Lisa Cannon-Albright

List of Publications by Year
in descending order

255 papers	21,954 citations	31902 53 h-index	9839 141 g-index
268 all docs	268 docs citations	268 times ranked	23970 citing authors

#	Article	IF	Citations
1	A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1. Science, 1994, 266, 66-71.	6.0	5,747
2	Localization of a breast cancer susceptibility gene, BRCA2, to chromosome 13q12-13. Science, 1994, 265, 2088-2090.	6.0	1,725
3	REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. American Journal of Human Genetics, 2016, 99, 877-885.	2.6	1,555
4	Systematic Population-Based Assessment of Cancer Risk in First-Degree Relatives of Cancer Probands. Journal of the National Cancer Institute, 1994, 86, 1600-1608.	3.0	923
5	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
6	A candidate prostate cancer susceptibility gene at chromosome 17p. Nature Genetics, 2001, 27, 172-180.	9.4	504
7	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	9.4	492
8	Common Inheritance of Susceptibility to Colonic Adenomatous Polyps and Associated Colorectal Cancers. New England Journal of Medicine, 1988, 319, 533-537.	13.9	464
9	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	9.4	422
10	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
11	Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. Nature Genetics, 2009, 41, 1116-1121.	9.4	389
12	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	9.4	265
13	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.	9.4	264
14	BRCA1, BRCA2, PALB2, and CDKN2A mutations in familial pancreatic cancer: a PACGENE study. Genetics in Medicine, 2015, 17, 569-577.	1.1	231
15	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	9.4	230
16	Population-Based Family Historyâ€“Specific Risks for Colorectal Cancer: A Constellation Approach. Gastroenterology, 2010, 138, 877-885.	0.6	198
17	Ovarian cancer risk in BRCA1 carriers is modified by the HRAS1 variable number of tandem repeat (VNTR) locus. Nature Genetics, 1996, 12, 309-311.	9.4	183
18	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	9.4	179

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19	Predisposition Locus for Major Depression at Chromosome 12q22-12q23.2. American Journal of Human Genetics, 2003, 73, 1271-1281.	2.6	176
20	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
21	HOXB13 is a susceptibility gene for prostate cancer: results from the International Consortium for Prostate Cancer Genetics (ICPCG). Human Genetics, 2013, 132, 5-14.	1.8	166
22	Risk modifiers in carriers of brca1 mutations. International Journal of Cancer, 1995, 64, 394-398.	2.3	161
23	Polygenic hazard score to guide screening for aggressive prostate cancer: development and validation in large scale cohorts. BMJ: British Medical Journal, 2018, 360, j5757.	2.4	153
24	Haplotype and Phenotype Analysis of Nine Recurrent BRCA2 Mutations in 111 Families: Results of an International Study. American Journal of Human Genetics, 1998, 62, 1381-1388.	2.6	150
25	Familial male breast cancer is not linked to the BRCA1 locus on chromosome 17q. Nature Genetics, 1994, 7, 103-107.	9.4	146
26	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.	2.6	138
27	GENETICS OF COLON CANCER: Impact of Inheritance on Colon Cancer Risk. Annual Review of Medicine, 1995, 46, 371-379.	5.0	128
28	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
29	Response to radiation therapy and prognosis in breast cancer patients with BRCA1 and BRCA2 mutations. Radiotherapy and Oncology, 1998, 47, 129-136.	0.3	114
30	Evidence for an Inherited Predisposition Contributing to the Risk for Rotator Cuff Disease. Journal of Bone and Joint Surgery - Series A, 2009, 91, 1136-1142.	1.4	94
31	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94
32	Population-Based Analysis of Prognostic Factors and Survival in Familial Melanoma. Journal of Clinical Oncology, 2005, 23, 7168-7177.	0.8	91
33	Prostate cancer risk prediction based on complete prostate cancer family history. Prostate, 2015, 75, 390-398.	1.2	91
34	Genome-wide linkage analyses of extended Utah pedigrees identifies loci that influence recurrent, early-onset major depression and anxiety disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 135B, 85-93.	1.1	90
35	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
36	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88

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37	Parapneumonic Empyema Deaths during Past Century, Utah. Emerging Infectious Diseases, 2009, 15, 44-48.	2.0	77
38	The effects of height and BMI on prostate cancer incidence and mortality: a Mendelian randomization study in 20,848 cases and 20,214 controls from the PRACTICAL consortium. Cancer Causes and Control, 2015, 26, 1603-1616.	0.8	77
39	Meta Association of Colorectal Cancer Confirms Risk Alleles at 8q24 and 18q21. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 616-621.	1.1	71
40	Shared Predispositions of Parkinsonism and Cancer. Archives of Neurology, 2012, 69, 1572.	4.9	71
41	Utah Family-Based Analysis: Past, Present and Future. Human Heredity, 2008, 65, 209-220.	0.4	69
42	Evidence for a heritable predisposition to Chronic Fatigue Syndrome. BMC Neurology, 2011, 11, 62.	0.8	68
43	Blood lipids and prostate cancer: a Mendelian randomization analysis. Cancer Medicine, 2016, 5, 1125-1136.	1.3	68
44	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	1.4	67
45	Linkage, whole genome sequence, and biological data implicate variants in RAB10 in Alzheimerâ€™s disease resilience. Genome Medicine, 2017, 9, 100.	3.6	67
46	At-Risk Populations for Osteosarcoma: The Syndromes and Beyond. Sarcoma, 2012, 2012, 1-9.	0.7	66
47	A Screening Study of Prostate Cancer in High Risk Families. Journal of Urology, 1992, 148, 826-827.	0.2	64
48	Confirmation of chromosome 7q11 locus for predisposition to intracranial aneurysm. Human Genetics, 2004, 114, 250-255.	1.8	62
49	Characterization of Common BRCA1 and BRCA2 Variants. Genetic Testing and Molecular Biomarkers, 2002, 6, 119-121.	1.7	59
50	Association of Rare Coding Mutations With Alzheimer Disease and Other Dementias Among Adults of European Ancestry. JAMA Network Open, 2019, 2, e191350.	2.8	58
51	Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1610-1616.	1.1	57
52	Comparison of compliance for colorectal cancer screening and surveillance by colonoscopy based on risk. Genetics in Medicine, 2011, 13, 737-743.	1.1	57
53	Evidence for an Inherited Predisposition to Lumbar Disc Disease. Journal of Bone and Joint Surgery - Series A, 2011, 93, 225-229.	1.4	56
54	A comprehensive survey of cancer risks in extended families. Genetics in Medicine, 2012, 14, 107-114.	1.1	56

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55	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. Cancer Discovery, 2015, 5, 368-379.	7.7	56
56	Risk Analysis of Prostate Cancer in PRACTICAL, a Multinational Consortium, Using 25 Known Prostate Cancer Susceptibility Loci. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1121-1129.	1.1	56
57	Localization of the 9p Melanoma Susceptibility Locus (MLM) to a 2-cM Region between D9S736 and D9S171. Genomics, 1994, 23, 265-268.	1.3	55
58	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	1.2	54
59	Independent Validation of Effect of HSD3B1 Genotype on Response to Androgen-Deprivation Therapy in Prostate Cancer. JAMA Oncology, 2017, 3, 856.	3.4	53
60	Significant Linkage Evidence for a Predisposition Gene for Pelvic Floor Disorders on Chromosome 9q21. American Journal of Human Genetics, 2009, 84, 678-682.	2.6	52
61	Significant evidence for a heritable contribution to cancer predisposition: a review of cancer familiality by site. BMC Cancer, 2012, 12, 138.	1.1	52
62	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	1.4	52
63	Interobserver concordance in discriminating clinical atypia of melanocytic nevi, and correlations with histologic atypia. Journal of the American Academy of Dermatology, 1996, 34, 618-625.	0.6	51
64	Population-Based Prevalence of CDKN2A Mutations in Utah Melanoma Families. Journal of Investigative Dermatology, 2006, 126, 660-666.	0.3	51
65	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
66	Evidence for a Heritable Component in Death Resulting From Aortic and Mitral Valve Diseases. Circulation, 2004, 110, 3143-3148.	1.6	49
67	Significant association of full-thickness rotator cuff tears and estrogen-related receptor-Î² (ESRRB). Journal of Shoulder and Elbow Surgery, 2015, 24, e31-e35.	1.2	48
68	Identification of Six Loci Associated With Pelvic Organ Prolapse Using Genome-Wide Association Analysis. Obstetrics and Gynecology, 2011, 118, 1345-1353.	1.2	47
69	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. Journal of Medical Genetics, 2011, 48, 477-484.	1.5	47
70	Familiality in brain tumors. Neurology, 2008, 71, 1015-1020.	1.5	46
71	Genome-wide association study for rotator cuffÂtears identifies two significant single-nucleotide polymorphisms. Journal of Shoulder and Elbow Surgery, 2016, 25, 174-179.	1.2	46
72	Associations of prostate cancer risk variants with disease aggressiveness: results of the NCI-SPORE Genetics Working Group analysis of 18,343 cases. Human Genetics, 2015, 134, 439-450.	1.8	45

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73	Relative risk for Alzheimer disease based on complete family history. Neurology, 2019, 92, e1745-e1753.	1.5	45
74	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	5.8	43
75	Pubertal development and prostate cancer risk: Mendelian randomization study in a population-based cohort. BMC Medicine, 2016, 14, 66.	2.3	42
76	Rarity of the Alzheimer Diseaseâ€“ProtectiveAPPA673T Variant in the United States. JAMA Neurology, 2015, 72, 209.	4.5	41
77	Population-based risks for cancer in patients with ALS. Neurology, 2016, 87, 289-294.	1.5	40
78	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. Nature Communications, 2021, 12, 1236.	5.8	40
79	Identification of excess clustering of coronary heart diseases among extended pedigrees in a genealogical population database. American Heart Journal, 2006, 152, 305-311.	1.2	38
80	A Genealogical Assessment of Heritable Predisposition to Asthma Mortality. American Journal of Respiratory and Critical Care Medicine, 2007, 176, 865-870.	2.5	38
81	Genetic Variants inXRCC2: New Insights Into Colorectal Cancer Tumorigenesis. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2476-2484.	1.1	38
82	Genome-wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients. Nature Communications, 2015, 6, 7539.	5.8	38
83	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	2.6	38
84	Characteristics of familial colon cancer in a large population data base. Cancer, 1989, 64, 1971-1975.	2.0	37
85	Identification of a genetic variant associated with rotator cuff repair healing. Journal of Shoulder and Elbow Surgery, 2016, 25, 865-872.	1.2	37
86	Genome-wide association of familial prostate cancer cases identifies evidence for a rare segregating haplotype at 8q24.21. Human Genetics, 2016, 135, 923-938.	1.8	37
87	Generation of an Integrated Transcription Map of theBRCA2Region on Chromosome 13q12â€“q13. Genomics, 1996, 36, 86-99.	1.3	36
88	Lobular breast cancer: Excess familiality observed in the Utah Population Database. International Journal of Cancer, 2005, 117, 655-661.	2.3	34
89	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
90	Familial clustering of ALS in a population-based resource. Neurology, 2014, 82, 17-22.	1.5	33

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91	Genetic predisposition to breast cancer. Cancer, 1992, 70, 1747-1754.	2.0	32
92	Report of a novel OCA2 gene mutation and an investigation of OCA2 variants on melanoma risk in a familial melanoma pedigree. Journal of Dermatological Science, 2013, 69, 30-37.	1.0	32
93	Cancer Risk in Families Fulfilling the Amsterdam Criteria for Lynch Syndrome. JAMA Oncology, 2017, 3, 1697.	3.4	32
94	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.	1.4	31
95	A genome wide linkage scan for dizygotic twinning in 525 families of mothers of dizygotic twins. Human Reproduction, 2010, 25, 1569-1580.	0.4	31
96	Consensus report of the 8 and 9th Weinman Symposia on Gene x Environment Interaction in carcinogenesis: novel opportunities for precision medicine. Cell Death and Differentiation, 2018, 25, 1885-1904.	5.0	31
97	Longitudinal Assessment of the Nevus Phenotype in a Melanoma Kindred. Journal of Investigative Dermatology, 2004, 123, 576-582.	0.3	30
98	Evidence of an Inherited Predisposition for Cervical Spondylotic Myelopathy. Spine, 2012, 37, 26-29.	1.0	30
99	Extracolonic Cancers Associated with Hereditary Nonpolyposis Colorectal Cancer in the Utah Population Database. American Journal of Gastroenterology, 2006, 101, 1591-1596.	0.2	29
100	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.	1.1	29
101	Joint effects of common genetic variants from multiple genes and pathways on the risk of premature coronary artery disease. American Heart Journal, 2010, 160, 250-256.e3.	1.2	29
102	Pancreatic cancer as a sentinel for hereditary cancer predisposition. BMC Cancer, 2018, 18, 697.	1.1	29
103	Microdissection, DOP-PCR, and comparative genomic hybridization of paraffin-embedded familial prostate cancers. Cancer Genetics and Cytogenetics, 2000, 122, 43-48.	1.0	28
104	Dissecting the genetic etiology of major depressive disorder using linkage analysis. Trends in Molecular Medicine, 2005, 11, 138-144.	3.5	28
105	Population-Based Assessment of Non-Melanoma Cancer Risk in Relatives of Cutaneous Melanoma Probands. Journal of Investigative Dermatology, 2007, 127, 183-188.	0.3	28
106	Alcohol consumption and prostate cancer incidence and progression: A Mendelian randomisation study. International Journal of Cancer, 2017, 140, 75-85.	2.3	28
107	A Breast Cancer Risk Haplotype in the Caspase-8 Gene. Cancer Research, 2009, 69, 2724-2728.	0.4	27
108	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	1.1	27

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109	Population-Based Relative Risks for Lung Cancer Based on Complete Family History of Lung Cancer. Journal of Thoracic Oncology, 2019, 14, 1184-1191.	0.5	27
110	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1731-1738.	1.1	27
111	Progress in prostate cancer. Nature Genetics, 1995, 9, 336-338.	9.4	26
112	A Role for XRCC4 in Age at Diagnosis and Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 1306-1310.	1.1	26
113	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.	0.4	26
114	Assessing the role of insulinâ€like growth factors and binding proteins in prostate cancer using Mendelian randomization: Genetic variants as instruments for circulating levels. International Journal of Cancer, 2016, 139, 1520-1533.	2.3	26
115	How well does family history predict who will get colorectal cancer? Implications for cancer screening and counseling. Genetics in Medicine, 2011, 13, 385-391.	1.1	25
116	A population-based survey of risk for cancer in individuals diagnosed with myotonic dystrophy. Muscle and Nerve, 2016, 54, 783-785.	1.0	25
117	A Robust Multipoint Linkage Statistic (tlod) for Mapping Complex Trait Loci. Genetic Epidemiology, 2001, 21, S492-7.	0.6	24
118	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.	1.8	24
119	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.	1.8	24
120	Evidence for pelvic organ prolapse predispositionÂgenesÂon chromosomes 10 and 17. American Journal of Obstetrics and Gynecology, 2015, 212, 771.e1-771.e7.	0.7	24
121	Familial Myeloma. New England Journal of Medicine, 2008, 359, 1734-1735.	13.9	23
122	Relative risks for comorbidities associated with myotonic dystrophy: A populationâ€based analysis. Muscle and Nerve, 2015, 52, 659-661.	1.0	23
123	Polyunsaturated fatty acids and prostate cancer risk: a Mendelian randomisation analysis from the PRACTICAL consortium. British Journal of Cancer, 2016, 115, 624-631.	2.9	23
124	A Nonsynonymous Variant in the GOLM1 Gene in Cutaneous Malignant Melanoma. Journal of the National Cancer Institute, 2018, 110, 1380-1385.	3.0	23
125	Germline Variant in HSD3B1 (1245 A > C) and Response to Abiraterone Acetate Plus Prednisone in Men With New-Onset Metastatic Castration-Resistant Prostate Cancer. Clinical Genitourinary Cancer, 2018, 16, 288-292.	0.9	23
126	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.	1.2	22

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127	Evidence for a heritable contribution to neuroendocrine tumors of the small intestine. Endocrine-Related Cancer, 2016, 23, 93-100.	1.6	22
128	Examination of ELN as a Candidate Gene in the Utah Intracranial Aneurysm Pedigrees. Stroke, 2005, 36, 1283-1284.	1.0	21
129	A heritable predisposition to pituitary tumors. Pituitary, 2010, 13, 130-137.	1.6	21
130	Fine-Mapping CASP8 Risk Variants in Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 176-181.	1.1	21
131	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.	1.8	21
132	The familiality of pelvic organ prolapse in the Utah Population Database. International Urogynecology Journal, 2013, 24, 413-418.	0.7	21
133	Evidence for a genetical contribution to non-smoking-related lung cancer. Thorax, 2015, 70, 1033-1039.	2.7	21
134	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 208-216.	1.1	21
135	Familial Associations between Cancer Sites. Journal of Biomedical Informatics, 1999, 32, 517-529.	0.7	20
136	Celiac Disease and Human Leukocyte Antigen Genotype: Accuracy of Diagnosis in Self-Diagnosed Individuals, Dosage Effect, and Sibling Risk. Journal of Pediatric Gastroenterology and Nutrition, 2000, 31, 22-27.	0.9	20
137	Genetic and Epidemiologic Evaluation of Dysplastic Nevi. Pigment Cell & Melanoma Research, 1988, 1, 144-151.	4.0	19
138	A Population-Based Description of Familial Clustering of Pancreatic Cancer. Clinical Gastroenterology and Hepatology, 2010, 8, 812-816.	2.4	19
139	Familiality analysis of provoked vestibulodynia treated by vestibulectomy supports genetic predisposition. American Journal of Obstetrics and Gynecology, 2016, 214, 609.e1-609.e7.	0.7	18
140	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.	1.1	18
141	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.3	18
142	Relative Risks for Lethal Prostate Cancer Based on Complete Family History of Prostate Cancer Death. Prostate, 2017, 77, 41-48.	1.2	18
143	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.	0.6	17
144	Identification of regions of positive selection using Shared Genomic Segment analysis. European Journal of Human Genetics, 2011, 19, 667-671.	1.4	17

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145	Gene and pathway level analyses of germline DNA-repair gene variants and prostate cancer susceptibility using the iCOGS-genotyping array. British Journal of Cancer, 2016, 114, 945-952.	2.9	17
146	Investigating the possible causal role of coffee consumption with prostate cancer risk and progression using Mendelian randomization analysis. International Journal of Cancer, 2017, 140, 322-328.	2.3	17
147	Use of a Genealogical Database Demonstrates Heritability of Pulmonary Fibrosis. Lung, 2013, 191, 475-481.	1.4	16
148	Familial clustering of endometrial cancer in a well-defined population. Gynecologic Oncology, 2011, 122, 75-78.	0.6	15
149	Lack of GNAQ and GNA11 Germ-Line Mutations in Familial Melanoma Pedigrees with Uveal Melanoma or Blue Nevi. Frontiers in Oncology, 2013, 3, 160.	1.3	15
150	A role for the MEGF6 gene in predisposition to osteoporosis. Annals of Human Genetics, 2021, 85, 58-72.	0.3	15
151	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.	1.2	14
152	Risk of Associated Conditions in Relatives of Subjects With Interstitial Cystitis. Female Pelvic Medicine and Reconstructive Surgery, 2015, 21, 93-98.	0.6	14
153	A novel ribosomal protein <scp>S20</scp> variant in a family with unexplained colorectal cancer and polyposis. Clinical Genetics, 2020, 97, 943-944.	1.0	14
154	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	1.4	14
155	Strong Evidence for a Genetic Contribution to Late-Onset Alzheimerâ€™s Disease Mortality: A Population-Based Study. PLoS ONE, 2013, 8, e77087.	1.1	14
156	Familial aggregation of Parkinson disease in Utah. Neurology: Genetics, 2016, 2, e65.	0.9	13
157	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members ofÂMelanoma Families. Journal of Investigative Dermatology, 2016, 136, 1066-1069.	0.3	13
158	Family history of cancer and the risk of childhood solid tumours: a Norwegian nationwide register-based cohort study. British Journal of Cancer, 2018, 118, 905-912.	2.9	13
159	Risk of pelvic organ prolapse treatment based onÂextended family history. American Journal of Obstetrics and Gynecology, 2020, 223, 105.e1-105.e8.	0.7	13
160	Associations of ATR and CHEK1 Single Nucleotide Polymorphisms with Breast Cancer. PLoS ONE, 2013, 8, e68578.	1.1	13
161	A New Nonparametric Linkage Statistic for Mapping Both Qualitative and Quantitative Trait Loci. Genetic Epidemiology, 2001, 21, S461-6.	0.6	12
162	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.	0.3	12

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163	A Population-Based Assessment of the Familial Component of Chronic Kidney Disease Mortality. American Journal of Nephrology, 2006, 26, 142-148.	1.4	12
164	High quality and quantity Genome-wide germline genotypes from FFPE normal tissue. BMC Research Notes, 2011, 4, 159.	0.6	12
165	Co-prevalence of other tumors in patients harboring pituitary tumors. Journal of Neurosurgery, 2014, 121, 1474-1477.	0.9	12
166	Inherited Variants in SULT1E1 and Response to Abiraterone Acetate by Men with Metastatic Castration Refractory Prostate Cancer. Journal of Urology, 2016, 196, 1112-1116.	0.2	12
167	Evidence for an Environmental and Inherited Predisposition Contributing to the Risk for Global Tendinopathies or Compression Neuropathies in Patients With Rotator Cuff Tears. Orthopaedic Journal of Sports Medicine, 2016, 4, 232596711664217.	0.8	12
168	Family history of cancer and risk of paediatric and young adultâ€™s testicular cancer: A Norwegian cohort study. British Journal of Cancer, 2019, 120, 1007-1014.	2.9	12
169	Failure to Detect Differences in Proliferation Status of Nevi from CDKN2A Mutation Carriers and Non-Carriers. Journal of Investigative Dermatology, 2002, 118, 386-387.	0.3	11
170	Statistical recombinant mapping in extended highâ€risk Utah pedigrees narrows the 8q24 prostate cancer locus to 2.0 Mb. Prostate, 2007, 67, 1456-1464.	1.2	11
171	Creation of a national resource with linked genealogy and phenotypic data: the Veterans Genealogy Project. Genetics in Medicine, 2013, 15, 541-547.	1.1	11
172	Identification of specific Y chromosomes associated with increased prostate cancer risk. Prostate, 2014, 74, 991-998.	1.2	11
173	SNP interaction pattern identifier (SIPI): an intensive search for SNPâ€“SNP interaction patterns. Bioinformatics, 2017, 33, 822-833.	1.8	11
174	Genetic Contribution to Nonsquamous, Nonâ€“Small Cell Lung Cancer in Nonsmokers. Journal of Thoracic Oncology, 2018, 13, 938-945.	0.5	11
175	Similar survival of patients with multiple versus single primary melanomas basedÂon Utah Surveillance, Epidemiology, and End Results data (1973-2011). Journal of the American Academy of Dermatology, 2018, 79, 238-244.	0.6	11
176	A Familial Component to Human Rectal Cancer, Independent of Colon Cancer Risk. Clinical Gastroenterology and Hepatology, 2007, 5, 1080-1084.	2.4	10
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