

Paolo Radice

List of Publications by Year in descending order

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Version: 2024-02-01

306
papers

28,308
citations

9428

76
h-index

7836

155
g-index

323
all docs

323
docs citations

323
times ranked

28455
citing authors

#	ARTICLE	IF	CITATIONS
1	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122.	3.0	19
2	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in <i>BRCA1</i> and <i>BRCA2</i> compared with those harboring protein truncating variants. <i>Genetics in Medicine</i> , 2022, 24, 119-129.	1.1	10
3	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	1.4	23
4	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	2.2	15
5	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	3.4	51
6	The Impact of Mediterranean Dietary Intervention on Metabolic and Hormonal Parameters According to <i>BRCA1/2</i> Variant Type. <i>Frontiers in Genetics</i> , 2022, 13, 820878.	1.1	2
7	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	3.6	19
8	Analysis of the mutational status of <i>SIX1/2</i> and microRNA processing genes in paired primary and relapsed Wilms tumors and association with relapse. <i>Cancer Gene Therapy</i> , 2021, 28, 1016-1024.	2.2	9
9	Functional evidence of transcripts and RNA-splicing outline. , 2021, , 121-144.		0
10	A case-only study to identify genetic modifiers of breast cancer risk for <i>BRCA1/BRCA2</i> mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	5.8	19
11	Breast Cancer Risk Genes Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	13.9	532
12	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. <i>Cancers</i> , 2021, 13, 2370.	1.7	4
13	Malignant salivary gland tumours in families with breast cancer susceptibility. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2021, 479, 221-226.	1.4	0
14	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100042.	1.0	6
15	The predictive ability of the 313 variant-based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous <i>BRCA1</i> or <i>BRCA2</i> pathogenic variant. <i>Genetics in Medicine</i> , 2021, 23, 1726-1737.	1.1	16
16	OCT Biomarkers in Neovascular Age-Related Macular Degeneration: A Narrative Review. <i>Journal of Ophthalmology</i> , 2021, 2021, 1-16.	0.6	21
17	Altered regulation of <i>BRCA1</i> exon 11 splicing is associated with breast cancer risk in carriers of <i>BRCA1</i> pathogenic variants. <i>Human Mutation</i> , 2021, 42, 1488-1502.	1.1	7
18	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145.	2.9	9

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19	Analysis of Italian BRCA1/2 Pathogenic Variants Identifies a Private Spectrum in the Population from the Bergamo Province in Northern Italy. <i>Cancers</i> , 2021, 13, 532.	1.7	8
20	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020, 80, 624-638.	0.4	39
21	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
22	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020, 38, 674-685.	0.8	270
23	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of <i>BRCA1</i> and <i>BRCA2</i> pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	1.1	82
24	<i>BRCA1/2</i> Variants and Metabolic Factors: Results From a Cohort of Italian Female Carriers. <i>Cancers</i> , 2020, 12, 3584.	1.7	2
25	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	2.6	39
26	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	9.4	265
27	Characterization of the Cancer Spectrum in Men With Germline <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>JAMA Oncology</i> , 2020, 6, 1218.	3.4	48
28	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
29	The Spectrum of <i>FANCM</i> Protein Truncating Variants in European Breast Cancer Cases. <i>Cancers</i> , 2020, 12, 292.	1.7	11
30	<i>BRCA1/2</i> Molecular Assay for Ovarian Cancer Patients: A Survey through Italian Departments of Oncology and Molecular and Genomic Diagnostic Laboratories. <i>Diagnostics</i> , 2019, 9, 146.	1.3	3
31	The <i>FANCM</i> :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	2.3	28
32	Two truncating variants in <i>FANCC</i> and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	1.6	5
33	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
34	GFP-Fragment Reassembly Screens for the Functional Characterization of Variants of Uncertain Significance in Protein Interaction Domains of the <i>BRCA1</i> and <i>BRCA2</i> Genes. <i>Cancers</i> , 2019, 11, 151.	1.7	4
35	Recommendations for the implementation of <i>BRCA</i> testing in ovarian cancer patients and their relatives. <i>Critical Reviews in Oncology/Hematology</i> , 2019, 140, 67-72.	2.0	51
36	Large scale multifactorial likelihood quantitative analysis of <i>BRCA1</i> and <i>BRCA2</i> variants: An ENIGMA resource to support clinical variant classification. <i>Human Mutation</i> , 2019, 40, 1557-1578.	1.1	102

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37	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. <i>British Journal of Cancer</i> , 2019, 121, 180-192.	2.9	19
38	Towards controlled terminology for reporting germline cancer susceptibility variants: an ENIGMA report. <i>Journal of Medical Genetics</i> , 2019, 56, 347-357.	1.5	32
39	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	5.8	90
40	Usefulness and Limitations of Comprehensive Characterization of mRNA Splicing Profiles in the Definition of the Clinical Relevance of BRCA1/2 Variants of Uncertain Significance. <i>Cancers</i> , 2019, 11, 295.	1.7	24
41	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	2.9	52
42	The association between weight at birth and breast cancer risk revisited using Mendelian randomisation. <i>European Journal of Epidemiology</i> , 2019, 34, 591-600.	2.5	16
43	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
44	Insight into genetic susceptibility to male breast cancer by multigene panel testing: Results from a multicenter study in Italy. <i>International Journal of Cancer</i> , 2019, 145, 390-400.	2.3	40
45	Height and Body Mass Index as Modifiers of Breast Cancer Risk in BRCA1/2 Mutation Carriers: A Mendelian Randomization Study. <i>Journal of the National Cancer Institute</i> , 2019, 111, 350-364.	3.0	30
46	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 795-806.	0.9	81
47	Evaluation of CYP17A1 and CYP1B1 polymorphisms in male breast cancer risk. <i>Endocrine Connections</i> , 2019, 8, 1224-1229.	0.8	6
48	The BRCA2 c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018, 39, 729-741.	1.1	19
49	Decapping protein EDC4 regulates DNA repair and phenocopies BRCA1. <i>Nature Communications</i> , 2018, 9, 967.	5.8	33
50	Mutational spectrum in a worldwide study of 29,700 families with BRCA1 or BRCA2 mutations. <i>Human Mutation</i> , 2018, 39, 593-620.	1.1	224
51	Survey of gynecological carcinosarcomas in families with breast and ovarian cancer predisposition. <i>Cancer Genetics</i> , 2018, 221, 38-45.	0.2	4
52	A possible role of FANCM mutations in male breast cancer susceptibility: Results from a multicenter study in Italy. <i>Breast</i> , 2018, 38, 92-97.	0.9	23
53	Individuals with FANCM biallelic mutations do not develop Fanconi anemia, but show risk for breast cancer, chemotherapy toxicity and may display chromosome fragility. <i>Genetics in Medicine</i> , 2018, 20, 452-457.	1.1	59
54	Contribution of MUTYH Variants to Male Breast Cancer Risk: Results From a Multicenter Study in Italy. <i>Frontiers in Oncology</i> , 2018, 8, 583.	1.3	25

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55	Two Missense Variants Detected in Breast Cancer Probands Preventing BRCA2-PALB2 Protein Interaction. <i>Frontiers in Oncology</i> , 2018, 8, 480.	1.3	11
56	<i>BRCA1</i> and <i>BRCA2</i> 5' noncoding region variants identified in breast cancer patients alter promoter activity and protein binding. <i>Human Mutation</i> , 2018, 39, 2025-2039.	1.1	15
57	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	9.4	184
58	Genetic and epigenetic analyses guided by high resolution whole-genome SNP array reveals a possible role of <i>CHEK2</i> in Wilms tumour susceptibility. <i>Oncotarget</i> , 2018, 9, 34079-34089.	0.8	25
59	Evaluation of copy-number variants as modifiers of breast and ovarian cancer risk for <i>BRCA1</i> pathogenic variant carriers. <i>European Journal of Human Genetics</i> , 2017, 25, 432-438.	1.4	26
60	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	75
61	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426
62	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
63	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
64	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
65	Association of breast cancer risk in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. <i>Breast Cancer Research and Treatment</i> , 2017, 161, 117-134.	1.1	18
66	Whole-exome sequencing and targeted gene sequencing provide insights into the role of <i>PALB2</i> as a male breast cancer susceptibility gene. <i>Cancer</i> , 2017, 123, 210-218.	2.0	31
67	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
68	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. <i>Journal of Clinical Oncology</i> , 2017, 35, 2240-2250.	0.8	152
69	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017, 8, 102769-102782.	0.8	9
70	A Targeted Approach to Genetic Counseling in Breast Cancer Patients: The Experience of an Italian Local Project. <i>Tumori</i> , 2016, 102, 45-50.	0.6	4
71	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016, 7, 80140-80163.	0.8	31
72	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>PLoS ONE</i> , 2016, 11, e0158801.	1.1	10

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73	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
74	Recommendations for the implementation of <i>BRCA</i> testing in the care and treatment pathways of ovarian cancer patients. Future Oncology, 2016, 12, 2071-2075.	1.1	21
75	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
76	Naturally occurring <i>BRCA2</i> alternative mRNA splicing events in clinically relevant samples. Journal of Medical Genetics, 2016, 53, 548-558.	1.5	69
77	Response: Table 1.. Journal of the National Cancer Institute, 2016, 108, djw173.	3.0	2
78	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
79	Mutation detection rates associated with specific selection criteria for BRCA1/2 testing in 1854 high-risk families: A monocentric Italian study. European Journal of Internal Medicine, 2016, 32, 65-71.	1.0	21
80	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
81	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
82	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59
83	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
84	Retina-derived POU domain factor 1 coordinates expression of genes relevant to renal and neuronal development. International Journal of Biochemistry and Cell Biology, 2016, 78, 162-172.	1.2	10
85	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	1.6	2
86	Haplotype analyses of the c.1027C>T and c.2167_2168delAT recurrent truncating mutations in the breast cancer-predisposing gene PALB2. Breast Cancer Research and Treatment, 2016, 160, 121-129.	1.1	11
87	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
88	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
89	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
90	The PALB2 p.Leu939Trp mutation is not associated with breast cancer risk. Breast Cancer Research, 2016, 18, 111.	2.2	11

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91	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. <i>Human Molecular Genetics</i> , 2016, 25, 2256-2268.	1.4	106
92	Personalized testing based on polygenic risk score is promising for more efficient population-based screening programs for common oncological diseases. <i>Annals of Oncology</i> , 2016, 27, 369-370.	0.6	5
93	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	9.4	125
94	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. <i>Human Genetics</i> , 2016, 135, 137-154.	1.8	8
95	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	3.0	77
96	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	0.6	18
97	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	1.1	26
98	Chromosomal anomalies at 1q, 3, 16q, and mutations of <i>SIX1</i> and <i>DROSHA</i> genes underlie Wilms tumor recurrences. <i>Oncotarget</i> , 2016, 7, 8908-8915.	0.8	26
99	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2015, 17, 61.	2.2	26
100	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	2.2	26
101	Androgen Receptor CAG Repeat Length and Estrogen Receptor Status in Postmenopausal Breast Cancer Prognosis. <i>International Journal of Biological Markers</i> , 2015, 30, 418-424.	0.7	3
102	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015, 70, 758-762.	0.2	0
103	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020.	1.1	34
104	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	428
105	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	1.4	40
106	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015, 96, 5-20.	2.6	76
107	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. <i>Carcinogenesis</i> , 2015, 36, 256-271.	1.3	14
108	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	9.4	221

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109	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	9.4	513
110	Novel and known genetic variants for male breast cancer risk at 8q24.21, 9p21.3, 11q13.3 and 14q24.1: Results from a multicenter study in Italy. <i>European Journal of Cancer</i> , 2015, 51, 2289-2295.	1.3	25
111	<i>FANCM</i>c.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. <i>Human Molecular Genetics</i> , 2015, 24, 5345-5355.	1.4	91
112	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , 2015, 97, 22-34.	2.6	37
113	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	56
114	Association of Type and Location of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Risk of Breast and Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1347.	3.8	390
115	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
116	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	3.0	99
117	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	1.1	24
118	Estimate of the penetrance of BRCA mutation and the COS software for the assessment of BRCA mutation probability. <i>Familial Cancer</i> , 2015, 14, 117-128.	0.9	12
119	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 285-298.	1.4	38
120	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 308-316.	1.1	22
121	Involvement of <i>MBD4</i> inactivation in mismatch repair-deficient tumorigenesis. <i>Oncotarget</i> , 2015, 6, 42892-42904.	0.8	43
122	Association between CASP8 652 6N Del Polymorphism (rs3834129) and Colorectal Cancer Risk: Results from a Multi-Centric Study. <i>PLoS ONE</i> , 2014, 9, e85538.	1.1	8
123	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	1.1	49
124	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	1.5	39
125	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. <i>PLoS Genetics</i> , 2014, 10, e1004256.	1.5	47
126	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111.	1.4	53

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127	Risk of desmoid tumours after open and laparoscopic colectomy in patients with familial adenomatous polyposis. <i>British Journal of Surgery</i> , 2014, 101, 558-565.	0.1	60
128	Association of SULT1A1 Arg213His polymorphism with male breast cancer risk: results from a multicenter study in Italy. <i>Breast Cancer Research and Treatment</i> , 2014, 148, 623-628.	1.1	7
129	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014, 16, 3419.	2.2	97
130	Breast-Cancer Risk in Families With Mutations in PALB2. <i>Obstetrical and Gynecological Survey</i> , 2014, 69, 659-660.	0.2	1
131	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2014, 16, 3416.	2.2	57
132	Comprehensive annotation of splice junctions supports pervasive alternative splicing at the BRCA1 locus: a report from the ENIGMA consortium. <i>Human Molecular Genetics</i> , 2014, 23, 3666-3680.	1.4	96
133	PALB2 sequencing in Italian familial breast cancer cases reveals a high-risk mutation recurrent in the province of Bergamo. <i>Genetics in Medicine</i> , 2014, 16, 688-694.	1.1	25
134	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. <i>Human Molecular Genetics</i> , 2014, 23, 1934-1946.	1.4	32
135	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. <i>British Journal of Cancer</i> , 2014, 110, 1088-1100.	2.9	21
136	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
137	Breast-Cancer Risk in Families with Mutations in <i>PALB2</i> . <i>New England Journal of Medicine</i> , 2014, 371, 497-506.	13.9	745
138	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	5.8	105
139	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014, 23, 6034-6046.	1.4	12
140	Comparison of mRNA Splicing Assay Protocols across Multiple Laboratories: Recommendations for Best Practice in Standardized Clinical Testing. <i>Clinical Chemistry</i> , 2014, 60, 341-352.	1.5	95
141	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , 2014, 16, R51.	2.2	14
142	Characterization of an Italian Founder Mutation in the RING-Finger Domain of BRCA1. <i>PLoS ONE</i> , 2014, 9, e86924.	1.1	24
143	miR-342 Regulates BRCA1 Expression through Modulation of ID4 in Breast Cancer. <i>PLoS ONE</i> , 2014, 9, e87039.	1.1	59
144	COMPLEXO: identifying the missing heritability of breast cancer via next generation collaboration. <i>Breast Cancer Research</i> , 2013, 15, 402.	2.2	36

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145	First description of an acinic cell carcinoma of the breast in a BRCA1 mutation carrier: a case report. <i>BMC Cancer</i> , 2013, 13, 46.	1.1	34
146	A Classification Model for BRCA2 DNA Binding Domain Missense Variants Based on Homology-Directed Repair Activity. <i>Cancer Research</i> , 2013, 73, 265-275.	0.4	103
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