# Daniele Campa

List of Publications by Year
in descending order



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|---|---|---|---|
| 168 papers | 7,846 citations | 81743 39 h-index | 60497 81 g-index |
| 176 all docs | 176 docs citations | 176 times ranked | 11718 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Germline genetic variability in pancreatic cancer risk and prognosis. Seminars in Cancer Biology, 2022, 79, 105-131. | 4.3 | 30 |
| 2 | TAS2R38 polymorphisms, Helicobacter pylori infection and susceptibility to gastric cancer and premalignant gastric lesions. European Journal of Cancer Prevention, 2022, 31, 401-407. | 0.6 | 1 |
| 3 | Genome-wide association study of mitochondrial copy number. Human Molecular Genetics, 2022, 31, 1346-1355. | 1.4 | 1 |
| 4 | A polygenic risk score for multiple myeloma risk prediction. European Journal of Human Genetics, 2022, 30, 474-479. | 1.4 | 5 |
| 5 | Maternal anthropometric variables and clinical factors shape neonatal microbiome. Scientific Reports, 2022, 12, 2875. | 1.6 | 2 |
| 6 | Genetically Determined Telomere Length Is Associated with Pancreatic Neuroendocrine Neoplasms Onset. Neuroendocrinology, 2022, 112, 1168-1176. | 1.2 | 3 |
| 7 | Validation and functional characterization of GWAS-identified variants for chronic lymphocytic leukemia: a CRuCIAL study. Blood Cancer Journal, 2022, 12, 79. | 2.8 | 1 |
| 8 | A polymorphic variant in telomere maintenance is associated with worrisome features and high-risk stigmata development in IPMNs. Carcinogenesis, 2022, 43, 728-735. | 1.3 | 5 |
| 9 | 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. | 3.0 | 45 |
| 10 | Polygenic and multifactorial scores for pancreatic ductal adenocarcinoma risk prediction. Journal of Medical Genetics, 2021, 58, 369-377. | 1.5 | 31 |
| 11 | Common gene variants within 3â€²â€untranslated regions as modulators of multiple myeloma risk and survival. International Journal of Cancer, 2021, 148, 1887-1894. | 2.3 | 3 |
| 12 | Do myeloproliferative neoplasms and multiple myeloma share the same genetic susceptibility loci?. International Journal of Cancer, 2021, 148, 1616-1624. | 2.3 | 7 |
| 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. | 2.9 | 5 |
| 14 | Genomeâ€wide scan of long noncoding <scp>RNA</scp> single nucleotide polymorphism<scp>s</scp> and pancreatic cancer susceptibility. International Journal of Cancer, 2021, 148, 2779-2788. | 2.3 | 23 |
| 15 | A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078. | 5.8 | 19 |
| 16 | Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. Cancer Research, 2021, 81, 3134-3143. | 0.4 | 8 |
| 17 | Polymorphic variants in Sweet and Umami taste receptor genes and birthweight. Scientific Reports, 2021, 11, 4971. | 1.6 | 4 |
| 18 | Expression quantitative trait loci of genes predicting outcome are associated with survival of multiple myeloma patients. International Journal of Cancer, 2021, 149, 327-336. | 2.3 | 3 |

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|---|---|---|---|
| 19 | Genetically determined telomere length and multiple myeloma risk and outcome. Blood Cancer Journal, 2021, 11, 74. | 2.8 | 10 |
| 20 | Telomere Length and Male Fertility. International Journal of Molecular Sciences, 2021, 22, 3959. | 1.8 | 18 |
| 21 | Lack of association of CD44-rs353630 and CHI3L2-rs684559 with pancreatic ductal adenocarcinoma survival. Scientific Reports, 2021, 11, 7570. | 1.6 | 2 |
| 22 | 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. | 2.6 | 6 |
| 23 | Associations between pancreatic expression quantitative traits and risk of pancreatic ductal adenocarcinoma. Carcinogenesis, 2021, 42, 1037-1045. | 1.3 | 14 |
| 24 | 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. | 2.2 | 7 |
| 25 | Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145. | 2.9 | 9 |
| 26 | Association of Genetic Variants Affecting microRNAs and Pancreatic Cancer Risk. Frontiers in Genetics, 2021, 12, 693933. | 1.1 | 10 |
| 27 | Genetic Polymorphisms Involved in Mitochondrial Metabolism and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2342-2345. | 1.1 | 4 |
| 28 | 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. | 1.1 | 19 |
| 29 | Polymorphisms within the TNFSF4 and MAPKAPK2 Loci Influence the Risk of Developing Invasive Aspergillosis: A Two-Stage Case Control Study in the Context of the aspBIOmics Consortium. Journal of Fungi (Basel, Switzerland), 2021, 7, 4. | 1.5 | 5 |
| 30 | Association between telomere length and mitochondrial copy number and cancer risk in humans: A meta-analysis on more than 300,000 individuals. Critical Reviews in Oncology/Hematology, 2021, 167, 103510. | 2.0 | 13 |
| 31 | Identification of Recessively Inherited Genetic Variants Potentially Linked to Pancreatic Cancer Risk. Frontiers in Oncology, 2021, 11, 771312. | 1.3 | 8 |
| 32 | Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228â€‰951 Women of European Descent. Journal of the National Cancer Institute, 2020, 112, 295-304. | 3.0 | 35 |
| 33 | Cereblon (CRBN) gene polymorphisms predict clinical response and progression-free survival in relapsed/refractory multiple myeloma patients treated with lenalidomide: a pharmacogenetic study from the IMMEnSE consortium. Leukemia and Lymphoma, 2020, 61, 699-706. | 0.6 | 3 |
| 34 | Host immune genetic variations influence the risk of developing acute myeloid leukaemia: results from the NuCLEAR consortium. Blood Cancer Journal, 2020, 10, 75. | 2.8 | 2 |
| 35 | Genetic polymorphisms associated with telomere length and risk of developing myeloproliferative neoplasms. Blood Cancer Journal, 2020, 10, 89. | 2.8 | 20 |
| 36 | Factors Associated With the Risk of Progression of Low-Risk Branch-Duct Intraductal Papillary Mucinous Neoplasms. JAMA Network Open, 2020, 3, e2022933. | 2.8 | 25 |

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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. | 9.4 | 265 |
| 38 | Role of OPRM1, clinical and anthropometric variants in neonatal pain reduction. Scientific Reports, 2020, 10, 7091. | 1.6 | 5 |
| 39 | Genome-Wide Geneâ€"Diabetes and Geneâ€"Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1784-1791. | 1.1 | 5 |
| 40 | Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688. | 1.6 | 2 |
| 41 | Mendelian randomisation study of the effects of known and putative risk factors on pancreatic cancer. Journal of Medical Genetics, 2020, 57, 820-828. | 1.5 | 40 |
| 42 | Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468. | 0.6 | 32 |
| 43 | Genomeâ€wide association study identifies an early onset pancreatic cancer risk locus. International Journal of Cancer, 2020, 147, 2065-2074. | 2.3 | 20 |
| 44 | Mitochondrial DNA Copy-Number Variation and Pancreatic Cancer Risk in the Prospective EPIC Cohort. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 681-686. | 1.1 | 16 |
| 45 | Genetic variants in taste-related genes and risk of pancreatic cancer. Mutagenesis, 2019, 34, 391-394. | 1.0 | 14 |
| 46 | The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38. | 2.3 | 28 |
| 47 | Genetic variability of the ABCC2 gene and clinical outcomes in pancreatic cancer patients. Carcinogenesis, 2019, 40, 544-550. | 1.3 | 8 |
| 48 | Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431. | 5.8 | 88 |
| 49 | Germline BRCA2 K3326X and CHEK2 I157T mutations increase risk for sporadic pancreatic ductal adenocarcinoma. International Journal of Cancer, 2019, 145, 686-693. | 2.3 | 20 |
| 50 | Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741. | 5.8 | 90 |
| 51 | Exome sequencing identifies germline variants in DIS3 in familial multiple myeloma. Leukemia, 2019, 33, 2324-2330. | 3.3 | 33 |
| 52 | Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657. | 2.9 | 52 |
| 53 | Genetic polymorphisms in inflammatory genes and pancreatic cancer risk: a two-phase study on more than 14 000 individuals. Mutagenesis, 2019, 34, 395-401. | 1.0 | 8 |
| 54 | Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34. | 2.6 | 711 |

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|---|---|---|---|
| 55 | Genetic polymorphisms in genes of class switch recombination and multiple myeloma risk and survival: an IMMEnSE study. Leukemia and Lymphoma, 2019, 60, 1803-1811. | 0.6 | 11 |
| 56 | Genetic determinants of telomere length and risk of pancreatic cancer: A PANDoRA study. International Journal of Cancer, 2019, 144, 1275-1283. | 2.3 | 36 |
| 57 | Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556. | 5.8 | 188 |
| 58 | Common genetic variants associated with pancreatic adenocarcinoma may also modify risk of pancreatic neuroendocrine neoplasms. Carcinogenesis, 2018, 39, 360-367. | 1.3 | 16 |
| 59 | Mitochondrial DNA copy number variation, leukocyte telomere length, and breast cancer risk in the European Prospective Investigation into Cancer and Nutrition (EPIC) study. Breast Cancer Research, 2018, 20, 29. | 2.2 | 44 |
| 60 | Do pancreatic cancer and chronic pancreatitis share the same genetic risk factors? A PANcreatic Disease ReseArch (PANDoRA) consortium investigation. International Journal of Cancer, 2018, 142, 290-296. | 2.3 | 14 |
| 61 | A comprehensive analysis of polymorphic variants in steroid hormone and insulinâ€like growth factorâ€1 metabolism and risk of in situ breast cancer: Results from the Breast and Prostate Cancer Cohort Consortium. International Journal of Cancer, 2018, 142, 1182-1188. | 2.3 | 0 |
| 62 | Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052. | 0.6 | 17 |
| 63 | Inherited variation in the xenobiotic transporter pathway and survival of multiple myeloma patients. British Journal of Haematology, 2018, 183, 375-384. | 1.2 | 11 |
| 64 | SLC22A3 polymorphisms do not modify pancreatic cancer risk, but may influence overall patient survival. Scientific Reports, 2017, 7, 43812. | 1.6 | 15 |
| 65 | Association between taste receptor (TAS) genes and the perception of wine characteristics. Scientific Reports, 2017, 7, 9239. | 1.6 | 22 |
| 66 | Lack of Association for Reported Endocrine Pancreatic Cancer Risk Loci in the PANDoRA Consortium. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1349-1351. | 1.1 | 5 |
| 67 | Taste receptor polymorphisms and male infertility. Human Reproduction, 2017, 32, 2324-2331. | 0.4 | 34 |
| 68 | Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822. | 0.9 | 45 |
| 69 | Association between polymorphisms of TAS2R16 and susceptibility to colorectal cancer. BMC Gastroenterology, 2017, 17, 104. | 0.8 | 21 |
| 70 | Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343. | 0.8 | 88 |
| 71 | Common germline variants within the CDKN2A/2B region affect risk of pancreatic neuroendocrine tumors. Scientific Reports, 2016, 6, 39565. | 1.6 | 15 |
| 72 | Association of genetic polymorphisms with survival of pancreatic ductal adenocarcinoma patients. Carcinogenesis, 2016, 37, 957-964. | 1.3 | 14 |

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|---|---|---|---|
| 73 | Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. Scientific Reports, 2016, 6, 25506. | 1.6 | 69 |
| 74 | Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979. | 5.8 | 50 |
| 75 | A common variant within the HNF1B gene is associated with overall survival of multiple myeloma patients: Results from the IMMEnSE consortium and meta-analysis. Oncotarget, 2016, 7, 59029-59048. | 0.8 | 16 |
| 76 | Functional single nucleotide polymorphisms within the cyclin-dependent kinase inhibitor 2A/2B region affect pancreatic cancer risk. Oncotarget, 2016, 7, 57011-57020. | 0.8 | 41 |
| 77 | Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58. | 2.2 | 26 |
| 78 | <scp>TERT</scp> gene harbors multiple variants associated with pancreatic cancer susceptibility. International Journal of Cancer, 2015, 137, 2175-2183. | 2.3 | 57 |
| 79 | Association of breast cancer risk loci with breast cancer survival. International Journal of Cancer, 2015, 137, 2837-2845. | 2.3 | 33 |
| 80 | Population-specific association of genes for telomere-associated proteins with longevity in an Italian population. Biogerontology, 2015, 16, 353-364. | 2.0 | 16 |
| 81 | A Genome-wide Pleiotropy Scan for Prostate Cancer Risk. European Urology, 2015, 67, 649-657. | 0.9 | 21 |
| 82 | Genetic risk variants associated with in situ breast cancer. Breast Cancer Research, 2015, 17, 82. | 2.2 | 25 |
| 83 | Genome-wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients. Nature Communications, 2015, 6, 7539. | 5.8 | 38 |
| 84 | Common variation at 2p13.3, 3q29, 7p13 and 17q25.1 associated with susceptibility to pancreatic cancer. Nature Genetics, 2015, 47, 911-916. | 9.4 | 224 |
| 85 | Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, . | 3.0 | 56 |
| 86 | Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889. | 5.8 | 88 |
| 87 | Type 2 diabetes-related variants influence the risk of developing multiple myeloma: results from the IMMEnSE consortium. Endocrine-Related Cancer, 2015, 22, 545-559. | 1.6 | 11 |
| 88 | Risk of multiple myeloma is associated with polymorphisms within telomerase genes and telomere length. International Journal of Cancer, 2015, 136, E351-8. | 2.3 | 30 |
| 89 | A Genome-Wide â€œPleiotropy Scanâ€•Does Not Identify New Susceptibility Loci for Estrogen Receptor Negative Breast Cancer. PLoS ONE, 2014, 9, e85955. | 1.1 | 8 |
| 90 | Factors associated with oxidative stress and cancer risk in the Breast and Prostate Cancer Cohort Consortium. Free Radical Research, 2014, 48, 380-386. | 1.5 | 38 |

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|---|---|---|---|
| 91 | Fine-Mapping the HOXB Region Detects Common Variants Tagging a Rare Coding Allele: Evidence for Synthetic Association in Prostate Cancer. PLoS Genetics, 2014, 10, e1004129. | 1.5 | 34 |
| 92 | Additive Interactions Between Susceptibility Single-Nucleotide Polymorphisms Identified in Genome-Wide Association Studies and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. American Journal of Epidemiology, 2014, 180, 1018-1027. | 1.6 | 36 |
| 93 | Post-GWAS geneâ€"environment interplay in breast cancer: results from the Breast and Prostate Cancer Cohort Consortium and a meta-analysis on 79 000 women. Human Molecular Genetics, 2014, 23, 5260-5270. | 1.4 | 37 |
| 94 | Coffee and tea consumption, genotype-basedCYP1A2andNAT2activity and colorectal cancer risk-Results from the EPIC cohort study. International Journal of Cancer, 2014, 135, 401-412. | 2.3 | 35 |
| 95 | Genetic Variants and Multiple Myeloma Risk: IMMEnSE Validation of the Best Reported Associationsâ€"An Extensive Replication of the Associations from the Candidate Gene Era. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 670-674. | 1.1 | 13 |
| 96 | Genetic association of gastric cancer with miRNA clusters including the cancerâ€related genes MIR29, MIR25, MIR93 and MIR106: Results from the EPICâ€EURGAST study. International Journal of Cancer, 2014, 135, 2065-2076. | 2.3 | 47 |
| 97 | Prostate Cancer (PCa) Risk Variants and Risk of Fatal PCa in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. European Urology, 2014, 65, 1069-1075. | 0.9 | 75 |
| 98 | The FOXE1 locus is a major genetic determinant for familial nonmedullary thyroid carcinoma. International Journal of Cancer, 2014, 134, 2098-2107. | 2.3 | 39 |
| 99 | Leukocyte Telomere Length in Relation to Pancreatic Cancer Risk: A Prospective Study. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2447-2454. | 1.1 | 36 |
| 100 | Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000. | 9.4 | 294 |
| 101 | Mitochondrial DNA copy number and future risk of B-cell lymphoma in a nested case-control study in the prospective EPIC cohort. Blood, 2014, 124, 530-535. | 0.6 | 46 |
| 102 | CD69, a New Potential Clinical Marker in Multiple Myeloma. Blood, 2014, 124, 2027-2027. | 0.6 | 2 |
| 103 | Cereblon (CRBN) Gene Polymorphisms Predict Clinical Response and Progression-Free Survival in Multiple Myeloma Patients Treated with Lenalidomide: A Pharmacogenetic Study of Immense Consortium. Blood, 2014, 124, 3628-3628. | 0.6 | 4 |
| 104 | Abstract 5078: Genome wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients. , 2014, , . | | 0 |
| 105 | Abstract 5064: Pleiotropy analysis identifies a novel prostate cancer variant at 6p21.33: The PAGE, PRACTICAL, and BPC3 Consortia. , 2014, , . | | 0 |
| 106 | Type 2 Diabetes-Related Variants Influence on the Risk of Developing Multiple Myeloma: Results from the Immense Consortium. Blood, 2014, 124, 2044-2044. | 0.6 | 0 |
| 107 | Impact of Drug Transporters ABCB1 and ABCG2 and Regulators of Xenobiotic Transport and Metabolism Pxr and CAR Gene Polymorphisms on Clinical Efficacy of Imatinib in Chronic Myeloid Leukemia (CML). Blood, 2014, 124, 5222-5222. | 0.6 | 0 |
| 108 | The International Multiple Myeloma Research (IMMEnSE) Consortium: Genetics of Multiple Myeloma Risk and Prognosis. Blood, 2014, 124, 3421-3421. | 0.6 | 0 |

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|---|---|---|---|
| 109 | Single nucleotide polymorphism detection by optical DNA-based sensing coupled with whole genomic amplification. Analytical and Bioanalytical Chemistry, 2013, 405, 985-993. | 1.9 | 16 |
| 110 | MAP3K7 and GSTZ1 are associated with human longevity: a two-stage caseâ€“control study using a multilocus genotyping. Age, 2013, 35, 1357-1366. | 3.0 | 8 |
| 111 | Genetic susceptibility to pancreatic cancer and its functional characterisation: The PANcreatic Disease ReseArch (PANDoRA) consortium. Digestive and Liver Disease, 2013, 45, 95-99. | 0.4 | 45 |
| 112 | Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 4239-4239. | 1.4 | 2 |
| 113 | Polymorphisms in regulators of xenobiotic transport and metabolism genes PXR and CAR do not affect multiple myeloma risk: a caseâ€“control study in the context of the IMMEnSE consortium. Journal of Human Genetics, 2013, 58, 155-159. | 1.1 | 5 |
| 114 | Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398. | 9.4 | 374 |
| 115 | Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391. | 9.4 | 492 |
| 116 | A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. Human Molecular Genetics, 2013, 22, 408-415. | 1.4 | 118 |
| 117 | Lack of Replication of Seven Pancreatic Cancer Susceptibility Loci Identified in Two Asian Populations. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 320-323. | 1.1 | 20 |
| 118 | Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528. | 1.4 | 100 |
| 119 | Genetic Variation in the Vitamin D Pathway in Relation to Risk of Prostate Cancerâ€"Results from the Breast and Prostate Cancer Cohort Consortium. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 688-696. | 1.1 | 36 |
| 120 | ABO blood groups and pancreatic cancer risk and survival: Results from the PANcreatic Disease ReseArch (PANDoRA) consortium. Oncology Reports, 2013, 29, 1637-1644. | 1.2 | 55 |
| 121 | Polymorphisms in the Gene Regions of the Adaptor Complex LAMTOR2/LAMTOR3 and Their Association with Breast Cancer Risk. PLoS ONE, 2013, 8, e53768. | 1.1 | 9 |
| 122 | Somatic Mutations in Exocrine Pancreatic Tumors: Association with Patient Survival. PLoS ONE, 2013, 8, e60870. | 1.1 | 47 |
| 123 | A Meta-Analysis Of Genome-Wide Association Studies Of Multiple Myeloma In Cases and Controls Of European Origin Identifies a Risk Locus In 12q23.1. Blood, 2013, 122, 3111-3111. | 0.6 | 2 |
| 124 | Replication of Five Prostate Cancer Loci Identified in an Asian Populationâ€"Results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 212-216. | 1.1 | 23 |
| 125 | Genetic variability in thePRKCIgene and prostate cancer risk. Cell Cycle, 2012, 11, 209-209. | 1.3 | 5 |
| 126 | Polymorphisms in xenobiotic transporters ABCB1, ABCG2, ABCC2, ABCC1, ABCC3 and multiple myeloma risk: a caseâ€“control study in the context of the International Multiple Myeloma rESEarch (IMMEnSE) consortium. Leukemia, 2012, 26, 1419-1422. | 3.3 | 14 |

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|---|---|---|---|
| 127 | Impact of polymorphic variation at 7p15.3, 3p22.1 and 2p23.3 loci on risk of multiple myeloma. British Journal of Haematology, 2012, 158, 805-809. | 1.2 | 19 |
| 128 | A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384. | 1.4 | 168 |
| 129 | A comprehensive study of polymorphisms in the ABCB1, ABCC2, ABCG2, NR1I2 genes and lymphoma risk. International Journal of Cancer, 2012, 131, 803-812. | 2.3 | 35 |
| 130 | A comprehensive study of polymorphisms in ABCB1, ABCC2 and ABCG2 and lung cancer chemotherapy response and prognosis. International Journal of Cancer, 2012, 131, 2920-2928. | 2.3 | 60 |
| 131 | Comprehensive investigation of genetic variation in the 8q24 region and multiple myeloma risk in the <scp>IMME</scp>n<scp>SE</scp> consortium. British Journal of Haematology, 2012, 157, 331-338. | 1.2 | 13 |
| 132 | A Comprehensive Investigation on Common Polymorphisms in the MDR1/ABCB1 Transporter Gene and Susceptibility to Colorectal Cancer. PLoS ONE, 2012, 7, e32784. | 1.1 | 30 |
| 133 | Bitter Taste Receptor Polymorphisms and Human Aging. PLoS ONE, 2012, 7, e45232. | 1.1 | 48 |
| 134 | Abstract 2621: Relative excess risk due to interactions between GWAS-identified susceptibility loci and other breast cancer risk factors. , 2012, , . | | 0 |
| 135 | Interactions Between Genetic Variants and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. Journal of the National Cancer Institute, 2011, 103, 1252-1263. | 3.0 | 147 |
| 136 | POMC and TP53 genetic variability and risk of basal cell carcinoma of skin: Interaction between host and genetic factors. Journal of Dermatological Science, 2011, 63, 47-54. | 1.0 | 15 |
| 137 | N-Acetyltransferase 2 Polymorphisms, Tobacco Smoking, and Breast Cancer Risk in the Breast and Prostate Cancer Cohort Consortium. American Journal of Epidemiology, 2011, 174, 1316-1322. | 1.6 | 31 |
| 138 | Genetic variability of the fatty acid synthase pathway is not associated with prostate cancer risk in the European Prospective Investigation on Cancer (EPIC). European Journal of Cancer, 2011, 47, 420-427. | 1.3 | 7 |
| 139 | Genetic Variability of the mTOR Pathway and Prostate Cancer Risk in the European Prospective Investigation on Cancer (EPIC). PLoS ONE, 2011, 6, e16914. | 1.1 | 12 |
| 140 | Pancreatic Cancer Susceptibility Loci and Their Role in Survival. PLoS ONE, 2011, 6, e27921. | 1.1 | 49 |
| 141 | Genetics and molecular epidemiology of multiple myeloma: The rationale for the IMMEnSE consortium (Review). International Journal of Oncology, 2011, 40, 625-38. | 1.4 | 14 |
| 142 | Genetic variability of the forkhead box O3 and prostate cancer risk in the European Prospective Investigation on Cancer. Oncology Reports, 2011, 26, 979-86. | 1.2 | 7 |
| 143 | Variation in genes coding for AMP-activated protein kinase (AMPK) and breast cancer risk in the European Prospective Investigation on Cancer (EPIC). Breast Cancer Research and Treatment, 2011, 127, 761-767. | 1.1 | 13 |
| 144 | Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791. | 9.4 | 265 |

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|---|---|---|---|
| 145 | Interaction between functional polymorphic variants in cytokine genes, established risk factors and susceptibility to basal cell carcinoma of skin. Carcinogenesis, 2011, 32, 1849-1854. | 1.3 | 20 |
| 146 | Characterizing Associations and SNP-Environment Interactions for GWAS-Identified Prostate Cancer Risk Markersâ€"Results from BPC3. PLoS ONE, 2011, 6, e17142. | 1.1 | 57 |
| 147 | Association Between TAS2R38 Gene Polymorphisms and Colorectal Cancer Risk: A Case-Control Study in Two Independent Populations of Caucasian Origin. PLoS ONE, 2011, 6, e20464. | 1.1 | 77 |
| 148 | Polymorphisms in Regulators of Xenobiotic Transport and Metabolism Genes NR1I2 and NR1I3 and Multiple Myeloma Risk: A Case-Control Study in the Context of IMMEnSE Consortium. Blood, 2011, 118, 5014-5014. | 0.6 | 0 |
| 149 | The INSIG2 rs7566605 polymorphism is not associated with body mass index and breast cancer risk. BMC Cancer, 2010, 10, 563. | 1.1 | 10 |
| 150 | Polymorphisms of genes coding for ghrelin and its receptor in relation to colorectal cancer risk: a two-step gene-wide case-control study. BMC Gastroenterology, 2010, 10, 112. | 0.8 | 23 |
| 151 | A gene-wide investigation on polymorphisms in the taste receptor 2R14 (TAS2R14) and susceptibility to colorectal cancer. BMC Medical Genetics, 2010, 11, 88. | 2.1 | 23 |
| 152 | 69 Post-GWAS pancreatic cancer susceptibility loci and their importance in survival. European Journal of Cancer, Supplement, 2010, 8, 18. | 2.2 | 0 |
| 153 | Outcome of experimental rat vaginitis by Candida albicans isolates with different karyotypes. Microbial Pathogenesis, 2010, 49, 47-50. | 1.3 | 6 |
| 154 | Genetic variation in genes of the fatty acid synthesis pathway and breast cancer risk. Breast Cancer Research and Treatment, 2009, 118, 565-574. | 1.1 | 20 |
| 155 | Association of ABCB1/MDR1 and OPRM1 Gene Polymorphisms With Morphine Pain Relief. Clinical Pharmacology and Therapeutics, 2008, 83, 559-566. | 2.3 | 303 |
| 156 | Could polymorphisms in ATP-binding cassette C3/multidrug resistance associated protein 3 (ABCC3/MRP3) modify colorectal cancer risk?. European Journal of Cancer, 2008, 44, 854-857. | 1.3 | 13 |
| 157 | A gene-wide investigation on polymorphisms in the ABCG2/BRCP transporter and susceptibility to colorectal cancer. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2008, 645, 56-60. | 0.4 | 41 |
| 158 | A comprehensive analysis of phase I and phase II metabolism gene polymorphisms and risk of non-small cell lung cancer in smokers. Carcinogenesis, 2008, 29, 1164-1169. | 1.3 | 123 |
| 159 | DNA Microarray Based on Arrayed-Primer Extension Technique for Identification of Pathogenic Fungi Responsible for Invasive and Superficial Mycoses. Journal of Clinical Microbiology, 2008, 46, 909-915. | 1.8 | 62 |
| 160 | Polymorphisms of dopamine receptor/transporter genes and risk of non-small cell lung cancer. Lung Cancer, 2007, 56, 17-23. | 0.9 | 37 |
| 161 | Association of common polymorphisms in inflammatory genes with risk of developing cancers of the upper aerodigestive tract. Cancer Causes and Control, 2007, 18, 449-455. | 0.8 | 25 |
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