

Kyriaki Michailidou

List of Publications by Year in descending order

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Version: 2024-02-01

175
papers

14,358
citations

26610

56
h-index

24232

110
g-index

191
all docs

191
docs citations

191
times ranked

18044
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	9.4	960
3	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
4	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
5	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
6	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
7	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	9.4	493
8	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
9	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
10	Genome-wide association studies identify four ER negative"specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	374
11	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
12	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
13	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 126-135.	1.1	278
14	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
15	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	9.4	256
16	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	2.6	201
17	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
18	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	5.8	178

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19	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	1.5	174
20	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012, 21, 5373-5384.	1.4	168
21	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	7.7	157
22	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. <i>Nature Genetics</i> , 2011, 43, 451-454.	9.4	141
23	A genome-wide association scan (GWAS) for mean telomere length within the COGS project: identified loci show little association with hormone-related cancer risk. <i>Human Molecular Genetics</i> , 2013, 22, 5056-5064.	1.4	130
24	A genome wide association study (GWAS) providing evidence of an association between common genetic variants and late radiotherapy toxicity. <i>Radiotherapy and Oncology</i> , 2014, 111, 178-185.	0.3	128
25	Breast cancer risk variants at 6q25 display different phenotype associations and regulate <i>ESR1</i> , <i>RMND1</i> and <i>CCDC170</i> . <i>Nature Genetics</i> , 2016, 48, 374-386.	9.4	125
26	Mendelian randomization study of adiposity-related traits and risk of breast, ovarian, prostate, lung and colorectal cancer. <i>International Journal of Epidemiology</i> , 2016, 45, 896-908.	0.9	124
27	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
28	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016, 13, e1002105.	3.9	118
29	Combined genetic and splicing analysis of <i>BRCA1</i> 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
30	Identification of a <i>BRCA2</i> -Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003173.	1.5	105
31	Evidence that breast cancer risk at the 2q35 locus is mediated through <i>IGFBP5</i> regulation. <i>Nature Communications</i> , 2014, 5, 4999.	5.8	105
32	A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76.	5.8	100
33	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
34	Fine-Scale Mapping of the <i>FGFR2</i> Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind <i>FOXA1</i> and <i>E2F1</i> . <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	2.6	98
35	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	1.5	94
36	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93

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37	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
38	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 526-536.	0.9	88
39	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
40	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. <i>Nature Communications</i> , 2020, 11, 3833.	5.8	88
41	Common genetic determinants of breast-cancer risk in East Asian women: a collaborative study of 23 637 breast cancer cases and 25 579 controls. <i>Human Molecular Genetics</i> , 2013, 22, 2539-2550.	1.4	86
42	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	4.1	83
43	Impact of the COVID-19 Pandemic on the Mental Health of Healthcare Workers. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 1435.	1.2	82
44	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
45	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
46	A Genome-wide Association Study of Early-Onset Breast Cancer Identifies <i>PCSK9</i> as a Novel Breast Cancer Gene and Supports a Common Genetic Spectrum for Breast Cancer at Any Age. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 658-669.	1.1	77
47	Five endometrial cancer risk loci identified through genome-wide association analysis. <i>Nature Genetics</i> , 2016, 48, 667-674.	9.4	77
48	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
49	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
50	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	75
51	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	5.8	75
52	Vaccine confidence among parents: Large scale study in eighteen European countries. <i>Vaccine</i> , 2020, 38, 1505-1512.	1.7	74
53	Meta-analysis of Genome Wide Association Studies Identifies Genetic Markers of Late Toxicity Following Radiotherapy for Prostate Cancer. <i>EBioMedicine</i> , 2016, 10, 150-163.	2.7	69
54	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. <i>Biological Psychiatry</i> , 2019, 85, 946-955.	0.7	69

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55	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. <i>Human Molecular Genetics</i> , 2015, 24, 5589-5602.	1.4	67
56	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	1.1	67
57	Evaluating Genome-Wide Association Study-Identified Breast Cancer Risk Variants in African-American Women. <i>PLoS ONE</i> , 2013, 8, e58350.	1.1	66
58	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1503-1510.	1.1	64
59	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2016, 23, 77-91.	1.6	62
60	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. <i>Cancer Medicine</i> , 2018, 7, 1978-1987.	1.3	62
61	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , 2016, 99, 903-911.	2.6	59
62	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	56
63	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. <i>Cancer Research</i> , 2015, 75, 2457-2467.	0.4	55
64	Mammographic Breast Density and Breast Cancer: Evidence of a Shared Genetic Basis. <i>Cancer Research</i> , 2012, 72, 1478-1484.	0.4	54
65	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
66	Prediction of breast cancer risk based on common genetic variants in women of East Asian ancestry. <i>Breast Cancer Research</i> , 2016, 18, 124.	2.2	52
67	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	2.3	51
68	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 1478-1492.	1.4	50
69	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	1.1	49
70	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. <i>PLoS ONE</i> , 2011, 6, e24987.	1.1	48
71	The care of adolescents and young adults with cancer: results of the ESMO/SIOPE survey. <i>ESMO Open</i> , 2017, 2, e000252.	2.0	48
72	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021, 113, 329-337.	3.0	45

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73	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	2.2	43
74	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. <i>International Journal of Epidemiology</i> , 2020, 49, 1117-1131.	0.9	41
75	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1168-1176.	3.0	41
76	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	1.4	40
77	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	1.5	39
78	Patient survival and tumor characteristics associated with CHEK2:p.I157T findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98.	2.2	39
79	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
80	Evaluating genetic variants associated with breast cancer risk in high and moderate-penetrance genes in Asians. <i>Carcinogenesis</i> , 2017, 38, 511-518.	1.3	38
81	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
82	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. <i>Scientific Reports</i> , 2015, 5, 17369.	1.6	35
83	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228,951 Women of European Descent. <i>Journal of the National Cancer Institute</i> , 2020, 112, 295-304.	3.0	35
84	Muscle-derived exosomes encapsulate myomiRs and are involved in local skeletal muscle tissue communication. <i>FASEB Journal</i> , 2021, 35, e21279.	0.2	35
85	Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. <i>Human Genetics</i> , 2015, 134, 231-245.	1.8	34
86	The spectrum of <i>BRCA1</i> and <i>BRCA2</i> pathogenic sequence variants in Middle Eastern, North African, and South European countries. <i>Human Mutation</i> , 2019, 40, e1-e23.	1.1	34
87	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016, 25, 3863-3876.	1.4	33
88	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
89	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
90	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

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91	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	2.2	31
92	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	2.3	28
93	Chromatin interactome mapping at 139 independent breast cancer risk signals. <i>Genome Biology</i> , 2020, 21, 8.	3.8	27
94	Polygenic risk scores for prediction of breast cancer risk in Asian populations. <i>Genetics in Medicine</i> , 2022, 24, 586-600.	1.1	27
95	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	2.2	26
96	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	1.1	26
97	Decreased breast cancer risk in systemic lupus erythematosus: the search for a genetic basis continues. <i>Lupus</i> , 2012, 21, 896-899.	0.8	25
98	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2015, 22, 851-861.	1.6	25
99	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
100	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. <i>Nature Communications</i> , 2021, 12, 4198.	5.8	24
101	Exome array analysis identifies GPR35 as a novel susceptibility gene for anthracycline-induced cardiotoxicity in childhood cancer. <i>Pharmacogenetics and Genomics</i> , 2017, 27, 445-453.	0.7	22
102	The Role of Perceived Organizational Support in Mental Health of Healthcare Workers During the COVID-19 Pandemic: A Cross-Sectional Study. <i>Frontiers in Psychiatry</i> , 2021, 12, 707293.	1.3	22
103	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
104	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. <i>Cancer Causes and Control</i> , 2016, 27, 679-693.	0.8	21
105	Type 2 Diabetes Susceptibility in the Greek-Cypriot Population: Replication of Associations with TCF7L2, FTO, HHEX, SLC30A8 and IGF2BP2 Polymorphisms. <i>Genes</i> , 2017, 8, 16.	1.0	21
106	Assessment of interactions between 205 breast cancer susceptibility loci and 13 established risk factors in relation to breast cancer risk, in the Breast Cancer Association Consortium. <i>International Journal of Epidemiology</i> , 2020, 49, 216-232.	0.9	21
107	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015, 6, 37979-37994.	0.8	20
108	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. <i>International Journal of Cancer</i> , 2017, 141, 1830-1840.	2.3	20

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109	Adapting the ACMG/AMP variant classification framework: A perspective from the ClinGen Hemoglobinopathy Variant Curation Expert Panel. <i>Human Mutation</i> , 2022, 43, 1089-1096.	1.1	20
110	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). <i>Scientific Reports</i> , 2016, 6, 32512.	1.6	19
111	The <i>BRCA2</i> 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
112	Oral health training, knowledge, attitudes and practices of primary care paediatricians: a European survey. <i>European Journal of Pediatrics</i> , 2018, 177, 675-681.	1.3	19
113	Wide phenotypic variability in RSPH9-associated primary ciliary dyskinesia: review of a case-series from Cyprus. <i>Journal of Thoracic Disease</i> , 2019, 11, 2067-2075.	0.6	19
114	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014, 5, 4051.	5.8	16
115	Patients with a High Polygenic Risk of Breast Cancer do not have An Increased Risk of Radiotherapy Toxicity. <i>Clinical Cancer Research</i> , 2016, 22, 1413-1420.	3.2	16
116	MicroRNAs as possible biomarkers for screening of aortic aneurysms: a systematic review and validation study. <i>Biomarkers</i> , 2018, 23, 253-264.	0.9	16
117	The Relationship between Common Genetic Markers of Breast Cancer Risk and Chemotherapy-Induced Toxicity: A Case-Control Study. <i>PLoS ONE</i> , 2016, 11, e0158984.	1.1	15
118	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	2.2	15
119	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. <i>Breast Cancer Research</i> , 2022, 24, 27.	2.2	15
120	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
121	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
122	Incorporating Functional Genomic Information in Genetic Association Studies Using an Empirical Bayes Approach. <i>Genetic Epidemiology</i> , 2016, 40, 176-187.	0.6	14
123	Re-evaluating genetic variants identified in candidate gene studies of breast cancer risk using data from nearly 280,000 women of Asian and European ancestry. <i>EBioMedicine</i> , 2019, 48, 203-211.	2.7	14
124	The International Hemoglobinopathy Research Network (<scp>INHERENT</scp>): An international initiative to study the role of genetic modifiers in hemoglobinopathies. <i>American Journal of Hematology</i> , 2021, 96, E416-E420.	2.0	14
125	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. <i>Oncotarget</i> , 2017, 8, 18381-18398.	0.8	14
126	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. <i>International Journal of Cancer</i> , 2020, 146, 2130-2138.	2.3	13

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127	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
128	Genome-wide association study of susceptibility loci for breast cancer in Sardinian population. <i>BMC Cancer</i> , 2015, 15, 383.	1.1	12
129	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	1.1	12
130	Epidemiology of ATTRV30M neuropathy in Cyprus and the modifier effect of complement C1q on the age of disease onset. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2018, 25, 220-226.	1.4	12
131	Novel Bayes Factors That Capture Expert Uncertainty in Prior Density Specification in Genetic Association Studies. <i>Genetic Epidemiology</i> , 2015, 39, 239-248.	0.6	10
132	Detecting rare copy number variants from Illumina genotyping arrays with the CamCNV pipeline: Segmentation of Δ scores improves detection and reliability. <i>Genetic Epidemiology</i> , 2021, 45, 237-248.	0.6	10
133	The functional ALDH2 polymorphism is associated with breast cancer risk: A pooled analysis from the Breast Cancer Association Consortium. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e707.	0.6	9
134	Effect of HBB genotype on survival in a cohort of transfusion-dependent thalassemia patients in Cyprus. <i>Haematologica</i> , 2021, 106, 2458-2468.	1.7	9
135	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
136	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017, 8, 102769-102782.	0.8	9
137	Meta-Analysis of Common and Rare Variants. <i>Methods in Molecular Biology</i> , 2018, 1793, 73-88.	0.4	8
138	NGS Panel Testing of Triple-Negative Breast Cancer Patients in Cyprus: A Study of BRCA-Negative Cases. <i>Cancers</i> , 2020, 12, 3140.	1.7	8
139	Implementation of multigene panel NGS diagnosis in the national primary ciliary dyskinesia cohort of Cyprus: An island with a high disease prevalence. <i>Human Mutation</i> , 2021, 42, e62-e77.	1.1	8
140	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. <i>Breast Cancer Research</i> , 2021, 23, 86.	2.2	7
141	Pathogenic and Low-Frequency Variants in Children With Central Precocious Puberty. <i>Frontiers in Endocrinology</i> , 2021, 12, 745048.	1.5	7
142	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. <i>BMC Cancer</i> , 2015, 15, 978.	1.1	6
143	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203.	2.6	6
144	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100041.	1.0	6

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145	Combination of a 15-SNP Polygenic Risk Score and Classical Risk Factors for the Prediction of Breast Cancer Risk in Cypriot Women. <i>Cancers</i> , 2021, 13, 4568.	1.7	6
146	Sigmoido-Cecal Fistula: A Rare Case of Complicated Recurrent Diverticulitis and a Review of the Literature. <i>American Journal of Case Reports</i> , 2018, 19, 1386-1392.	0.3	6
147	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	2.0	6
148	A Genome-Wide Gene-Based Gene-Environment Interaction Study of Breast Cancer in More than 90,000 Women. <i>Cancer Research Communications</i> , 2022, 2, 211-219.	0.7	6
149	Novel variants in the ACTA2 and MYH11 genes in a Cypriot family with thoracic aortic aneurysms: a case report. <i>BMC Medical Genetics</i> , 2018, 19, 208.	2.1	5
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