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	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
2	Breast-Cancer Risk in Families with Mutations in PALB2. New England Journal of Medicine, 2014, 371, 497-506.	13.9	745
3	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
4	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
5	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
6	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
7	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
8	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
9	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
10	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
11	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
12	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
13	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
14	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
15	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
16	Elastin point mutations cause an obstructive vascular disease, supravalvular aortic stenosis. Human Molecular Genetics, 1997, 6, 1021-1028.	1.4	233
17	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	1.1	224
18	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221

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19	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
20	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
21	Benchmarking short sequence mapping tools. BMC Bioinformatics, 2013, 14, 184.	1.2	170
22	Implementation of Germline Testing for Prostate Cancer: Philadelphia Prostate Cancer Consensus Conference 2019. Journal of Clinical Oncology, 2020, 38, 2798-2811.	0.8	170
23	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
24	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
25	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
26	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
27	Epigenetic alterations in the breast: Implications for breast cancer detection, prognosis and treatment. Seminars in Cancer Biology, 2009, 19, 165-171.	4.3	136
28	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
29	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
30	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
31	Identification of Breast Tumor Mutations in BRCA1 That Abolish Its Function in Homologous DNA Recombination. Cancer Research, 2010, 70, 988-995.	0.4	116
32	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
33	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
34	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
35	Haploinsufficiency for BRCA1 leads to cell-type-specific genomic instability and premature senescence. Nature Communications, 2015, 6, 7505.	5.8	101
36	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

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37	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
38	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
39	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
40	Merkel Cell Polyomavirus in Cutaneous Squamous Cell Carcinoma of Immunocompetent Individuals. Journal of Investigative Dermatology, 2009, 129, 2868-2874.	0.3	93
41	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
42	Keratinocyte Carcinomas: Current Concepts and Future Research Priorities. Clinical Cancer Research, 2019, 25, 2379-2391.	3.2	91
43	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
44	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	0.8	90
45	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
46	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
47	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	1.5	85
48	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
49	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
50	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
51	Clinically Applicable Models to CharacterizeBRCA1andBRCA2Variants of Uncertain Significance. Journal of Clinical Oncology, 2008, 26, 5393-5400.	0.8	77
52	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
53	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
54	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

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55	Epidemiology of keratinocyte carcinomas after organ transplantation. British Journal of Dermatology, 2017, 177, 1208-1216.	1.4	67
56	Differential mutation frequencies in metastatic cutaneous squamous cell carcinomas versus primary tumors. Cancer, 2017, 123, 1184-1193.	2.0	64
57	The pathogenesis of cutaneous squamous cell carcinoma in organ transplant recipients. British Journal of Dermatology, 2017, 177, 1217-1224.	1.4	58
58	Methylation not a frequent â€œsecond hitâ€•in tumors with germline BRCA mutations. Familial Cancer, 2009, 8, 339-346.	0.9	57
59	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
60	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
61	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
62	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
63	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
64	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
65	Use of Whole Genome Sequencing for Diagnosis and Discovery in the Cancer Genetics Clinic. EBioMedicine, 2015, 2, 74-81.	2.7	50
66	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
67	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
68	BRCA1/2 Functional Loss Defines a Targetable Subset in Leiomyosarcoma. Oncologist, 2019, 24, 973-979.	1.9	49
69	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
70	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
71	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
72	mrSNP: Software to detect SNP effects on microRNA binding. BMC Bioinformatics, 2014, 15, 73.	1.2	46

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73	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
74	The Impact of 3â€²UTR Variants on Differential Expression of Candidate Cancer Susceptibility Genes. PLoS ONE, 2013, 8, e58609.	1.1	44
75	Clinical testing of BRCA1 and BRCA2: a worldwide snapshot of technological practices. Npj Genomic Medicine, 2018, 3, 7.	1.7	44
76	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44
77	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
78	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
79	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
80	Germline Variants Impact Somatic Events during Tumorigenesis. Trends in Genetics, 2019, 35, 515-526.	2.9	39
81	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
82	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
83	The Role of Parental and Grandparental Epigenetic Alterations in Familial Cancer Risk. Cancer Research, 2008, 68, 9116-9121.	0.4	35
84	Germline Variation Controls the Architecture of Somatic Alterations in Tumors. PLoS Genetics, 2010, 6, e1001136.	1.5	35
85	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
86	Ovarian cancer susceptibility alleles and risk of ovarian cancer inBRCA1andBRCA2mutation carriers. Human Mutation, 2012, 33, 690-702.	1.1	34
87	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
88	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
89	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
90	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

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91	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
92	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
93	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
94	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
95	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2020, 11, 820.	5.8	30
96	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
97	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
98	The Role for Oxidative Stress in Aberrant DNA Methylation in Alzheimerâ€™s Disease. Current Alzheimer Research, 2012, 9, 1077-1096.	0.7	27
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	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
101	BRCA1andBRCA2pathogenic sequence variants in women of African origin or ancestry. Human Mutation, 2019, 40, 1781-1796.	1.1	26
102	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
103	Characterization of BRCA1 ring finger variants of uncertain significance. Breast Cancer Research and Treatment, 2010, 119, 737-743.	1.1	25
104	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
105	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
106	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
107	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
108	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

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109	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
110	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
111	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
112	Salivary Gland Cancer inBRCA-Positive Families. JAMA Otolaryngology - Head and Neck Surgery, 2014, 140, 1213.	1.2	21
113	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
114	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
115	Genetic Testing to Guide Risk-Stratified Screens for Breast Cancer. Journal of Personalized Medicine, 2019, 9, 15.	1.1	21
116	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
117	Differential expression ofmiR-1, a putative tumor suppressing microRNA, in cancer resistant and cancer susceptible mice. PeerJ, 2013, 1, e68.	0.9	20
118	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
119	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
120	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
121	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
122	PTPRJ Haplotypes and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2782-2785.	1.1	18
123	Haplotype structure in Ashkenazi Jewish BRCA1 and BRCA2 mutation carriers. Human Genetics, 2011, 130, 685-699.	1.8	18
124	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
125	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
126	Sequence divergence of Mus spretus and Mus musculus across a skin cancer susceptibility locus. BMC Genomics, 2008, 9, 626.	1.2	16

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127	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
128	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
129	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
130	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
131	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
132	Identifying colorectal cancer caused by biallelic MUTYH pathogenic variants using tumor mutational signatures. Nature Communications, 2022, 13, .	5.8	15
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	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
135	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
136	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
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	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
139	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
140	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
141	<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
142	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
143	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
144	Metastatic breast cancer patient perceptions of somatic tumor genomic testing. BMC Cancer, 2020, 20, 389.	1.1	8

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145	Association between Smoking and Molecular Subtypes of Colorectal Cancer. JNCI Cancer Spectrum, 2021, 5, pkab056.	1.4	8
146	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
147	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
148	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
149	Polygenic Risk Scores in Prostate Cancer Risk Assessment and Screening. Urologic Clinics of North America, 2021, 48, 387-399.	0.8	7
150	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
151	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
152	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
153	Chromosomal aberrations in UVBâ€induced tumors of immunosuppressed mice. Genes Chromosomes and Cancer, 2009, 48, 490-501.	1.5	5
154	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
155	Variants in an Hdac9 intronic enhancer plasmid impact Twist1 expression in vitro. Mammalian Genome, 2016, 27, 99-110.	1.0	5
156	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
157	Oncogenetic network estimation with disjunctive Bayesian networks. Computational and Systems Oncology, 2021, 1, e1027.	1.1	5
158	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
159	Linking distant relatives with <scp>BRCA</scp> gene mutations: potential for cost savings. Clinical Genetics, 2014, 85, 54-58.	1.0	4
160	F-Box Protein-Mediated Resistance to PARP Inhibitor Therapy. Molecular Cell, 2019, 73, 195-196.	4.5	4
161	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
162	Maternal age at delivery and fertility of the next generation. Paediatric and Perinatal Epidemiology, 2020, 34, 629-636.	0.8	4

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163	Genetic analysis of a malignant meningioma and associated metastases. Acta Neurochirurgica, 2022, 164, 1401-1405.	0.9	4
164	Genetic polymorphism in Methylenetetrahydrofolate Reductase chloride transport protein 6 (MTHFR) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Skin Health and Disease, 0, , .	0.7	4
165	Polygenic risk scores for prostate cancer: testing considerations. Canadian Journal of Urology, 2019, 26, 17-18.	0.0	4
166	MicroRNA Expression Profiling of Cutaneous Squamous Cell Carcinomas Arising in Different Sites. Otolaryngology - Head and Neck Surgery, 2020, 163, 538-545.	1.1	3
167	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
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