Amanda E Toland

List of Publications by Year
in descending order

183 papers	14,341 citations	26567 56 h-index	23472 111 g-index
192 all docs	192 docs citations	192 times ranked	18953 citing authors

#	Article	IF	Citations
1	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	3.0	19
2	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in BRCA1 and BRCA2 compared with those harboring protein truncating variants. Genetics in Medicine, 2022, 24, 119-129.	1.1	10
3	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	0.8	90
4	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
5	Genetic analysis of a malignant meningioma and associated metastases. Acta Neurochirurgica, 2022, 164, 1401-1405.	0.9	4
6	Differences in somatic TP53 mutation type in breast tumors by race and receptor status. Breast Cancer Research and Treatment, 2022, 192, 639-648.	1.1	7
7	Diabetes mellitus in relation to colorectal tumor molecular subtypes â€•a pooled analysis of more than 9,000 cases. International Journal of Cancer, 2022, , .	2.3	2
8	loss drives aggressive tumor phenotypes in cutaneous squamous cell carcinoma.. American Journal of Cancer Research, 2022, 12, 1309-1322.	1.4	0
9	Association between germline variants and somatic mutations in colorectal cancer. Scientific Reports, 2022, 12, .	1.6	1
10	Identifying colorectal cancer caused by biallelic MUTYH pathogenic variants using tumor mutational signatures. Nature Communications, 2022, 13, .	5.8	15
11	The p.Ser64Leu and p.Pro104Leu missense variants of PALB2 identified in familial pancreatic cancer patients compromise the DNA damage response. Human Mutation, 2021, 42, 150-163.	1.1	0
12	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
13	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44
14	Albert de la Chapelle (1933â€“2020). American Journal of Human Genetics, 2021, 108, 214-216.	2.6	0
15	Machine learning approaches reveal subtle differences in breathing and sleep fragmentation inPhox2b-derived astrocytes ablated mice. Journal of Neurophysiology, 2021, 125, 1164-1179.	0.9	3
16	Oncogenetic network estimation with disjunctive Bayesian networks. Computational and Systems Oncology, 2021, 1, e1027.	1.1	5
17	Association between Smoking and Molecular Subtypes of Colorectal Cancer. JNCI Cancer Spectrum, 2021, 5, pkab056.	1.4	8
18	The predictive ability of the 313 variantâ€“based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	1.1	16

#	Article	IF	Citations
19	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	2.6	6
20	Polygenic Risk Scores in Prostate Cancer Risk Assessment and Screening. Urologic Clinics of North America, 2021, 48, 387-399.	0.8	7
21	Impact of Previous Genetic Counseling and Objective Numeracy on Accurate Interpretation of a Pharmacogenetics Test Report. Public Health Genomics, 2021, 24, 26-32.	0.6	11
22	The influence of sex, age and sunlight exposure on mutational processes in melanoma. British Journal of Dermatology, 2021, 184, 197-198.	1.4	0
23	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
24	Developing risk prediction models for melanoma: balancing better predictive value with ease of clinical implementation. British Journal of Dermatology, 2020, 182, 1089-1090.	1.4	0
25	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
26	Cumulative Burden of Colorectal Cancerâ€"Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	0.6	110
27	Sequencing technology status of BRCA1/2 testing in Latin American Countries. Npj Genomic Medicine, 2020, 5, 22.	1.7	1
28	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	1.1	82
29	Intake of Dietary Fruit, Vegetables, and Fiber and Risk of Colorectal Cancer According to Molecular Subtypes: A Pooled Analysis of 9 Studies. Cancer Research, 2020, 80, 4578-4590.	0.4	26
30	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
31	MicroRNA Expression Profiling of Cutaneous Squamous Cell Carcinomas Arising in Different Sites. Otolaryngology - Head and Neck Surgery, 2020, 163, 538-545.	1.1	3
32	Metastatic breast cancer patient perceptions of somatic tumor genomic testing. BMC Cancer, 2020, 20, 389.	1.1	8
33	Implementation of Germline Testing for Prostate Cancer: Philadelphia Prostate Cancer Consensus Conference 2019. Journal of Clinical Oncology, 2020, 38, 2798-2811.	0.8	170
34	Maternal age at delivery and fertility of the next generation. Paediatric and Perinatal Epidemiology, 2020, 34, 629-636.	0.8	4
35	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
36	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32

#	Article	IF	Citations
37	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2020, 11, 820.	5.8	30
38	POT 1 pathogenic variants: not all telomere pathway genes are equal in risk of hereditary cutaneous melanoma. British Journal of Dermatology, 2019, 181, 14-15.	1.4	1
39	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
40	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
41	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
42	F-Box Protein-Mediated Resistance to PARP Inhibitor Therapy. Molecular Cell, 2019, 73, 195-196.	4.5	4
43	Large scale multifactorial likelihood quantitative analysis of BRCA1 and BRCA2 variants: An ENIGMA resource to support clinical variant classification. Human Mutation, 2019, 40, 1557-1578.	1.1	102
44	BRCA1/2 Functional Loss Defines a Targetable Subset in Leiomyosarcoma. Oncologist, 2019, 24, 973-979.	1.9	49
45	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. British Journal of Cancer, 2019, 121, 180-192.	2.9	19
46	BRCA1andBRCA2pathogenic sequence variants in women of African origin or ancestry. Human Mutation, 2019, 40, 1781-1796.	1.1	26
47	Germline Variants Impact Somatic Events during Tumorigenesis. Trends in Genetics, 2019, 35, 515-526.	2.9	39
48	Understanding BRCA Mutation Carriersâ€™ Preferences for Communication of Genetic Modifiers of Breast Cancer Risk. Journal of Health Communication, 2019, 24, 377-384.	1.2	7
49	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
50	Genetic Testing to Guide Risk-Stratified Screens for Breast Cancer. Journal of Personalized Medicine, 2019, 9, 15.	1.1	21
51	Genomeâ€wide association studies and polygenic risk scores for skin cancer: clinically useful yet?. British Journal of Dermatology, 2019, 181, 1146-1155.	1.4	49
52	Exploring genetic counselorsâ€™ perceptions of usefulness and intentions to use refined risk models in clinical care based on the Technology Acceptance Model (TAM). Journal of Genetic Counseling, 2019, 28, 664-672.	0.9	4
53	Single Nucleotide Polymorphisms in Î²-Carotene Oxygenase 1 are Associated with Plasma Lycopene Responses to a Tomato-Soy Juice Intervention in Men with Prostate Cancer. Journal of Nutrition, 2019, 149, 381-397.	1.3	35
54	Keratinocyte Carcinomas: Current Concepts and Future Research Priorities. Clinical Cancer Research, 2019, 25, 2379-2391.	3.2	91

#	Article	IF	Citations
55	Lessons learned from two decades of BRCA1 and BRCA2 genetic testing: the evolution of data sharing and variant classification. Genetics in Medicine, 2019, 21, 1476-1480.	1.1	2
56	Height and Body Mass Index as Modifiers of Breast Cancer Risk in BRCA1/2 Mutation Carriers: A Mendelian Randomization Study. Journal of the National Cancer Institute, 2019, 111, 350-364.	3.0	30
57	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
58	Polygenic risk scores for prostate cancer: testing considerations. Canadian Journal of Urology, 2019, 26, 17-18.	0.0	4
59	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	1.1	19
60	Operationalizing the Reciprocal Engagement Model of Genetic Counseling Practice: a Framework for the Scalable Delivery of Genomic Counseling and Testing. Journal of Genetic Counseling, 2018, 27, 1111-1129.	0.9	25
61	Clinical testing of BRCA1 and BRCA2: a worldwide snapshot of technological practices. Npj Genomic Medicine, 2018, 3, 7.	1.7	44
62	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	1.1	224
63	Involvement and Influence of Healthcare Providers, Family Members, and Other Mutation Carriers in the Cancer Risk Management Decisionâ€Making Process of BRCA1 and BRCA2 Mutation Carriers. Journal of Genetic Counseling, 2018, 27, 1291-1301.	0.9	6
64	The BRCA1 c. 5096G>A p.Arg1699Gln (R1699Q) intermediate risk variant: breast and ovarian cancer risk estimation and recommendations for clinical management from the ENIGMA consortium. Journal of Medical Genetics, 2018, 55, 15-20.	1.5	50
65	Association of BRCA2 K3326* With Small Cell Lung Cancer and Squamous Cell Cancer of the Skin. Journal of the National Cancer Institute, 2018, 110, 967-974.	3.0	29
66	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.4	54
67	Early Outcome Data Assessing Utility of a Post-Test Genomic Counseling Framework for the Scalable Delivery of Precision Health. Journal of Personalized Medicine, 2018, 8, 25.	1.1	7
68	<scp>EMR</scp> documentation of physicianâ€“patient communication following genomic counseling for actionable complex disease and pharmacogenomic results. Clinical Genetics, 2017, 91, 545-556.	1.0	9
69	Variants at theOCA2/HERC2locus affect time to first cutaneous squamous cell carcinoma in solid organ transplant recipients collected using two different study designs. British Journal of Dermatology, 2017, 177, 1066-1073.	1.4	9
70	Differential mutation frequencies in metastatic cutaneous squamous cell carcinomas versus primary tumors. Cancer, 2017, 123, 1184-1193.	2.0	64
71	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
72	Outcomes of a Randomized Controlled Trial of Genomic Counseling for Patients Receiving Personalized and Actionable Complex Disease Reports. Journal of Genetic Counseling, 2017, 26, 980-998.	0.9	15

#	Article	IF	Citations
73	Counseleesâ€™ Perspectives of Genomic Counseling Following Online Receipt of Multiple Actionable Complex Disease and Pharmacogenomic Results: a Qualitative Research Study. Journal of Genetic Counseling, 2017, 26, 738-751.	0.9	16
74	Epidemiology of keratinocyte carcinomas after organ transplantation. British Journal of Dermatology, 2017, 177, 1208-1216.	1.4	67
75	Risk prediction tools for keratinocyte carcinoma after solid organ transplantation: a review of the literature. British Journal of Dermatology, 2017, 177, 1202-1207.	1.4	23
76	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
77	DNA repair-related functional assays for the classification of BRCA1 and BRCA2 variants: a critical review and needs assessment. Journal of Medical Genetics, 2017, 54, 721-731.	1.5	33
78	The pathogenesis of cutaneous squamous cell carcinoma in organ transplant recipients. British Journal of Dermatology, 2017, 177, 1217-1224.	1.4	58
79	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. Breast Cancer Research and Treatment, 2017, 161, 117-134.	1.1	18
80	IRF4 Polymorphism Is Associated with Cutaneous Squamous Cell Carcinoma inÂOrgan Transplant Recipients: A Pigment-Independent Phenomenon. Journal of Investigative Dermatology, 2017, 137, 251-253.	0.3	13
81	Organ transplantation and cutaneous squamous cell carcinoma: progress, pitfalls and priorities in immunosuppressionâ€associated keratinocyte carcinoma. British Journal of Dermatology, 2017, 177, 1150-1151.	1.4	9
82	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
83	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	3.9	118
84	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	1.1	10
85	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
86	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
87	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	2.2	31
88	Variants in an Hdac9 intronic enhancer plasmid impact Twist1 expression in vitro. Mammalian Genome, 2016, 27, 99-110.	1.0	5
89	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	0.8	21
90	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	2.2	88

#	Article	IF	Citations
91	High risk cutaneous squamous cell carcinoma of the head and neck. World Journal of Otorhinolaryngology - Head and Neck Surgery, 2016, 2, 136-140.	0.7	16
92	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	1.4	33
93	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	2.2	42
94	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
95	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
96	Micro<scp>RNA</scp> expression profiling in metastatic cutaneous squamous cell carcinoma. Journal of the European Academy of Dermatology and Venereology, 2016, 30, 1043-1045.	1.3	18
97	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
98	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	2.2	26
99	Functional Analysis of BARD1 Missense Variants in Homology-Directed Repair of DNA Double Strand Breaks. Human Mutation, 2015, 36, 1205-1214.	1.1	27
100	Alleleâ€specific imbalance mapping at human orthologs of mouse susceptibility to colon cancer (Scc) loci. International Journal of Cancer, 2015, 137, 2323-2331.	2.3	5
101	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34
102	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
103	Use of Whole Genome Sequencing for Diagnosis and Discovery in the Cancer Genetics Clinic. EBioMedicine, 2015, 2, 74-81.	2.7	50
104	Germline Mutation in BRCA1 or BRCA2 and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. Clinical Cancer Research, 2015, 21, 652-657.	3.2	138
105	Inherited Mutations in 17 Breast Cancer Susceptibility Genes Among a Large Triple-Negative Breast Cancer Cohort Unselected for Family History of Breast Cancer. Journal of Clinical Oncology, 2015, 33, 304-311.	0.8	521
106	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
107	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	2.6	76
108	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	1.3	14

#	Article	IF	Citations
109	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
110	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
111	Haploinsufficiency for BRCA1 leads to cell-type-specific genomic instability and premature senescence. Nature Communications, 2015, 6, 7505.	5.8	101
112	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	2.6	37
113	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
114	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
115	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
116	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	1.1	24
117	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.	1.4	38
118	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	1.1	22
119	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
120	Design and Implementation of a Randomized Controlled Trial of Genomic Counseling for Patients with Chronic Disease. Journal of Personalized Medicine, 2014, 4, 1-19.	1.1	20
121	Melanoma Incidence Rates in Active Duty Military Personnel Compared With a Population-Based Registry in the United States, 2000â€“2007. Military Medicine, 2014, 179, 247-253.	0.4	22
122	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	1.5	47
123	Expression of cancer-testis antigens MAGEA1, MAGEA3, ACRBP, PRAME, SSX2, and CTAG2 in myxoid and round cell liposarcoma. Modern Pathology, 2014, 27, 1238-1245.	2.9	55
124	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
125	mrSNP: Software to detect SNP effects on microRNA binding. BMC Bioinformatics, 2014, 15, 73.	1.2	46
126	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	2.2	97

#	Article	IF	Citations
127	Breast-Cancer Risk in Families With Mutations in PALB2. Obstetrical and Gynecological Survey, 2014, 69, 659-660.	0.2	1
128	Salivary Gland Cancer inBRCA-Positive Families. JAMA Otolaryngology - Head and Neck Surgery, 2014, 140, 1213.	1.2	21
129	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	2.2	57
130	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	1.4	32
131	Linking distant relatives with <scp>BRCA</scp> gene mutations: potential for cost savings. Clinical Genetics, 2014, 85, 54-58.	1.0	4
132	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. Carcinogenesis, 2014, 35, 1012-1019.	1.3	145
133	Alleleâ€specific imbalance mapping identifies HDAC9 as a candidate gene for cutaneous squamous cell carcinoma. International Journal of Cancer, 2014, 134, 244-248.	2.3	14
134	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. British Journal of Cancer, 2014, 110, 1088-1100.	2.9	21
135	Breast-Cancer Risk in Families with Mutations in PALB2. New England Journal of Medicine, 2014, 371, 497-506.	13.9	745
136	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
137	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	1.4	12
138	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	2.2	14
139	Benchmarking short sequence mapping tools. BMC Bioinformatics, 2013, 14, 184.	1.2	170
140	Analysis of BRCA1 Variants in Double-Strand Break Repair by Homologous Recombination and Single-Strand Annealing. Human Mutation, 2013, 34, 439-445.	1.1	52
141	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	2.6	201
142	The cancer-testis antigen NY-ESO-1 is highly expressed in myxoid and round cell subset of liposarcomas. Modern Pathology, 2013, 26, 282-288.	2.9	44
143	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
144	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	1.5	244

#	Article	IF	Citations
145	The Impact of 3â€²UTR Variants on Differential Expression of Candidate Cancer Susceptibility Genes. PLoS ONE, 2013, 8, e58609.	1.1	44
146	Differential expression ofmiR-1, a putative tumor suppressing microRNA, in cancer resistant and cancer susceptible mice. PeerJ, 2013, 1, e68.	0.9	20
147	Interaction Between Genetics and Epigenetics in Cancer. , 2013, , 209-229.		0
148	Abstract 2998: Identification of AURKA- and PTPRJ-interacting human colorectal cancer susceptibility alleles.. , 2013, , .		0
149	A Nonsynonymous Polymorphism in IRS1 Modifies Risk of Developing Breast and Ovarian Cancers in BRCA1 and Ovarian Cancer in BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1362-1370.	1.1	23
150	BRCA1 R1699Q variant displaying ambiguous functional abrogation confers intermediate breast and ovarian cancer risk. Journal of Medical Genetics, 2012, 49, 525-532.	1.5	97
151	The Role for Oxidative Stress in Aberrant DNA Methylation in Alzheimerâ€™s Disease. Current Alzheimer Research, 2012, 9, 1077-1096.	0.7	27
152	Pathology of Breast and Ovarian Cancers among BRCA1 and BRCA2 Mutation Carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 134-147.	1.1	513
153	Association Between <emph type="ital">BRCA1</emph> and <emph type="ital">BRCA2</emph> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. JAMA - Journal of the American Medical Association, 2012, 307, 382.	3.8	546
154	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. Breast Cancer Research, 2012, 14, R33.	2.2	78
155	Ovarian cancer susceptibility alleles and risk of ovarian cancer inBRCA1andBRCA2mutation carriers. Human Mutation, 2012, 33, 690-702.	1.1	34
156	Aberrant Epigenetic Regulation in Breast Cancer. , 2012, , 91-122.		2
157	Abstract 103: DCPS as a cutaneous squamous cell carcinoma susceptibility gene. , 2012, , .		1
158	Evaluation of Allele-Specific Somatic Changes of Genome-Wide Association Study Susceptibility Alleles in Human Colorectal Cancers. PLoS ONE, 2012, 7, e37672.	1.1	8
159	Common breast cancer susceptibility alleles are associated with tumour subtypes in BRCA1 and BRCA2 mutation carriers: results from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2011, 13, R110.	2.2	71
160	Haplotype structure in Ashkenazi Jewish BRCA1 and BRCA2 mutation carriers. Human Genetics, 2011, 130, 685-699.	1.8	18
161	Common alleles at 6q25.1 and 1p11.2 are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2011, 20, 3304-3321.	1.4	68
162	The Combined Influence of Oral Contraceptives and Human Papillomavirus Virus on Cutaneous Squamous Cell Carcinoma. Clinical Medicine Insights: Oncology, 2011, 5, CMO.S6905.	0.6	4

#	Article	IF	Citations
163	Common variants of the BRCA1 wild-type allele modify the risk of breast cancer in BRCA1 mutation carriers. Human Molecular Genetics, 2011, 20, 4732-4747.	1.4	32
164	Characterization of BRCA1 ring finger variants of uncertain significance. Breast Cancer Research and Treatment, 2010, 119, 737-743.	1.1	25
165	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptorâ€“negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	9.4	309
166	Germline Variation Controls the Architecture of Somatic Alterations in Tumors. PLoS Genetics, 2010, 6, e1001136.	1.5	35
167	Common Breast Cancer Susceptibility Alleles and the Risk of Breast Cancer for BRCA1 and BRCA2 Mutation Carriers: Implications for Risk Prediction. Cancer Research, 2010, 70, 9742-9754.	0.4	169
168	Identification of Breast Tumor Mutations in BRCA1 That Abolish Its Function in Homologous DNA Recombination. Cancer Research, 2010, 70, 988-995.	0.4	116
169	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	1.5	85
170	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2009, 18, 4442-4456.	1.4	99
171	Epigenetic alterations in the breast: Implications for breast cancer detection, prognosis and treatment. Seminars in Cancer Biology, 2009, 19, 165-171.	4.3	136
172	Chromosomal aberrations in UVBâ€induced tumors of immunosuppressed mice. Genes Chromosomes and Cancer, 2009, 48, 490-501.	1.5	5
173	Methylation not a frequent â€œsecond hitâ€in tumors with germline BRCA mutations. Familial Cancer, 2009, 8, 339-346.	0.9	57
174	Merkel Cell Polyomavirus in Cutaneous Squamous Cell Carcinoma of Immunocompetent Individuals. Journal of Investigative Dermatology, 2009, 129, 2868-2874.	0.3	93
175	Evaluation of a candidate breast cancer associated SNP in ERCC4 as a risk modifier in BRCA1 and BRCA2 mutation carriers. Results from the Consortium of Investigators of Modifiers of BRCA1/BRCA2 (CIMBA). British Journal of Cancer, 2009, 101, 2048-2054.	2.9	15
176	Sequence divergence of Mus spretus and Mus musculus across a skin cancer susceptibility locus. BMC Genomics, 2008, 9, 626.	1.2	16
177	Clinically Applicable Models to CharacterizeBRCA1andBRCA2Variants of Uncertain Significance. Journal of Clinical Oncology, 2008, 26, 5393-5400.	0.8	77
178	PTPRJ Haplotypes and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2782-2785.	1.1	18
179	The Role of Parental and Grandparental Epigenetic Alterations in Familial Cancer Risk. Cancer Research, 2008, 68, 9116-9121.	0.4	35
180	Mouse Models. , 2008, , 1957-1961.		0

#	Article	IF	Citations
181	Lack of Germ-Line Promoter Methylation in BRCA1-Negative Families with Familial Breast Cancer. Genetic Testing and Molecular Biomarkers, 2006, 10, 281-284.	1.7	24
182	Elastin point mutations cause an obstructive vascular disease, supravalvular aortic stenosis. Human Molecular Genetics, 1997, 6, 1021-1028.	1.4	233
183	Genetic polymorphism in Methylenetetrahydrofolate Reductase chloride transport protein 6 (MTHFR) Tj ETQq1 1 0.784314 rgBT /Ov Skin Health and Disease, 0, , .	0.7	4