Nicola J Camp

List of Publications by Year
in descending order

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	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
2	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
3	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
4	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
5	Shared genomic segment analysis in a large high-risk chronic lymphocytic leukemia pedigree implicates CXCR4 in inherited risk. , 2021, 5, 189-199.		0
6	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
7	Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. , 2021, 5, 200-217.		0
8	Duo Shared Genomic Segment analysis identifies a genome-wide significant risk locus at 18q21.33 in myeloma pedigrees. , 2021, 5, 112-123.		0
9	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
10	Sequencing at lymphoid neoplasm susceptibility loci maps six myeloma risk genes. Human Molecular Genetics, 2021, 30, 1142-1153.	2.9	2
11	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
12	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
13	Natural history of monoclonal B-cell lymphocytosis among relatives in CLL families. Blood, 2021, 137, 2046-2056.	1.4	16
14	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
15	Neurexin 1 variants as risk factors for suicide death. Molecular Psychiatry, 2021, , .	7.9	5
16	Genetic determinants of multiple myeloma risk within the Wnt/beta-catenin signaling pathway. Cancer Epidemiology, 2021, 73, 101972.	1.9	0
17	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
18	CD229 CAR T Cell Therapy for the Treatment of Relapsed B Cell Lymphoma. Blood, 2021, 138, 2800-2800.	1.4	0

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19	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
20	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
21	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
22	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
23	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
24	Coinherited genetics of multiple myeloma and its precursor, monoclonal gammopathy of undetermined significance. Blood Advances, 2020, 4, 2789-2797.	5.2	20
25	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
26	Association of elevated serumfree light chains with chronic lymphocytic leukemia and monoclonal B-cell lymphocytosis. Blood Cancer Journal, 2019, 9, 59.	6.2	9
27	Shared genomic segments in highâ€risk multigenerational pedigrees with gastroschisis. Birth Defects Research, 2019, 111, 1655-1664.	1.5	4
28	Genetic overlap between autoimmune diseases and nonâ€Hodgkin lymphoma subtypes. Genetic Epidemiology, 2019, 43, 844-863.	1.3	28
29	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
30	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
31	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
32	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
33	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
34	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539.	2.8	6
35	Association between a Polygenic Risk Score for Multiple Myeloma Risk and Overall Survival. Blood, 2019, 134, 4366-4366.	1.4	0
36	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

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37	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
38	Germline Lysine-Specific Demethylase 1 (LSD1/KDM1A) Mutations Confer Susceptibility to Multiple Myeloma. Cancer Research, 2018, 78, 2747-2759.	0.9	56
39	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
40	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
41	Novel pedigree analysis implicates DNA repair and chromatin remodeling in multiple myeloma risk. PLoS Genetics, 2018, 14, e1007111.	3.5	30
42	Large-Scale Linkage Analysis of Multiple Myeloma (MM) and Monoclonal Gammopathy of Undetermined Significance (MGUS) Families. Blood, 2018, 132, 4501-4501.	1.4	0
43	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
44	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	12.8	75
45	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
46	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
47	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
48	Discordant Haplotype Sequencing Identifies Functional Variants at the 2q33 Breast Cancer Risk Locus. Cancer Research, 2016, 76, 1916-1925.	0.9	7
49	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
50	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	12.8	94
51	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
52	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
53	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
54	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

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55	Genome-wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients. Nature Communications, 2015, 6, 7539.	12.8	38
56	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
57	Exome Sequencing in Myeloma Pedigrees Implicates RAS1 and NOTCH Signaling Are Involved in Inherited Myeloma Risk. Blood, 2015, 126, 2976-2976.	1.4	0
58	Disruption of the SUMO Pathway in a High-Risk B-Cell Non-Hodgkin Lymphoma Pedigree. Blood, 2015, 126, 2682-2682.	1.4	0
59	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
60	Elevated Rates of Monoclonal Gammopathy in High-Risk Chronic Lymphocytic Leukemia Pedigrees. Blood, 2015, 126, 1449-1449.	1.4	0
61	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
62	Inherited Giant Platelet Disorder, Kashmiri Thrombocytopenia, a Common Syndrome Found in Srinagar, India. Blood, 2014, 124, 4211-4211.	1.4	2
63	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
64	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
65	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	21.4	179
66	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
67	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
68	Genetic evidence of PTPN22 effects on chronic lymphocytic leukemia. Blood, 2013, 121, 237-238.	1.4	10
69	Associations of ATR and CHEK1 Single Nucleotide Polymorphisms with Breast Cancer. PLoS ONE, 2013, 8, e68578.	2.5	13
70	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
71	Fine-Mapping CASP8 Risk Variants in Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 176-181.	2.5	21
72	Shared Genomic Segment Analysis: The Power to Find Rare Disease Variants. Annals of Human Genetics, 2012, 76, 500-509.	0.8	18

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73	Common variation at 6p21.31 (BAK1) influences the risk of chronic lymphocytic leukemia. Blood, 2012, 120, 843-846.	1.4	76
74	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
75	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
76	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
77	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
78	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
79	Genome-wide association study identifies a novel susceptibility locus at 6p21.3 among familial CLL. Blood, 2011, 117, 1911-1916.	1.4	118
80	Identification of regions of positive selection using Shared Genomic Segment analysis. European Journal of Human Genetics, 2011, 19, 667-671.	2.8	17
81	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. Journal of Medical Genetics, 2011, 48, 477-484.	3.2	47
82	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
83	Haplotype association analyses in resources of mixed structure using Monte Carlo testing. BMC Bioinformatics, 2010, 11, 592.	2.6	3
84	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
85	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
86	Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32. Nature Genetics, 2010, 42, 661-664.	21.4	152
87	Genetic Susceptibility Variants for Chronic Lymphocytic Leukemia. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1098-1102.	2.5	31
88	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
89	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
90	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

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91	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
92	Genetic Variants inXRCC2: New Insights Into Colorectal Cancer Tumorigenesis. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2476-2484.	2.5	38
93	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
94	Monoclonal B-Cell Lymphocytosis Is Commonly Observed Among Unaffected Members of High Risk CLL Families.. Blood, 2009, 114, 1232-1232.	1.4	2
95	Family-Associated Monoclonal B Lymphocytosis Shows Differences From CLL That Suggest An Indolent Biology.. Blood, 2009, 114, 1241-1241.	1.4	0
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	Further mapping of 10q26 supports strong association of HTRA1 polymorphisms with age-related macular degeneration. Vision Research, 2008, 48, 685-689.	1.4	44
98	hapConstructor: automatic construction and testing of haplotypes in a Monte Carlo framework. Bioinformatics, 2008, 24, 2105-2107.	4.1	17
99	Familial Myeloma. New England Journal of Medicine, 2008, 359, 1734-1735.	27.0	23
100	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
101	Genome-Wide Scans Meta-Analysis for Pulse Pressure. Hypertension, 2007, 50, 557-564.	2.7	22
102	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
103	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
104	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
105	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
106	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
107	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
108	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

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109	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
110	A Variant of the HTRA1 Gene Increases Susceptibility to Age-Related Macular Degeneration. Science, 2006, 314, 992-993.	12.6	735
111	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
112	Lobular breast cancer: Excess familiality observed in the Utah Population Database. International Journal of Cancer, 2005, 117, 655-661.	5.1	34
113	Confirmation of the HPCX prostate cancer predisposition locus in large Utah prostate cancer pedigrees. Human Genetics, 2005, 116, 179-185.	3.8	24
114	Populationâ€based risk assessment for other cancers in relatives of hereditary prostate cancer (HPC) cases. Prostate, 2005, 64, 347-355.	2.3	24
115	Genomic search for prostate cancer predisposition loci in Utah pedigrees. Prostate, 2005, 65, 365-374.	2.3	27
116	Evidence for Linkage on Chromosome 3q25â€“27 in a Large Autism Extended Pedigree. Human Heredity, 2005, 60, 220-226.	0.8	17
117	Examination of ELN as a Candidate Gene in the Utah Intracranial Aneurysm Pedigrees. Stroke, 2005, 36, 1283-1284.	2.0	21
118	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
119	Dissecting the genetic etiology of major depressive disorder using linkage analysis. Trends in Molecular Medicine, 2005, 11, 138-144.	6.7	28
120	Evidence for a Heritable Component in Death Resulting From Aortic and Mitral Valve Diseases. Circulation, 2004, 110, 3143-3148.	1.6	49
121	Model-fitting and linkage analysis of sodiumâ€“lithium countertransport. European Journal of Human Genetics, 2004, 12, 1055-1061.	2.8	4
122	Confirmation of chromosome 7q11 locus for predisposition to intracranial aneurysm. Human Genetics, 2004, 114, 250-255.	3.8	62
123	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
124	Graphical Modeling of the Joint Distribution of Alleles at Associated Loci. American Journal of Human Genetics, 2004, 74, 1088-1101.	6.2	38
125	Predisposition Locus for Major Depression at Chromosome 12q22-12q23.2. American Journal of Human Genetics, 2003, 73, 1271-1281.	6.2	176
126	Genome-Wide Multipoint Parametric Linkage Analysis of Pulse Pressure in Large, Extended Utah Pedigrees. Hypertension, 2003, 42, 322-328.	2.7	47

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127	A genealogical assessment of heritable predisposition to aneurysms. Journal of Neurosurgery, 2003, 99, 637-643.	1.6	46
128	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
129	HLA DQA1-DQB1 genotypes in Bedouin families with celiac disease. Human Immunology, 2002, 63, 502-507.	2.4	15
130	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
131	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
132	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
133	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
134	A candidate prostate cancer susceptibility gene at chromosome 17p. Nature Genetics, 2001, 27, 172-180.	21.4	504
135	Interleukin-1 Receptor Antagonist Gene Polymorphism and Coronary Artery Disease. Circulation, 1999, 99, 861-866.	1.6	217
136	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
137	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
138	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
139	The effect of selective sampling on mapping quantitative trait loci. , 1997, 14, 767-772.		4
140	Does a Multiple Myeloma Polygenic Risk Score Predict Overall Survival of Myeloma Patients?. Cancer Epidemiology Biomarkers and Prevention, 0, , .	2.5	2