# Nicola J Camp

List of Publications by Year
in descending order



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|---|---|---|---|
| 140 papers | 6,148 citations | 101543 36 h-index | 76900 74 g-index |
| 143 all docs | 143 docs citations | 143 times ranked | 9086 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | A Variant of the HTRA1 Gene Increases Susceptibility to Age-Related Macular Degeneration. Science, 2006, 314, 992-993. | 12.6 | 735 |
| 2 | 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 |
| 3 | A candidate prostate cancer susceptibility gene at chromosome 17p. Nature Genetics, 2001, 27, 172-180. | 21.4 | 504 |
| 4 | Interleukin-1 Receptor Antagonist Gene Polymorphism and Coronary Artery Disease. Circulation, 1999, 99, 861-866. | 1.6 | 217 |
| 5 | Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876. | 21.4 | 179 |
| 6 | An Analysis of Linkage Disequilibrium in the Interleukin-1 Gene Cluster, Using a Novel Grouping Method for Multiallelic Markers. American Journal of Human Genetics, 1998, 62, 1180-1188. | 6.2 | 176 |
| 7 | Predisposition Locus for Major Depression at Chromosome 12q22-12q23.2. American Journal of Human Genetics, 2003, 73, 1271-1281. | 6.2 | 176 |
| 8 | HOXB13 is a susceptibility gene for prostate cancer: results from the International Consortium for Prostate Cancer Genetics (ICPCG). Human Genetics, 2013, 132, 5-14. | 3.8 | 166 |
| 9 | Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. Nature Genetics, 2010, 42, 661-664. | 21.4 | 152 |
| 10 | A Combined Genomewide Linkage Scan of 1,233 Families for Prostate Cancerâ€"Susceptibility Genes Conducted by the International Consortium for Prostate Cancer Genetics. American Journal of Human Genetics, 2005, 77, 219-229. | 6.2 | 138 |
| 11 | Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73. | 21.4 | 120 |
| 12 | Genome-wide association study identifies a novel susceptibility locus at 6p21.3 among familial CLL. Blood, 2011, 117, 1911-1916. | 1.4 | 118 |
| 13 | Genomewide Transmission/Disequilibrium Testingâ€"Consideration of the Genotypic Relative Risks at Disease Loci. American Journal of Human Genetics, 1997, 61, 1424-1430. | 6.2 | 109 |
| 14 | Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933. | 12.8 | 94 |
| 15 | Classification tree analysis: a statistical tool to investigate risk factor interactions with an example for colon cancer (United States). Cancer Causes and Control, 2002, 13, 813-823. | 1.8 | 81 |
| 16 | Primary biliary cirrhosis shows association with genetic polymorphism of tumour necrosis factor alpha promoter region. Journal of Hepatology, 1999, 31, 242-247. | 3.7 | 76 |
| 17 | Common variation at 6p21.31 (BAK1) influences the risk of chronic lymphocytic leukemia. Blood, 2012, 120, 843-846. | 1.4 | 76 |
| 18 | Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175. | 12.8 | 75 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353. | 12.8 | 75 |
| 20 | Genomewide Multipoint Linkage Analysis of Seven Extended Palauan Pedigrees with Schizophrenia, by a Markov-Chain Monte Carlo Method. American Journal of Human Genetics, 2001, 69, 1278-1289. | 6.2 | 67 |
| 21 | Confirmation of chromosome 7q11 locus for predisposition to intracranial aneurysm. Human Genetics, 2004, 114, 250-255. | 3.8 | 62 |
| 22 | Common occurrence of monoclonal Bâ€cell lymphocytosis among members of highâ€risk CLL families. British Journal of Haematology, 2010, 151, 152-158. | 2.5 | 61 |
| 23 | Multiple-polymorphism associations of 7 matrix metalloproteinase and tissue inhibitor metalloproteinase genes with myocardial infarction and angiographic coronary artery disease. American Heart Journal, 2007, 154, 751-758. | 2.7 | 58 |
| 24 | Pooled genome linkage scan of aggressive prostate cancer: results from the International Consortium for Prostate Cancer Genetics. Human Genetics, 2006, 120, 471-485. | 3.8 | 57 |
| 25 | Germline Lysine-Specific Demethylase 1 (LSD1/KDM1A) Mutations Confer Susceptibility to Multiple Myeloma. Cancer Research, 2018, 78, 2747-2759. | 0.9 | 56 |
| 26 | Linkage of creatinine clearance to chromosome 10 in Utah pedigrees replicates a locus for end-stage renal disease in humans and renal failure in the fawn-hooded rat. Kidney International, 2002, 62, 1143-1148. | 5.2 | 55 |
| 27 | Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676. | 2.9 | 52 |
| 28 | Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744. | 7.1 | 51 |
| 29 | Evidence for a Heritable Component in Death Resulting From Aortic and Mitral Valve Diseases. Circulation, 2004, 110, 3143-3148. | 1.6 | 49 |
| 30 | Genome-Wide Multipoint Parametric Linkage Analysis of Pulse Pressure in Large, Extended Utah Pedigrees. Hypertension, 2003, 42, 322-328. | 2.7 | 47 |
| 31 | A role for XRCC2 gene polymorphisms in breast cancer risk and survival. Journal of Medical Genetics, 2011, 48, 477-484. | 3.2 | 47 |
| 32 | Meta-Analysis of Associations of the Ser217Leu and Ala541Thr Variants in ELAC2 (HPC2) and Prostate Cancer. American Journal of Human Genetics, 2002, 71, 1475-1478. | 6.2 | 46 |
| 33 | A genealogical assessment of heritable predisposition to aneurysms. Journal of Neurosurgery, 2003, 99, 637-643. | 1.6 | 46 |
| 34 | Further mapping of 10q26 supports strong association of HTRA1 polymorphisms with age-related macular degeneration. Vision Research, 2008, 48, 685-689. | 1.4 | 44 |
| 35 | Multiple myeloma and family history of lymphohaematopoietic cancers: Results from the International Multiple Myeloma Consortium. British Journal of Haematology, 2016, 175, 87-101. | 2.5 | 43 |
| 36 | Genome-wide significant regions in 43 Utah high-risk families implicate multiple genes involved in risk for completed suicide. Molecular Psychiatry, 2020, 25, 3077-3090. | 7.9 | 40 |

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|---|---|---|---|
| 37 | Graphical Modeling of the Joint Distribution of Alleles at Associated Loci. American Journal of Human Genetics, 2004, 74, 1088-1101. | 6.2 | 38 |
| 38 | Identification of excess clustering of coronary heart diseases among extended pedigrees in a genealogical population database. American Heart Journal, 2006, 152, 305-311. | 2.7 | 38 |
| 39 | Genetic Variants inXRCC2: New Insights Into Colorectal Cancer Tumorigenesis. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2476-2484. | 2.5 | 38 |
| 40 | Genome-wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients. Nature Communications, 2015, 6, 7539. | 12.8 | 38 |
| 41 | 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 |
| 42 | Linkage of serum creatinine and glomerular filtration rate to chromosome 2 in Utah pedigrees*1. American Journal of Hypertension, 2004, 17, 511-515. | 2.0 | 36 |
| 43 | Whole transcriptome profiling of patient-derived xenograft models as a tool to identify both tumor and stromal specific biomarkers. Oncotarget, 2016, 7, 20773-20787. | 1.8 | 36 |
| 44 | A comprehensive study of polymorphisms in the ABCB1, ABCC2, ABCG2, NR1I2 genes and lymphoma risk. International Journal of Cancer, 2012, 131, 803-812. | 5.1 | 35 |
| 45 | Lobular breast cancer: Excess familiality observed in the Utah Population Database. International Journal of Cancer, 2005, 117, 655-661. | 5.1 | 34 |
| 46 | HLA Class I and II Diversity Contributes to the Etiologic Heterogeneity of Non-Hodgkin Lymphoma Subtypes. Cancer Research, 2018, 78, 4086-4096. | 0.9 | 34 |
| 47 | Young Adult and Usual Adult Body Mass Index and Multiple Myeloma Risk: A Pooled Analysis in the International Multiple Myeloma Consortium (IMMC). Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 876-885. | 2.5 | 33 |
| 48 | Compelling evidence for a prostate cancer gene at 22q12.3 by the International Consortium for Prostate Cancer Genetics. Human Molecular Genetics, 2007, 16, 1271-1278. | 2.9 | 31 |
| 49 | Genetic Susceptibility Variants for Chronic Lymphocytic Leukemia. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1098-1102. | 2.5 | 31 |
| 50 | Novel pedigree analysis implicates DNA repair and chromatin remodeling in multiple myeloma risk. PLoS Genetics, 2018, 14, e1007111. | 3.5 | 30 |
| 51 | Replication of the 10q11 and Xp11 Prostate Cancer Risk Variants: Results from a Utah Pedigree-Based Study. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1290-1294. | 2.5 | 29 |
| 52 | Dissecting the genetic etiology of major depressive disorder using linkage analysis. Trends in Molecular Medicine, 2005, 11, 138-144. | 6.7 | 28 |
| 53 | Genetic overlap between autoimmune diseases and nonâ€Hodgkin lymphoma subtypes. Genetic Epidemiology, 2019, 43, 844-863. | 1.3 | 28 |
| 54 | Genomic search for prostate cancer predisposition loci in Utah pedigrees. Prostate, 2005, 65, 365-374. | 2.3 | 27 |

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|---|---|---|---|
| 55 | Localization of a Prostate Cancer Predisposition Gene to an 880-kb Region on Chromosome 22q12.3 in Utah High-Risk Pedigrees. Cancer Research, 2006, 66, 10205-10212. | 0.9 | 26 |
| 56 | Confirmation of the HPCX prostate cancer predisposition locus in large Utah prostate cancer pedigrees. Human Genetics, 2005, 116, 179-185. | 3.8 | 24 |
| 57 | Populationâ€based risk assessment for other cancers in relatives of hereditary prostate cancer (HPC) cases. Prostate, 2005, 64, 347-355. | 2.3 | 24 |
| 58 | A unique genome-wide association analysis in extended Utah high-risk pedigrees identifies a novel melanoma risk variant on chromosome arm 10q. Human Genetics, 2012, 131, 77-85. | 3.8 | 24 |
| 59 | Association analysis of 9,560 prostate cancer cases from the International Consortium of Prostate Cancer Genetics confirms the role of reported prostate cancer associated SNPs for familial disease. Human Genetics, 2014, 133, 347-356. | 3.8 | 24 |
| 60 | Familial Myeloma. New England Journal of Medicine, 2008, 359, 1734-1735. | 27.0 | 23 |
| 61 | Association of common missense changes in ELAC2 (HPC2) with prostate cancer in a Japanese caseâ€“control series. Journal of Human Genetics, 2002, 47, 0641-0648. | 2.3 | 22 |
| 62 | Genome-Wide Scans Meta-Analysis for Pulse Pressure. Hypertension, 2007, 50, 557-564. | 2.7 | 22 |
| 63 | Genomeâ€wide linkage analysis of 1,233 prostate cancer pedigrees from the International Consortium for prostate cancer Genetics using novel sumLINK and sumLOD analyses. Prostate, 2010, 70, 735-744. | 2.3 | 22 |
| 64 | Examination of ELN as a Candidate Gene in the Utah Intracranial Aneurysm Pedigrees. Stroke, 2005, 36, 1283-1284. | 2.0 | 21 |
| 65 | Multiple Less Common Genetic Variants Explain the Association of the Cholesteryl Ester Transfer Protein Gene With Coronary Artery Disease. Journal of the American College of Cardiology, 2007, 49, 2053-2060. | 2.8 | 21 |
| 66 | Fine-Mapping CASP8 Risk Variants in Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 176-181. | 2.5 | 21 |
| 67 | Validation of prostate cancer risk-related loci identified from genome-wide association studies using family-based association analysis: evidence from the International Consortium for Prostate Cancer Genetics (ICPCG). Human Genetics, 2012, 131, 1095-1103. | 3.8 | 21 |
| 68 | Consensus Analysis of Whole Transcriptome Profiles from Two Breast Cancer Patient Cohorts Reveals Long Non-Coding RNAs Associated with Intrinsic Subtype and the Tumour Microenvironment. PLoS ONE, 2016, 11, e0163238. | 2.5 | 21 |
| 69 | Association of polygenic risk score with the risk of chronic lymphocytic leukemia and monoclonal B-cell lymphocytosis. Blood, 2018, 131, 2541-2551. | 1.4 | 21 |
| 70 | Coinherited genetics of multiple myeloma and its precursor, monoclonal gammopathy of undetermined significance. Blood Advances, 2020, 4, 2789-2797. | 5.2 | 20 |
| 71 | A Pooled Analysis of Alcohol Consumption and Risk of Multiple Myeloma in the International Multiple Myeloma Consortium. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1620-1627. | 2.5 | 19 |
| 72 | 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 |

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|---|---|---|---|
| 73 | Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51. | 8.2 | 19 |
| 74 | Shared Genomic Segment Analysis: The Power to Find Rare Disease Variants. Annals of Human Genetics, 2012, 76, 500-509. | 0.8 | 18 |
| 75 | A Meta-analysis of Multiple Myeloma Risk Regions in African and European Ancestry Populations Identifies Putatively Functional Loci. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1609-1618. | 2.5 | 18 |
| 76 | Characterization of linkage disequilibrium structure, mutation history, and tagging SNPs, and their use in association analyses:ELAC2 and familial early-onset prostate cancer. Genetic Epidemiology, 2005, 28, 232-243. | 1.3 | 17 |
| 77 | Evidence for Linkage on Chromosome 3q25â€“27 in a Large Autism Extended Pedigree. Human Heredity, 2005, 60, 220-226. | 0.8 | 17 |
| 78 | hapConstructor: automatic construction and testing of haplotypes in a Monte Carlo framework. Bioinformatics, 2008, 24, 2105-2107. | 4.1 | 17 |
| 79 | Identification of regions of positive selection using Shared Genomic Segment analysis. European Journal of Human Genetics, 2011, 19, 667-671. | 2.8 | 17 |
| 80 | A Pooled Analysis of Cigarette Smoking and Risk of Multiple Myeloma from the International Multiple Myeloma Consortium. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 631-634. | 2.5 | 17 |
| 81 | Panel sequencing of 264 candidate susceptibility genes and segregation analysis in a cohort of non-BRCA1, non-BRCA2 breast cancer families. Breast Cancer Research and Treatment, 2017, 166, 937-949. | 2.5 | 16 |
| 82 | Natural history of monoclonal B-cell lymphocytosis among relatives in CLL families. Blood, 2021, 137, 2046-2056. | 1.4 | 16 |
| 83 | HLA DQA1-DQB1 genotypes in Bedouin families with celiac disease. Human Immunology, 2002, 63, 502-507. | 2.4 | 15 |
| 84 | Chromosomes 4 and 8 implicated in a genome wide SNP linkage scan of 762 prostate cancer families collected by the ICPCG. Prostate, 2012, 72, 410-426. | 2.3 | 14 |
| 85 | Re-interpretation of PAM50 gene expression as quantitative tumor dimensions shows utility for clinical trials: application to prognosis and response to paclitaxel in breast cancer. Breast Cancer Research and Treatment, 2019, 175, 129-139. | 2.5 | 14 |
| 86 | Rare proteinâ€coding variants implicate genes involved in risk of suicide death. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 508-520. | 1.7 | 14 |
| 87 | Common variants within 6p21.31 locus are associated with chronic lymphocytic leukaemia and, potentially, other non-Hodgkin lymphoma subtypes. British Journal of Haematology, 2012, 159, n/a-n/a. | 2.5 | 13 |
| 88 | Mapping of the IRF8 Gene Identifies a 3â€²UTR Variant Associated with Risk of Chronic Lymphocytic Leukemia but not Other Common Non-Hodgkin Lymphoma Subtypes. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 461-466. | 2.5 | 13 |
| 89 | Lipid Trait Variants and the Risk of Non-Hodgkin Lymphoma Subtypes: A Mendelian Randomization Study. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1074-1078. | 2.5 | 13 |
| 90 | Associations of ATR and CHEK1 Single Nucleotide Polymorphisms with Breast Cancer. PLoS ONE, 2013, 8, e68578. | 2.5 | 13 |

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|---|---|---|---|
| 91 | High-Resolution Characterization of Linkage Disequilibrium Structure and Selection of Tagging Single Nucleotide Polymorphisms: Application to the Cholesteryl Ester Transfer Protein Gene. Annals of Human Genetics, 2006, 70, 524-534. | 0.8 | 12 |
| 92 | Pooled study of occupational exposure to aromatic hydrocarbon solvents and risk of multiple myeloma. Occupational and Environmental Medicine, 2018, 75, 798-806. | 2.8 | 12 |
| 93 | Statistical recombinant mapping in extended highâ€risk Utah pedigrees narrows the 8q24 prostate cancer locus to 2.0 Mb. Prostate, 2007, 67, 1456-1464. | 2.3 | 11 |
| 94 | Family Study Designs Informed by Tumor Heterogeneity and Multi-Cancer Pleiotropies: The Power of the Utah Population Database. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 807-815. | 2.5 | 11 |
| 95 | Genetic evidence of PTPN22 effects on chronic lymphocytic leukemia. Blood, 2013, 121, 237-238. | 1.4 | 10 |
| 96 | A parallel genetic algorithm to discover patterns in genetic markers that indicate predisposition to multifactorial disease. Computers in Biology and Medicine, 2008, 38, 826-836. | 7.0 | 9 |
| 97 | Reparameterization of PAM50 Expression Identifies Novel Breast Tumor Dimensions and Leads to Discovery of a Genome-Wide Significant Breast Cancer Locus at 12q15. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 644-652. | 2.5 | 9 |
| 98 | Association of elevated serumfree light chains with chronic lymphocytic leukemia and monoclonal B-cell lymphocytosis. Blood Cancer Journal, 2019, 9, 59. | 6.2 | 9 |
| 99 | Predictors of Response Outcomes for Research Recruitment Through a Central Cancer Registry: Evidence From 17 Recruitment Efforts for Population-Based Studies. American Journal of Epidemiology, 2019, 188, 928-939. | 3.4 | 9 |
| 100 | Significant evidence for linkage to chromosome 5q13 in a genome-wide scan for asthma in an extended pedigree resource. European Journal of Human Genetics, 2009, 17, 636-643. | 2.8 | 8 |
| 101 | Discordant Haplotype Sequencing Identifies Functional Variants at the 2q33 Breast Cancer Risk Locus. Cancer Research, 2016, 76, 1916-1925. | 0.9 | 7 |
| 102 | A Pooled Analysis of Reproductive Factors, Exogenous Hormone Use, and Risk of Multiple Myeloma among Women in the International Multiple Myeloma Consortium. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 217-221. | 2.5 | 6 |
| 103 | Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539. | 2.8 | 6 |
| 104 | Neurexin 1 variants as risk factors for suicide death. Molecular Psychiatry, 2021, , . | 7.9 | 5 |
| 105 | The effect of selective sampling on mapping quantitative trait loci. , 1997, 14, 767-772. | | 4 |
| 106 | Model-fitting and linkage analysis of sodiumâ€“lithium countertransport. European Journal of Human Genetics, 2004, 12, 1055-1061. | 2.8 | 4 |
| 107 | Shared genomic segments in highâ€risk multigenerational pedigrees with gastroschisis. Birth Defects Research, 2019, 111, 1655-1664. | 1.5 | 4 |
| 108 | Harnessing Population Pedigree Data and Machine Learning Methods to Identify Patterns of Familial Bladder Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 918-926. | 2.5 | 4 |

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| 109 | 21-gene recurrence score testing utilization among older women from different races: A population-based study. Journal of Geriatric Oncology, 2021, 12, 206-211. | 1.0 | 4 |
| 110 | Common genetic polymorphisms contribute to the association between chronic lymphocytic leukaemia and non-melanoma skin cancer. International Journal of Epidemiology, 2021, 50, 1325-1334. | 1.9 | 4 |
| 111 | Genetic Investigation by Shared Genomic Segment and Linkage Study of a Unique Family with Primary Familial and Congenital Polycythemia. Blood, 2010, 116, 4783-4783. | 1.4 | 4 |
| 112 | Haplotype association analyses in resources of mixed structure using Monte Carlo testing. BMC Bioinformatics, 2010, 11, 592. | 2.6 | 3 |
| 113 | Elevated IgM and abnormal free light chain ratio are increased in relatives from high-risk chronic lymphocytic leukemia pedigrees. Blood Cancer Journal, 2019, 9, 25. | 6.2 | 3 |
| 114 | Expression quantitative trait loci of genes predicting outcome are associated with survival of multiple myeloma patients. International Journal of Cancer, 2021, 149, 327-336. | 5.1 | 3 |
| 115 | Identification of a Major Susceptibility Locus for Lethal Graft-versus-Host Disease in MHC-Matched Mice. Journal of Immunology, 2009, 183, 462-469. | 0.8 | 2 |
| 116 | Validity and power of association testing in family-based sampling designs: evidence for and against the common wisdom. Genetic Epidemiology, 2011, 35, 174-181. | 1.3 | 2 |
| 117 | Browser-based Data Annotation, Active Learning, and Real-Time Distribution of Artificial Intelligence Models: From Tumor Tissue Microarrays to COVID-19 Radiology. Journal of Pathology Informatics, 2021, 12, 38. | 1.7 | 2 |
| 118 | Sequencing at lymphoid neoplasm susceptibility loci maps six myeloma risk genes. Human Molecular Genetics, 2021, 30, 1142-1153. | 2.9 | 2 |
| 119 | Family-Associated Monoclonal B Lymphocytosis Is Commonly Oligoclonal and Expresses Markers Associated with Adverse Risk in CLL. Blood, 2008, 112, 3144-3144. | 1.4 | 2 |
| 120 | Monoclonal B-Cell Lymphocytosis Is Commonly Observed Among Unaffected Members of High Risk CLL Families.. Blood, 2009, 114, 1232-1232. | 1.4 | 2 |
| 121 | Inherited Giant Platelet Disorder, Kashmiri Thrombocytopenia, a Common Syndrome Found in Srinagar, India. Blood, 2014, 124, 4211-4211. | 1.4 | 2 |
| 122 | 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. | 1.4 | 2 |
| 123 | Familial risk of epithelial ovarian cancer after accounting for gynaecological surgery: a population-based study. Journal of Medical Genetics, 2023, 60, 119-127. | 3.2 | 2 |
| 124 | Does a Multiple Myeloma Polygenic Risk Score Predict Overall Survival of Myeloma Patients?. Cancer Epidemiology Biomarkers and Prevention, 0, , . | 2.5 | 2 |
| 125 | SA18SIGNIFICANT OVERLAP OF GENOMIC REGIONS FROM EXTENDED HIGH-RISK AUTISM FAMILIES WITH EVOLUTIONARILY ACCELERATED REGIONS IN A SPECIES WITH HIGHLY UNUSUAL SOCIAL BEHAVIOR. European Neuropsychopharmacology, 2019, 29, S1197. | 0.7 | 0 |
| 126 | 66ANALYSES OF DISEASE-ASSOCIATED AND LIKELY FUNCTIONAL VARIANTS FROM PSYCHARRAY IMPLICATE GENES INVOLVED IN RISK FOR COMPLETED SUICIDE. European Neuropsychopharmacology, 2019, 29, S1105. | 0.7 | 0 |

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|---|---|---|---|
| 127 | Shared genomic segment analysis in a large high-risk chronic lymphocytic leukemia pedigree implicates CXCR4 in inherited risk. , 2021, 5, 189-199. | | 0 |
| 128 | Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. , 2021, 5, 200-217. | | 0 |
| 129 | Duo Shared Genomic Segment analysis identifies a genome-wide significant risk locus at 18q21.33 in myeloma pedigrees. , 2021, 5, 112-123. | | 0 |
| 130 | Genetic determinants of multiple myeloma risk within the Wnt/beta-catenin signaling pathway. Cancer Epidemiology, 2021, 73, 101972. | 1.9 | 0 |
| 131 | Family-Associated Monoclonal B Lymphocytosis Shows Differences From CLL That Suggest An Indolent Biology.. Blood, 2009, 114, 1241-1241. | 1.4 | 0 |
| 132 | Investigation of CLL-Susceptibility Loci with Monoclonal B-Cell Lymphocytosis (MBL) Risk and Confirmation of Recently Reported CLL-Susceptibility Loci. Blood, 2010, 116, 2443-2443. | 1.4 | 0 |
| 133 | Exome Sequencing in a Family with Chronic Lymphocytic Leukemia, Mantle Cell Lymphoma and Autoimmune Disease Uncovers Potential Germline Risk-Alleles. Blood, 2014, 124, 5629-5629. | 1.4 | 0 |
| 134 | Exome Sequencing in Myeloma Pedigrees Implicates RAS1 and NOTCH Signaling Are Involved in Inherited Myeloma Risk. Blood, 2015, 126, 2976-2976. | 1.4 | 0 |
| 135 | Disruption of the SUMO Pathway in a High-Risk B-Cell Non-Hodgkin Lymphoma Pedigree. Blood, 2015, 126, 2682-2682. | 1.4 | 0 |
| 136 | A Genome-Wide Association Study of Myeloma Survival in Utah Uncovers Germline Variants That May Influence Survival of Multiple Myeloma Patients. Blood, 2015, 126, 2993-2993. | 1.4 | 0 |
| 137 | Elevated Rates of Monoclonal Gammopathy in High-Risk Chronic Lymphocytic Leukemia Pedigrees. Blood, 2015, 126, 1449-1449. | 1.4 | 0 |
| 138 | Large-Scale Linkage Analysis of Multiple Myeloma (MM) and Monoclonal Gammopathy of Undetermined Significance (MGUS) Families. Blood, 2018, 132, 4501-4501. | 1.4 | 0 |
| 139 | Association between a Polygenic Risk Score for Multiple Myeloma Risk and Overall Survival. Blood, 2019, 134, 4366-4366. | 1.4 | 0 |
| 140 | CD229 CAR T Cell Therapy for the Treatment of Relapsed B Cell Lymphoma. Blood, 2021, 138, 2800-2800. | 1.4 | 0 |