7	21
63	Polymorphic loci of E2F2, CCND1 and CCND3 are associated with HER2 status of breast tumors. International Journal of Cancer, 2009, 124, 2077-2081.	5.1	20
64	The earwax-associated SNP c.538G>A (G180R) in ABCC11 is not associated with breast cancer risk in Europeans. Breast Cancer Research and Treatment, 2011, 129, 993-999.	2.5	20
65	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	12.8	19
66	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
67	Polymorphisms of the nuclear receptor pregnane X receptor and organic anion transporter polypeptides 1A2, 1B1, 1B3, and 2B1 are not associated with breast cancer risk. Breast Cancer Research and Treatment, 2011, 125, 563-569.	2.5	18
68	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
69	Combined UGT1A1 and UGT1A6 genotypes together with a stressful life event increase breast cancer risk. Breast Cancer Research and Treatment, 2010, 124, 289-292.	2.5	14
70	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
71	Exploring the association between genetic variation in the <scp>SUMO</scp> isopeptidase gene <scp>USPL1</scp> and breast cancer through integration of data from the populationâ€based <scp>GENICA</scp> study and external genetic databases. International Journal of Cancer, 2013, 133, 362-372.	5.1	13
72	No evidence that GATA3 rs570613 SNP modifies breast cancer risk. Breast Cancer Research and Treatment, 2009, 117, 371-379.	2.5	12

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73	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
74	Breast Cancer Risk and 6q22.33: Combined Results from Breast Cancer Association Consortium and Consortium of Investigators on Modifiers of BRCA1/2. PLoS ONE, 2012, 7, e35706.	2.5	11
75	Preoperative Metastatic Brain Tumor-Associated Intracerebral Hemorrhage Is Associated With Dismal Prognosis. Frontiers in Oncology, 2021, 11, 699860.	2.8	11
76	Confirmation of the reduction of hormone replacement therapy-related breast cancer risk for carriers of the HSD17B1_937_G variant. Breast Cancer Research and Treatment, 2013, 138, 543-548.	2.5	10
77	The Impact of Prolonged Mechanical Ventilation on Overall Survival in Patients With Surgically Treated Brain Metastases. Frontiers in Oncology, 2021, 11, 658949.	2.8	10
78	The frameshift polymorphism CYP3A43_74_delA is associated with poor differentiation of breast tumors. Cancer, 2010, 116, 5358-5364.	4.1	9
79	Variation in the Calpain-10 gene is not associated with gestational diabetes mellitus. Scandinavian Journal of Clinical and Laboratory Investigation, 2014, 74, 59-66.	1.2	9
80	The UGT1A6_19_GG genotype is a breast cancer risk factor. Frontiers in Genetics, 2013, 4, 104.	2.3	8
81	Quantum Cascade Laser-Based Infrared Imaging as a Label-Free and Automated Approach to Determine Mutations in Lung Adenocarcinoma. American Journal of Pathology, 2021, 191, 1269-1280.	3.8	7
82	The postmenopausal hormone replacement therapy-related breast cancer risk is decreased in women carrying the CYP2C19*17 variant. Breast Cancer Research and Treatment, 2012, 131, 347-350.	2.5	6
83	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
84	7q21-rs6964587 and breast cancer risk: an extended case-control study by the Breast Cancer Association Consortium. Journal of Medical Genetics, 2011, 48, 698-702.	3.2	5
85	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	3.7	4
86	No association of polymorphisms in the cell polarity gene SCRIB with breast cancer risk. Breast Cancer Research and Treatment, 2011, 127, 259-264.	2.5	2
87	Evaluation of patient-reported severity of handâ€“foot syndrome under capecitabine using a Markov modeling approach. Cancer Chemotherapy and Pharmacology, 2020, 86, 435-444.	2.3	2
88	Epigenetic quantification of circulating immune cells in peripheral blood of triple-negative breast cancer patients. Clinical Epigenetics, 2021, 13, 207.	4.1	2