Shannon K Mcdonnell

List of Publications by Year
in descending order

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114	13,522	31902 53	22764 112
papers	citations	h-index	g-index

119	119	119	16954
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	Efficacy of Bilateral Prophylactic Mastectomy in Women with a Family History of Breast Cancer. New England Journal of Medicine, 1999, 340, 77-84.	13.9	1,343
3	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
4	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	9.4	492
5	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
6	Anxiety disorders and depressive disorders preceding Parkinson's disease: A case-control study. Movement Disorders, 2000, 15, 669-677.	2.2	407
7	Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. Nature Genetics, 2009, 41, 1116-1121.	9.4	389
8	Incidence of progressive supranuclear palsy and multiple system atrophy in Olmsted County, Minnesota, 1976 to 1990. Neurology, 1997, 49, 1284-1288.	1.5	361
9	Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. Nature Genetics, 2008, 40, 281-283.	9.4	357
10	Risk tables for parkinsonism and Parkinson's disease. Journal of Clinical Epidemiology, 2002, 55, 25-31.	2.4	304
11	The Frequency of Hereditary Defective Mismatch Repair in a Prospective Series of Unselected Colorectal Carcinomas. American Journal of Human Genetics, 2001, 69, 780-790.	2.6	303
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	Mutations in CHEK2 Associated with Prostate Cancer Risk. American Journal of Human Genetics, 2003, 72, 270-280.	2.6	264
14	Risk SNP-Mediated Promoter-Enhancer Switching Drives Prostate Cancer through lncRNA PCAT19. Cell, 2018, 174, 564-575.e18.	13.5	264
15	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
16	Efficacy of Contralateral Prophylactic Mastectomy in Women With a Personal and Family History of Breast Cancer. Journal of Clinical Oncology, 2001, 19, 3938-3943.	0.8	257
17	Evidence for a Prostate Cancerâ€“Susceptibility Locus on Chromosome 20. American Journal of Human Genetics, 2000, 67, 82-91.	2.6	213
18	A Germline DNA Polymorphism Enhances Alternative Splicing of the KLF6 Tumor Suppressor Gene and Is Associated with Increased Prostate Cancer Risk. Cancer Research, 2005, 65, 1213-1222.	0.4	202

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19	Evidence for Autosomal Dominant Inheritance of Prostate Cancer. American Journal of Human Genetics, 1998, 62, 1425-1438.	2.6	198
20	Hysterectomy, menopause, and estrogen use preceding Parkinson's disease: An exploratory case-control study. Movement Disorders, 2001, 16, 830-837.	2.2	194
21	Survival Study of Parkinson Disease in Olmsted County, Minnesota. Archives of Neurology, 2003, 60, 91.	4.9	178
22	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
23	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
24	Multiple Novel Prostate Cancer Predisposition Loci Confirmed by an International Study: The PRACTICAL Consortium. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2052-2061.	1.1	148
25	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
26	Comparison of Microsatellites Versus Single-Nucleotide Polymorphisms in a Genome Linkage Screen for Prostate Cancerâ€“Susceptibility Loci. American Journal of Human Genetics, 2004, 75, 948-965.	2.6	129
27	Genetic heterogeneity in Peutz-Jeghers syndrome. Human Mutation, 2000, 16, 23-30.	1.1	125
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	Nonparametric Tests of Association of Multiple Genes with Human Disease. American Journal of Human Genetics, 2005, 76, 780-793.	2.6	117
30	Influence of strict, intermediate, and broad diagnostic criteria on the age- and sex-specific incidence of Parkinson's disease. Movement Disorders, 2000, 15, 819-825.	2.2	112
31	A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. Cancer Discovery, 2015, 5, 878-891.	7.7	111
32	Analysis of the RNASEL Gene in Familial and Sporadic Prostate Cancer. American Journal of Human Genetics, 2002, 71, 116-123.	2.6	105
33	Evaluation of Genetic Variations in the Androgen and Estrogen Metabolic Pathways as Risk Factors for Sporadic and Familial Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 969-978.	1.1	101
34	Two Common Chromosome 8q24 Variants Are Associated with Increased Risk for Prostate Cancer. Cancer Research, 2007, 67, 2944-2950.	0.4	100
35	Nonfatal Cancer Preceding Parkinsonâ€™s Disease: A Case-Control Study. Epidemiology, 2002, 13, 157-164.	1.2	96
36	Familial aggregation of Parkinson's disease: The Mayo Clinic family study. Annals of Neurology, 2004, 56, 495-502.	2.8	96

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37	Linkage Analyses at the Chromosome 1 Loci 1q24-25 (HPC1), 1q42.2-43 (PCAP), and 1p36 (CAPB) in Families with Hereditary Prostate Cancer. American Journal of Human Genetics, 2000, 66, 539-546.	2.6	91
38	Genome-wide analyses as part of the international FTLD-TDP whole-genome sequencing consortium reveals novel disease risk factors and increases support for immune dysfunction in FTLD. Acta Neuropathologica, 2019, 137, 879-899.	3.9	90
39	Caution on Pedigree Haplotype Inference with Software That Assumes Linkage Equilibrium. American Journal of Human Genetics, 2002, 71, 992-995.	2.6	88
40	Confirmation of a Positive Association between Prostate Cancer Risk and a Locus at Chromosome 8q24. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 809-814.	1.1	88
41	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
42	Pathologic characteristics of breast parenchyma in patients with hereditary breast carcinoma, including BRCA1 and BRCA2 mutation carriers. Cancer, 2003, 97, 1-11.	2.0	87
43	Multiple Genetic Variant Association Testing by Collapsing and Kernel Methods With Pedigree or Population Structured Data. Genetic Epidemiology, 2013, 37, 409-418.	0.6	87
44	Validation of a Telephone Questionnaire for Parkinsonâ€™s Disease. Journal of Clinical Epidemiology, 1998, 51, 517-523.	2.4	83
45	Increased risk of essential tremor in first-degree relatives of patients with Parkinson's disease. Movement Disorders, 2007, 22, 1607-1614.	2.2	81
46	Common variation at 6p21.31 (BAK1) influences the risk of chronic lymphocytic leukemia. Blood, 2012, 120, 843-846.	0.6	76
47	Microsatellite instability and hMLH1/hMSH2 expression in young endometrial carcinoma patients: Associations with family history and histopathology. , 2000, 86, 60-66.		73
48	Prospective Validation of HLA-DRB1*07:01 Allele Carriage As a Predictive Risk Factor for Lapatinib-Induced Liver Injury. Journal of Clinical Oncology, 2014, 32, 2296-2303.	0.8	69
49	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
50	Genome-Wide Transcriptional Profiling Reveals MicroRNA-Correlated Genes and Biological Processes in Human Lymphoblastoid Cell Lines. PLoS ONE, 2009, 4, e5878.	1.1	64
51	No association of germline alteration of MSR1 with prostate cancer risk. Nature Genetics, 2003, 35, 128-129.	9.4	60
52	Risk of cancer after the diagnosis of Parkinson's disease: A historical cohort study. Movement Disorders, 2005, 20, 719-725.	2.2	57
53	Pooled genome linkage scan of aggressive prostate cancer: results from the International Consortium for Prostate Cancer Genetics. Human Genetics, 2006, 120, 471-485.	1.8	57
54	Case-control study of the extended tau gene haplotype in Parkinson's disease. Annals of Neurology, 2001, 50, 658-661.	2.8	54

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55	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	1.2	54
56	Analysis of the Prostate Cancerâ€“Susceptibility Locus HPC20 in 172 Families Affected by Prostate Cancer. American Journal of Human Genetics, 2001, 68, 795-801.	2.6	51
57	Incorporating Functional Annotations for Fine-Mapping Causal Variants in a Bayesian Framework Using Summary Statistics. Genetics, 2016, 204, 933-958.	1.2	51
58	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
59	Role of the Nijmegen Breakage Syndrome 1 Gene in Familial and Sporadic Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 935-938.	1.1	49
60	Genome linkage screen for prostate cancer susceptibility loci: Results from the Mayo Clinic familial prostate cancer study. Prostate, 2003, 57, 335-346.	1.2	48
61	Polymorphisms in Mitochondrial Genes and Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 3558-3566.	1.1	48
62	Risk of Cognitive Impairment or Dementia in Relatives of Patients With Parkinson Disease. Archives of Neurology, 2007, 64, 1458.	4.9	47
63	Prostate cancer and genetic susceptibility: A genome scan incorporating disease aggressiveness. Prostate, 2006, 66, 317-325.	1.2	45
64	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
65	Case-control study of debrisoquine 4-hydroxylase, n-acetyltransferase 2, and apolipoprotein e gene polymorphisms in Parkinson's disease. Movement Disorders, 2000, 15, 714-719.	2.2	44
66	Mapping Complex Traits in a Diversity Outbred F1 Mouse Population Identifies Germline Modifiers of Metastasis in Human Prostate Cancer. Cell Systems, 2017, 4, 31-45.e6.	2.9	44
67	Genome-wide linkage scan for prostate cancer aggressiveness loci using families from the University of Michigan Prostate Cancer Genetics Project. Prostate, 2006, 66, 173-179.	1.2	42
68	Complex segregation analysis of Parkinson's disease: The Mayo Clinic Family Study. Annals of Neurology, 2006, 59, 788-795.	2.8	41
69	Association of Peutz-Jeghers-like Mucocutaneous Pigmentation with Breast and Gynecologic Carcinomas in Women. Medicine (United States), 2000, 79, 293-298.	0.4	38
70	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	2.6	38
71	Identification of Novel Variants in Colorectal Cancer Families by High-Throughput Exome Sequencing. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1239-1251.	1.1	37
72	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

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73	Using the gene ontology to scan multilevel gene sets for associations in genome wide association studies. Genetic Epidemiology, 2012, 36, 3-16.	0.6	32
74	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
75	FIRE: functional inference of genetic variants that regulate gene expression. Bioinformatics, 2017, 33, 3895-3901.	1.8	30
76	Two-stage Study of Familial Prostate Cancer by Whole-exome Sequencing and Custom Capture Identifies 10 Novel Genes Associated with the Risk of Prostate Cancer. European Urology, 2021, 79, 353-361.	0.9	28
77	Regression Models for Linkage Heterogeneity Applied to Familial Prostate Cancer. American Journal of Human Genetics, 2001, 68, 1189-1196.	2.6	27
78	The Mayo Clinic Family Study of Parkinsonâ€™s Disease: Study Design, Instruments, and Sample Characteristics. Neuroepidemiology, 2005, 24, 151-167.	1.1	27
79	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	1.1	27
80	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
81	Dense genome-wide SNP linkage scan in 301 hereditary prostate cancer families identifies multiple regions with suggestive evidence for linkage. Human Molecular Genetics, 2009, 18, 1839-1848.	1.4	25
82	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
83	Genome-wide linkage scan of prostate cancer Gleason score and confirmation of chromosome 19q. Human Genetics, 2007, 121, 729-735.	1.8	23
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.	1.2	22
85	Incidence of Medically Recognized Migraine: A 1989-1990 Study in Olmsted County, Minnesota. Headache, 2000, 40, 216-223.	1.8	21
86	Family-based association analysis of 42 hereditary prostate cancer families identifies the Apolipoprotein L3 region on chromosome 22q12 as a risk locus. Human Molecular Genetics, 2010, 19, 3852-3862.	1.4	21
87	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
88	Gluthatione-S-transferase P1 polymorphism I105V in familial and sporadic prostate cancer. Cancer Genetics and Cytogenetics, 2004, 155, 82-86.	1.0	20
89	Luteinizing hormone ? polymorphism and risk of familial and sporadic prostate cancer. Prostate, 2003, 56, 30-36.	1.2	19
90	Case-control study of estrogen receptor gene polymorphisms in Parkinson's disease. Movement Disorders, 2002, 17, 509-512.	2.2	16

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91	Mutational landscape of candidate genes in familial prostate cancer. Prostate, 2014, 74, 1371-1378.	1.2	16
92	Detection of Preclinical Parkinson Disease in At-Risk Family Members With Use of [123I]Î²-CIT and SPECT: An Exploratory Study. Mayo Clinic Proceedings, 1999, 74, 681-685.	1.4	14
93	Frequency of Defective DNA Mismatch Repair in Colorectal Cancer among the Alaska Native People. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 2344-2350.	1.1	14
94	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
95	Detecting genomic clustering of risk variants from sequence data: cases versus controls. Human Genetics, 2013, 132, 1301-1309.	1.8	14
96	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	1.4	14
97	Estimation of genotype relative risks from pedigree data by retrospective likelihoods. Genetic Epidemiology, 2010, 34, 287-298.	0.6	13
98	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.	1.2	13
99	Whole exome sequencing in 75 high-risk families with validation and replication in independent case-control studies identifies TANGO2, OR5H14, and CHAD as new prostate cancer susceptibility genes. Oncotarget, 2017, 8, 1495-1507.	0.8	11
100	Identification of missing variants by combining multiple analytic pipelines. BMC Bioinformatics, 2018, 19, 139.	1.2	10
101	Polygenic risk for prostate cancer: Decreasing relative risk with age but little impact on absolute risk. American Journal of Human Genetics, 2022, 109, 900-908.	2.6	10
102	Truncating Variants in p53AIP1 Disrupting DNA Damageâ€“Induced Apoptosis Are Associated with Prostate Cancer Risk. Cancer Research, 2006, 66, 10302-10307.	0.4	9
103	Fine mapping of familial prostate cancer families narrows the interval for a susceptibility locus on chromosome 22q12.3 to 1.36ÂMb. Human Genetics, 2008, 123, 65-75.	1.8	9
104	How well do whole exome sequencing results correlate with medical findings? A study of 89 Mayo Clinic Biobank samples. Frontiers in Genetics, 2015, 6, 244.	1.1	9
105	Genome-wide linkage analyses of hereditary prostate cancer families with colon cancer provide further evidence for a susceptibility locus on 15q11â€“q14. European Journal of Human Genetics, 2010, 18, 1141-1147.	1.4	7
106	Germline miRNA DNA variants and the risk of colorectal cancer by subtype. Genes Chromosomes and Cancer, 2017, 56, 177-184.	1.5	7
107	Analysis of Xq27-28 linkage in the international consortium for prostate cancer genetics (ICPCG) families. BMC Medical Genetics, 2012, 13, 46.	2.1	5
108	An expanded variant list and assembly annotation identifies multiple novel coding and noncoding genes for prostate cancer risk using a normal prostate tissue eQTL data set. PLoS ONE, 2019, 14, e0214588.	1.1	5

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109	Affected relative pairs and simultaneous search for two-locus linkage in the presence of epistasis. Genetic Epidemiology, 2007, 31, 431-449.	0.6	3
110	A microRNA Transcriptome-wide Association Study of Prostate Cancer Risk. Frontiers in Genetics, 2022, 13, 836841.	1.1	3
111	Network-directed cis-mediator analysis of normal prostate tissue expression profiles reveals downstream regulatory associations of prostate cancer susceptibility loci. Oncotarget, 2017, 8, 85896-85908.	0.8	2
112	Lack of Referral Bias in Genetic Studies of Prostate Cancer. Epidemiology, 2002, 13, 612-613.	1.2	1
113	Searching for epistasis and linkage heterogeneity by correlations of pedigreeâ€specific linkage scores. Genetic Epidemiology, 2008, 32, 464-475.	0.6	0
114	Familial recurrence risk with varying amount of family history. Genetic Epidemiology, 2019, 43, 440-448.	0.6	0