Therese Truong

List of Publications by Year in descending order

143 papers	12,979 citations	38738 50 h-index	28296 105 g-index
160 all docs	160 docs citations	160 times ranked	16094 citing authors

#	Article	IF	Citations
1	Performance of African-ancestry-specific polygenic hazard score varies according to local ancestry in 8q24. Prostate Cancer and Prostatic Diseases, 2022, 25, 229-237.	3.9	9
2	Metabolic Syndrome and Risk of Gastrointestinal Cancers: An Investigation Using Large-scale Molecular Data. Clinical Gastroenterology and Hepatology, 2022, 20, e1338-e1352.	4.4	12
3	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
4	Leveraging pleiotropic association using sparse group variable selection in genomics data. BMC Medical Research Methodology, 2022, 22, 9.	3.1	1
5	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
6	Associations between plasma levels of brominated flame retardants and methylation of DNA from peripheral blood: A cross-sectional study in a cohort of French women. Environmental Research, 2022, 210, 112788.	7.5	3
7	A Genome-Wide Gene-Based Geneâ€“Environment Interaction Study of Breast Cancer in More than 90,000 Women. Cancer Research Communications, 2022, 2, 211-219.	1.7	6
8	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199.	3.3	2
9	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
10	Inflammatory potential of the diet and association with risk of differentiated thyroid cancer in the European Prospective Investigation into Cancer and Nutrition (EPIC) cohort. European Journal of Nutrition, 2022, 61, 3625-3635.	3.9	4
11	Blood polyphenol concentrations and differentiated thyroid carcinoma in women from the European Prospective Investigation into Cancer and Nutrition (EPIC) study. American Journal of Clinical Nutrition, 2021, 113, 162-171.	4.7	12
12	Africanâ€specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer. International Journal of Cancer, 2021, 148, 99-105.	5.1	24
13	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	6.4	5
14	Geneâ€•and pathwayâ€level analyses of iCOGS variants highlight novel signaling pathways underlying familial breast cancer susceptibility. International Journal of Cancer, 2021, 148, 1895-1909.	5.1	5
15	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	21.4	264
16	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
17	Multiethnic genomeâ€wide association study of differentiated thyroid cancer in the <scp>EPITHYR</scp> consortium. International Journal of Cancer, 2021, 148, 2935-2946.	5.1	11
18	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

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19	Penalized partial least squares for pleiotropy. BMC Bioinformatics, 2021, 22, 86.	2.6	2
20	Fine-mapping of two differentiated thyroid carcinoma susceptibility loci at 2q35 and 8p12 in Europeans, Melanesians and Polynesians. Oncotarget, 2021, 12, 493-506.	1.8	6
21	Gene network and biological pathways associated with susceptibility to differentiated thyroid carcinoma. Scientific Reports, 2021, 11, 8932.	3.3	7
22	Role of DNA Repair Variants and Diagnostic Radiology Exams in Differentiated Thyroid Cancer Risk: A Pooled Analysis of Two Caseâ€“Control Studies. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1208-1217.	2.5	2
23	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
24	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6
25	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	5.0	7
26	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
27	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
28	1107Dietary polyphenol intake and differentiated thyroid cancer risk: a population-based case-control study in New Caledonia. International Journal of Epidemiology, 2021, 50, .	1.9	0
29	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	2.5	19
30	Adapted dietary inflammatory index and differentiated thyroid carcinoma risk in two French population-based caseâ€“control studies. European Journal of Nutrition, 2021, , 1.	3.9	4
31	Bayesian metaâ€analysis models for cross cancer genomic investigation of pleiotropic effects using group structure. Statistics in Medicine, 2021, 40, 1498-1518.	1.6	2
32	Assessment of interactions between 205 breast cancer susceptibility loci and 13 established risk factors in relation to breast cancer risk, in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2020, 49, 216-232.	1.9	21
33	Polyphenol intake and differentiated thyroid cancer risk in the European Prospective Investigation into Cancer and Nutrition (EPIC) cohort. International Journal of Cancer, 2020, 146, 1841-1850.	5.1	20
34	Dietary Inflammatory Index and Differentiated Thyroid Carcinoma Risk: A Population-Based Case-Control Study in New Caledonia. American Journal of Epidemiology, 2020, 189, 95-107.	3.4	14
35	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
36	Appraising causal relationships of dietary, nutritional and physical-activity exposures with overall and aggressive prostate cancer: two-sample Mendelian-randomization study based on 79â€‰148 prostate-cancer cases and 61â€‰106 controls. International Journal of Epidemiology, 2020, 49, 587-596.	1.9	36

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37	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
38	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
39	Circadian genes polymorphisms, night work and prostate cancer risk: Findings from the <scp>EPICAP</scp> study. International Journal of Cancer, 2020, 147, 3119-3129.	5.1	16
40	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
41	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
42	Role of GSTM1 and GSTT1 genotypes in differentiated thyroid cancer and interaction with lifestyle factors: Results from case-control studies in France and New Caledonia. PLoS ONE, 2020, 15, e0228187.	2.5	3
43	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
44	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
45	Circadian genes and risk of prostate cancer: Findings from the EPICAP study. International Journal of Cancer, 2019, 145, 1745-1753.	5.1	17
46	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
47	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
48	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
49	Association of breast cancer risk with polymorphisms in genes involved in the metabolism of xenobiotics and interaction with tobacco smoking: A geneâ€set analysis. International Journal of Cancer, 2019, 144, 1896-1908.	5.1	14
50	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
51	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	2.5	19
52	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2018, 47, 526-536.	1.9	88
53	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
54	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88

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55	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
56	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
57	Hormonal and reproductive risk factors of papillary thyroid cancer: A population-based case-control study in France. Cancer Epidemiology, 2017, 48, 78-84.	1.9	23
58	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
59	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
60	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
61	Geneâ€“environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	5.1	20
62	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
63	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
64	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	1.8	31
65	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	8.4	118
66	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
67	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
68	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
69	Night work and breast cancer risk defined by human epidermal growth factor receptor-2 (HER2) and hormone receptor status: A population-based caseâ€“control study in France. Chronobiology International, 2016, 33, 783-787.	2.0	23
70	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
71	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	1.8	21
72	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	6.2	59

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73	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	2.9	33
74	rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	3.3	2
75	Weight and weight changes throughout life and postmenopausal breast cancer risk: a case-control study in France. BMC Cancer, 2016, 16, 761.	2.6	6
76	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
77	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
78	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	3.3	19
79	Fine-mapping of two differentiated thyroid carcinoma susceptibility loci at 9q22.33 and 14q13.3 detects novel candidate functional SNPs in Europeans from metropolitan France and Melanesians from New Caledonia. International Journal of Cancer, 2016, 139, 617-627.	5.1	11
80	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
81	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
82	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. Human Genetics, 2016, 135, 137-154.	3.8	8
83	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
84	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
85	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
86	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
87	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
88	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
89	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
90	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

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91	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
92	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
93	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	6.2	37
94	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
95	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
96	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	2.5	24
97	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
98	Abstract 4638: Fine mapping of two GWAS at 9q22 and 14q13 associated with differentiated thyroid cancer risk. , 2015, , .		0
99	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
100	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
101	Education and Lung Cancer Among Never Smokers. Epidemiology, 2014, 25, 934-935.	2.7	3
102	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
103	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
104	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
105	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28
106	Breast cancer risk, nightwork, and circadian clock gene polymorphisms. Endocrine-Related Cancer, 2014, 21, 629-638.	3.1	71
107	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. British Journal of Cancer, 2014, 110, 1088-1100.	6.4	21
108	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105

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109	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
110	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
111	Night work and breast cancer: A populationâ€based caseâ€“control study in France (the CECILE study). International Journal of Cancer, 2013, 132, 924-931.	5.1	98
112	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
113	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
114	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	6.2	201
115	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
116	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
117	A genome-wide association study to identify genetic susceptibility loci that modify ductal and lobular postmenopausal breast cancer risk associated with menopausal hormone therapy use: a two-stage design with replication. Breast Cancer Research and Treatment, 2013, 138, 529-542.	2.5	18
118	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genomeâ€“wide interaction study. Endocrine-Related Cancer, 2013, 20, 875-887.	3.1	26
119	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
120	Risk of Breast Cancer by Type of Menopausal Hormone Therapy: a Case-Control Study among Post-Menopausal Women in France. PLoS ONE, 2013, 8, e78016.	2.5	106
121	Abstract 141: Nonsteroidal anti-inflammatory drugs (NSAIDs), cyclooxygenase-2 polymorphisms, and breast cancer risk.. , 2013, , .		0
122	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
123	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
124	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1783-1791.	2.5	17
125	Family history of malignant and benign thyroid diseases and risk of thyroid cancer: a population-based caseâ€“control study in New Caledonia. Cancer Causes and Control, 2012, 23, 745-755.	1.8	23
126	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35

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127	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	2.5	51
128	Abstract 655: Menopausal hormone therapy and breast cancer risk: The CECILE Study. , 2012, , .		0
129	Abstract 657: Perinatal factors and breast cancer risk: The CECILE study. , 2012, , .		0
130	Abstract 2611: Role of circadian genes in breast cancer: Analysis of the CECILE study, a population-based case-control study conducted in France. , 2012, , .		0
131	Determinants of serum concentrations of 1,1-dichloro-2,2-bis(p-chlorophenyl)ethylene and polychlorinated biphenyls among French women in the CECILE study. Environmental Research, 2011, 111, 861-870.	7.5	43
132	A Genome-Wide Association Study of Upper Aerodigestive Tract Cancers Conducted within the INHANCE Consortium. PLoS Genetics, 2011, 7, e1001333.	3.5	158
133	Breast cancer risk by occupation and industry: Analysis of the CECILE study, a populationâ€based caseâ€“control study in France. American Journal of Industrial Medicine, 2011, 54, 499-509.	2.1	46
134	A Sex-Specific Association between a 15q25 Variant and Upper Aerodigestive Tract Cancers. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 658-664.	2.5	14
135	Abstract 3728: Night work and breast cancer risk: CECILE study. , 2011, , .		0
136	Role of dietary iodine and cruciferous vegetables in thyroid cancer: a countrywide caseâ€“control study in New Caledonia. Cancer Causes and Control, 2010, 21, 1183-1192.	1.8	80
137	Replication of Lung Cancer Susceptibility Loci at Chromosomes 15q25, 5p15, and 6p21: A Pooled Analysis From the International Lung Cancer Consortium. Journal of the National Cancer Institute, 2010, 102, 959-971.	6.3	174
138	International Lung Cancer Consortium: Coordinated association study of 10 potential lung cancer susceptibility variants. Carcinogenesis, 2010, 31, 625-633.	2.8	56
139	Pooled Analysis of Two Caseâ€“Control Studies in New Caledonia and French Polynesia of Body Mass Index and Differentiated Thyroid Cancer: The Importance of Body Surface Area. Thyroid, 2010, 20, 1285-1293.	4.5	56
140	Abstract 3861: A genome-wide association study of upper aerodigestive tract cancers identifies 4q21, 4q23, and 12q24 as susceptibility loci. , 2010, , .		0
141	Alcohol Drinking, Tobacco Smoking, and Anthropometric Characteristics as Risk Factors for Thyroid Cancer: A Countrywide Case-Control Study in New Caledonia. American Journal of Epidemiology, 2007, 166, 1140-1149.	3.4	95
142	Time trends and geographic variations for thyroid cancer in New Caledonia, a very high incidence area (1985â€“1999). European Journal of Cancer Prevention, 2007, 16, 62-70.	1.3	61
143	Role of Goiter and of Menstrual and Reproductive Factors in Thyroid Cancer: A Population-based Case-Control Study in New Caledonia (South Pacific), a Very High Incidence Area. American Journal of Epidemiology, 2005, 161, 1056-1065.	3.4	80