# Therese Truong

## List of Publications by Year in Descending Order



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| 133 papers | 8,557 citations | 47 h-index | 91 g-index |
| 160 ext. papers | 11,089 ext. citations | 10.6 avg, IF | 3.97 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 133 | Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65 | 6.7 | 0 |
| 132 | Leveraging pleiotropic association using sparse group variable selection in genomics data.. *BMC Medical Research Methodology*, **2022**, 22, 9 | 4.7 | |
| 131 | Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. *JAMA Oncology*, **2022**, | 13.4 | 4 |
| 130 | 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**, 112788 | 7.9 | |
| 129 | A Genome-Wide Gene-Based Gene-Environment Interaction Study of Breast Cancer in More than 90,000 Women. *Cancer Research Communications*, **2022**, 2, 211-219 | | 0 |
| 128 | Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women.. *Scientific Reports*, **2022**, 12, 6199 | 4.9 | |
| 127 | Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51 | 14.4 | 0 |
| 126 | Adapted dietary inflammatory index and differentiated thyroid carcinoma risk in two French population-based case-control studies. *European Journal of Nutrition*, **2021**, 1 | 5.2 | 2 |
| 125 | Bayesian meta-analysis models for cross cancer genomic investigation of pleiotropic effects using group structure. *Statistics in Medicine*, **2021**, 40, 1498-1518 | 2.3 | 1 |
| 124 | Gene network and biological pathways associated with susceptibility to differentiated thyroid carcinoma. *Scientific Reports*, **2021**, 11, 8932 | 4.9 | 1 |
| 123 | Role of DNA Repair Variants and Diagnostic Radiology Exams in Differentiated Thyroid Cancer Risk: A Pooled Analysis of Two Case-Control Studies. *Cancer Epidemiology Biomarkers and Prevention*, **2021**, 30, 1208-1217 | 4 | 1 |
| 122 | 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 | 11 | 1 |
| 121 | African-specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer. *International Journal of Cancer*, **2021**, 148, 99-105 | 7.5 | 7 |
| 120 | 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 | 8.7 | 2 |
| 119 | Gene- and pathway-level analyses of iCOGS variants highlight novel signaling pathways underlying familial breast cancer susceptibility. *International Journal of Cancer*, **2021**, 148, 1895-1909 | 7.5 | 2 |
| 118 | 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 | 36.3 | 62 |
| 117 | A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. *Nature Communications*, **2021**, 12, 1078 | 17.4 | 4 |

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| 116 | Multiethnic genome-wide association study of differentiated thyroid cancer in the EPITHYR consortium. *International Journal of Cancer*, **2021**, 148, 2935-2946 | 7.5 | 5 |
| 115 | Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439 | 59.2 | 143 |
| 114 | Penalized partial least squares for pleiotropy. *BMC Bioinformatics*, **2021**, 22, 86 | 3.6 | 0 |
| 113 | Fine-mapping of two differentiated thyroid carcinoma susceptibility loci at 2q35 and 8p12 in Europeans, Melanesians and Polynesians. *Oncotarget*, **2021**, 12, 493-506 | 3.3 | 2 |
| 112 | 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 | 8.3 | 1 |
| 111 | Mendelian randomisation study of smoking exposure in relation to breast cancer risk. *British Journal of Cancer*, **2021**, 125, 1135-1145 | 8.7 | 0 |
| 110 | Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397 | 50.4 | 28 |
| 109 | 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 | 4 | 4 |
| 108 | Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. *Nature Genetics*, **2020**, 52, 572-581 | 36.3 | 76 |
| 107 | Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Scientific Reports*, **2020**, 10, 9688 | 4.9 | 2 |
| 106 | Circadian genes polymorphisms, night work and prostate cancer risk: Findings from the EPICAP study. *International Journal of Cancer*, **2020**, 147, 3119-3129 | 7.5 | 7 |
| 105 | Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468 | 2.6 | 9 |
| 104 | A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312 | 17.4 | 20 |
| 103 | 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 | 3.7 | 2 |
| 102 | Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73 | 36.3 | 56 |
| 101 | Appraising causal relationships of dietary, nutritional and physical-activity exposures with overall and aggressive prostate cancer: two-sample Mendelian-randomization study based on 79 148 prostate-cancer cases and 61 106 controls. *International Journal of Epidemiology*, **2020**, 49, 587-596 | 7.8 | 16 |
| 100 | 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 | 7.8 | 13 |
| 99 | 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 | 7.5 | 9 |

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| 98 | 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 | 3.8 | 8 |
| 97 | 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*, **2020**, | 7 | 2 |
| 96 | Two truncating variants in FANCC and breast cancer risk. *Scientific Reports*, **2019**, 9, 12524 | 4.9 | 2 |
| 95 | Circadian genes and risk of prostate cancer: Findings from the EPICAP study. *International Journal of Cancer*, **2019**, 145, 1745-1753 | 7.5 | 8 |
| 94 | Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741 | 17.4 | 47 |
| 93 | Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657 | 8.7 | 28 |
| 92 | The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. *Npj Breast Cancer*, **2019**, 5, 38 | 7.8 | 12 |
| 91 | Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34 | 11 | 363 |
| 90 | Association of breast cancer risk with polymorphisms in genes involved in the metabolism of xenobiotics and interaction with tobacco smoking: A gene-set analysis. *International Journal of Cancer*, **2019**, 144, 1896-1908 | 7.5 | 8 |
| 89 | Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2019**, 48, 795-806 | 7.8 | 52 |
| 88 | The BRCA2 c.68-7T□□A variant is not pathogenic: A model for clinical calibration of spliceogenicity. *Human Mutation*, **2018**, 39, 729-741 | 4.7 | 16 |
| 87 | 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 | 7.8 | 53 |
| 86 | Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. *Nature Genetics*, **2018**, 50, 928-936 | 36.3 | 340 |
| 85 | Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. *Nature Communications*, **2018**, 9, 2256 | 17.4 | 57 |
| 84 | A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978 | 36.3 | 101 |
| 83 | Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799 | 10.1 | 49 |
| 82 | Hormonal and reproductive risk factors of papillary thyroid cancer: A population-based case-control study in France. *Cancer Epidemiology*, **2017**, 48, 78-84 | 2.8 | 17 |
| 81 | 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 | 36.3 | 257 |

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| 80 | Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94 | 50.4 | 643 |
| 79 | Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778 | 36.3 | 186 |
| 78 | Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. *Breast Cancer Research*, **2017**, 19, 119 | 8.3 | 26 |
| 77 | Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. *International Journal of Cancer*, **2017**, 141, 1830-1840 | 7.5 | 13 |
| 76 | - a novel candidate breast cancer susceptibility locus on 6q14.1. *Oncotarget*, **2017**, 8, 102769-102782 | 3.3 | 3 |
| 75 | No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401 | 4.9 | 15 |
| 74 | 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 | 5.6 | 24 |
| 73 | rs2735383, located at a microRNA binding site in the 3ꞌUTR of NBS1, is not associated with breast cancer risk. *Scientific Reports*, **2016**, 6, 36874 | 4.9 | 2 |
| 72 | Weight and weight changes throughout life and postmenopausal breast cancer risk: a case-control study in France. *BMC Cancer*, **2016**, 16, 761 | 4.8 | 5 |
| 71 | Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375 | 17.4 | 64 |
| 70 | Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675 | 17.4 | 53 |
| 69 | 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 | 4.9 | 16 |
| 68 | 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, 617-27 | 7.5 | 9 |
| 67 | No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. *Journal of Medical Genetics*, **2016**, 53, 298-309 | 5.8 | 83 |
| 66 | Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. *Nature Genetics*, **2016**, 48, 374-86 | 36.3 | 93 |
| 65 | 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, 137-54 | 6.3 | 6 |
| 64 | BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. *Journal of the National Cancer Institute*, **2016**, 108, | 9.7 | 65 |
| 63 | RAD51B in Familial Breast Cancer. *PLoS ONE*, **2016**, 11, e0153788 | 3.7 | 18 |

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| 62 | 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 | 3.3 | 21 |
| 61 | 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 | 11.6 | 80 |
| 60 | Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. *PLoS ONE*, **2016**, 11, e0160316 | 3.7 | 11 |
| 59 | Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. *International Journal of Cancer*, **2016**, 139, 1303-1317 | 7.5 | 26 |
| 58 | PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811 | 5.8 | 121 |
| 57 | Night work and breast cancer risk defined by human epidermal growth factor receptor-2 (HER2) and hormone receptor status: A population-based case-control study in France. *Chronobiology International*, **2016**, 33, 783-7 | 3.6 | 14 |
| 56 | Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2016**, 18, 22 | 8.3 | 31 |
| 55 | Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. *Cancer Causes and Control*, **2016**, 27, 679-93 | 2.8 | 15 |
| 54 | 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 | 11 | 43 |
| 53 | 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, 256-71 | 4.6 | 12 |
| 52 | Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nature Genetics*, **2015**, 47, 373-80 | 36.3 | 406 |
| 51 | 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 | 11 | 26 |
| 50 | Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303 | 36.3 | 226 |
| 49 | Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107, | 9.7 | 74 |
| 48 | Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 1680-91 | 4 | 17 |
| 47 | Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. *Human Molecular Genetics*, **2015**, 24, 285-98 | 5.6 | 35 |
| 46 | Investigation of gene-environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. *International Journal of Cancer*, **2015**, 136, E685-96 | 7.5 | 26 |
| 45 | 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 | 2.4 | |

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| 44 | Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107, | 9.7 | 324 |
| 43 | Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84 | 5.6 | 36 |
| 42 | 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 | 11 | 59 |
| 41 | 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, 1934-46 | 5.6 | 28 |
| 40 | Identification of new genetic susceptibility loci for breast cancer through consideration of gene-environment interactions. *Genetic Epidemiology*, **2014**, 38, 84-93 | 2.6 | 24 |
| 39 | Breast cancer risk, nightwork, and circadian clock gene polymorphisms. *Endocrine-Related Cancer*, **2014**, 21, 629-38 | 5.7 | 57 |
| 38 | FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. *British Journal of Cancer*, **2014**, 110, 1088-100 | 8.7 | 20 |
| 37 | Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999 | 17.4 | 87 |
| 36 | Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. *Human Molecular Genetics*, **2014**, 23, 6034-46 | 5.6 | 11 |
| 35 | Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. *Breast Cancer Research*, **2014**, 16, R51 | 8.3 | 12 |
| 34 | MicroRNA related polymorphisms and breast cancer risk. *PLoS ONE*, **2014**, 9, e109973 | 3.7 | 37 |
| 33 | Genetic predisposition to in situ and invasive lobular carcinoma of the breast. *PLoS Genetics*, **2014**, 10, e1004285 | 6 | 38 |
| 32 | Education and lung cancer among never smokers. *Epidemiology*, **2014**, 25, 934-5 | 3.1 | 3 |
| 31 | Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2014**, 23, 6096-111 | 5.6 | 48 |
| 30 | DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. *Human Molecular Genetics*, **2014**, 23, 2490-7 | 5.6 | 35 |
| 29 | Night work and breast cancer: a population-based case-control study in France (the CECILE study). *International Journal of Cancer*, **2013**, 132, 924-31 | 7.5 | 78 |
| 28 | 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, 1046-60 | 11 | 80 |
| 27 | Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2 | 36.3 | 422 |

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| 26 | 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 | 11 | 167 |
| 25 | Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2 | 36.3 | 327 |
| 24 | Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2 | 36.3 | 813 |
| 23 | 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 | 4.4 | 14 |
| 22 | Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genome-wide interaction study. *Endocrine-Related Cancer*, **2013**, 20, 875-87 | 5.7 | 19 |
| 21 | Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors. *PLoS Genetics*, **2013**, 9, e1003284 | 6 | 112 |
| 20 | 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 | 3.7 | 82 |
| 19 | Genome-wide association analysis identifies three new breast cancer susceptibility loci. *Nature Genetics*, **2012**, 44, 312-8 | 36.3 | 237 |
| 18 | 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, 1783-91 | 4 | 17 |
| 17 | Family history of malignant and benign thyroid diseases and risk of thyroid cancer: a population-based case-control study in New Caledonia. *Cancer Causes and Control*, **2012**, 23, 745-55 | 2.8 | 20 |
| 16 | 11q13 is a susceptibility locus for hormone receptor positive breast cancer. *Human Mutation*, **2012**, 33, 1123-32 | 4.7 | 33 |
| 15 | 19p13.1 is a triple-negative-specific breast cancer susceptibility locus. *Cancer Research*, **2012**, 72, 1795-803 | 8.1 | 93 |
| 14 | 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 | 3.7 | 49 |
| 13 | 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, 861-70 | 7.9 | 37 |
| 12 | A genome-wide association study of upper aerodigestive tract cancers conducted within the INHANCE consortium. *PLoS Genetics*, **2011**, 7, e1001333 | 6 | 136 |
| 11 | Breast cancer risk by occupation and industry: analysis of the CECILE study, a population-based case-control study in France. *American Journal of Industrial Medicine*, **2011**, 54, 499-509 | 2.7 | 39 |
| 10 | A sex-specific association between a 15q25 variant and upper aerodigestive tract cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2011**, 20, 658-64 | 4 | 14 |
| 9 | 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, 959-71 | 9.7 | 153 |

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| 8 | International Lung Cancer Consortium: coordinated association study of 10 potential lung cancer susceptibility variants. *Carcinogenesis*, **2010**, 31, 625-33 | 4.6 | 46 |
| 7 | Pooled analysis of two case-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, 1285-93 | 6.2 | 49 |
| 6 | Role of dietary iodine and cruciferous vegetables in thyroid cancer: a countrywide case-control study in New Caledonia. *Cancer Causes and Control*, **2010**, 21, 1183-92 | 2.8 | 65 |
| 5 | 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, 1140-9 | 3.8 | 86 |
| 4 | Time trends and geographic variations for thyroid cancer in New Caledonia, a very high incidence area (1985-1999). *European Journal of Cancer Prevention*, **2007**, 16, 62-70 | 2 | 47 |
| 3 | 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, 1056-65 | 3.8 | 73 |
| 2 | African-specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer | | 1 |
| 1 | Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses | | 2 |