

Anja Rudolph

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

131
papers

9,047
citations

46
h-index

93
g-index

132
ext. papers

10,921
ext. citations

9.7
avg, IF

4.05
L-index

#	Paper	IF	Citations
131	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. <i>International Journal of Cancer</i> , 2018 , 143, 746-757	7.5	9
130	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	7.8	53
129	Prognostic impact of surgery for early-stage invasive breast cancer on breast cancer-specific survival, overall survival, and recurrence risk: a population-based analysis. <i>Breast Cancer Research and Treatment</i> , 2018 , 170, 381-390	4.4	3
128	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	36.3	101
127	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017 , 77, 2789-2799	10.1	49
126	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017 , 49, 680-691	36.3	190
125	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
124	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1767-1778	36.3	186
123	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017 , 19, 119	8.3	26
122	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. <i>International Journal of Cancer</i> , 2017 , 141, 1830-1840	7.5	13
121	Genistein and enterolactone in relation to Ki-67 expression and HER2 status in postmenopausal breast cancer patients. <i>Molecular Nutrition and Food Research</i> , 2017 , 61, 1700449	5.9	8
120	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017 , 19, 599-603		51
119	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017 , 46, 1814-1822	7.8	27
118	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	5.6	24
117	A splicing variant of TERT identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. <i>International Journal of Cancer</i> , 2016 , 139, 2646-2654	7.5	6
116	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, 1052-67	24.4	104
115	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64

114	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016 , 7, 12675	17.4	53
113	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	4.9	16
112	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. <i>Breast Cancer Research</i> , 2016 , 18, 104	8.3	44
111	Relationship between menopausal hormone therapy and mortality after breast cancer The MARIEplus study, a prospective case cohort. <i>International Journal of Cancer</i> , 2016 , 138, 2098-108	7.5	9
110	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016 , 34, 2750-60	2.2	107
109	Gene-environment interaction and risk of breast cancer. <i>British Journal of Cancer</i> , 2016 , 114, 125-33	8.7	108
108	CYP24A1 variant modifies the association between use of oestrogen plus progestogen therapy and colorectal cancer risk. <i>British Journal of Cancer</i> , 2016 , 114, 221-9	8.7	16
107	Circulating miRNAs with prognostic value in metastatic breast cancer and for early detection of metastasis. <i>Carcinogenesis</i> , 2016 , 37, 461-70	4.6	102
106	Assessment of Multifactor Gene-Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 780-90	4	8
105	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , 2016 , 2, 138-53	5.3	16
104	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	5.6	55
103	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016 , 53, 298-309	5.8	83
102	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016 , 48, 374-86	36.3	93
101	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, 137-54	6.3	6
100	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	65
99	Evidence of a genetic link between endometriosis and ovarian cancer. <i>Fertility and Sterility</i> , 2016 , 105, 35-43.e1-10	4.8	26
98	Genome-Wide Interaction Analyses between Genetic Variants and Alcohol Consumption and Smoking for Risk of Colorectal Cancer. <i>PLoS Genetics</i> , 2016 , 12, e1006296	6	30
97	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016 , 11, e0153788	3.7	18

96	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. <i>Oncotarget</i> , 2016 , 7, 69097-69110	3.3	4
95	Association of circulating inflammatory biomarkers and dietary inflammation potential with postmenopausal breast cancer prognosis.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 1566-1566	2.2	
94	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	3.3	21
93	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	11.6	80
92	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016 , 11, e0160316	3.7	11
91	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016 , 45, 884-95	7.8	45
90	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016 , 139, 1303-1317	7.5	26
89	Plasma hyaluronic acid level as a prognostic and monitoring marker of metastatic breast cancer. <i>International Journal of Cancer</i> , 2016 , 138, 2499-509	7.5	28
88	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016 , 53, 800-811	5.8	121
87	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	8.3	26
86	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	8.3	25
85	Phyto-oestrogens and colorectal cancer risk: a systematic review and dose-response meta-analysis of observational studies. <i>British Journal of Nutrition</i> , 2016 , 116, 2115-2128	3.6	25
84	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016 , 135, 741-56	6.3	18
83	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016 , 18, 22	8.3	31
82	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, 679-93	2.8	15
81	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016 , 45, 1619-1630	7.8	77
80	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	11	43
79	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, 256-71	4.6	12

78	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015 , 47, 164-71	36.3	177
77	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015 , 47, 373-80	36.3	406
76	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1574-84	4	24
75	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	11	26
74	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	38
73	Evaluating the ovarian cancer gonadotropin hypothesis: a candidate gene study. <i>Gynecologic Oncology</i> , 2015 , 136, 542-8	4.9	12
72	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, 231-45	6.3	30
71	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. <i>Breast Cancer Research</i> , 2015 , 17, 18	8.3	17
70	Statin use and survival after colorectal cancer: the importance of comprehensive confounder adjustment. <i>Journal of the National Cancer Institute</i> , 2015 , 107, djv045	9.7	72
69	Association of aspirin and NSAID use with risk of colorectal cancer according to genetic variants. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 313, 1133-42	27.4	135
68	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015 , 6, 8234	17.4	40
67	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	36.3	226
66	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. <i>Human Genetics</i> , 2015 , 134, 1249-1262	6.3	25
65	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015 , 36, 1341-53	4.6	20
64	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015 , 24, 5955-64	5.6	48
63	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	74
62	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, 1680-91	4	17
61	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, 285-98	5.6	35

60	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015 , 24, 1478-92	5.6	46
59	Candidate genetic modifiers for breast and ovarian cancer risk in BRCA1 and BRCA2 mutation carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 308-16	4	20
58	Investigation of gene-environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. <i>International Journal of Cancer</i> , 2015 , 136, E685-96	7.5	26
57	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015 , 39, 689-97	2.6	18
56	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015 , 17, 58	8.3	24
55	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. <i>Breast Cancer Research</i> , 2015 , 17, 110	8.3	13
54	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015 , 10, e0128106	3.7	15
53	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015 , 6, 37979-94	3.3	19
52	Prediction of breast cancer risk based on profiling with common genetic variants. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	324
51	Dietary inflammation potential and postmenopausal breast cancer risk in a German case-control study. <i>Breast</i> , 2015 , 24, 491-6	3.6	49
50	Mendelian randomization study of height and risk of colorectal cancer. <i>International Journal of Epidemiology</i> , 2015 , 44, 662-72	7.8	44
49	Mendelian Randomization Study of Body Mass Index and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1024-31	4	54
48	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2015 , 24, 3595-607	5.6	32
47	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
46	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	11	59
45	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). <i>Journal of Genetics and Genome Research</i> , 2015 , 2,		22
44	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, 1934-46	5.6	28
43	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. <i>Human Genetics</i> , 2014 , 133, 481-97	6.3	21

42	Identification of new genetic susceptibility loci for breast cancer through consideration of gene-environment interactions. <i>Genetic Epidemiology</i> , 2014 , 38, 84-93	2.6	24
41	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. <i>Carcinogenesis</i> , 2014 , 35, 1012-9	4.6	121
40	Consortium analysis of gene and gene-folate interactions in purine and pyrimidine metabolism pathways with ovarian carcinoma risk. <i>Molecular Nutrition and Food Research</i> , 2014 , 58, 2023-35	5.9	8
39	Alcohol consumption and survival after a breast cancer diagnosis: a literature-based meta-analysis and collaborative analysis of data for 29,239 cases. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 934-45	4	29
38	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
37	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
36	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014 , 23, 6034-46	5.6	11
35	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	8.3	12
34	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37
33	Gene-environment interaction involving recently identified colorectal cancer susceptibility Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 1824-33	4	40
32	No evidence of gene-calcium interactions from genome-wide analysis of colorectal cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 2971-6	4	9
31	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. <i>PLoS Genetics</i> , 2014 , 10, e1004285	6	38
30	Genome-wide diet-gene interaction analyses for risk of colorectal cancer. <i>PLoS Genetics</i> , 2014 , 10, e1004228	4.28	66
29	Variation in NF- κ B signaling pathways and survival in invasive epithelial ovarian cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 1421-7	4	11
28	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014 , 5, 4051	17.4	13
27	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014 , 23, 6096-111	5.6	48
26	Post-GWAS gene-environment interplay in breast cancer: results from the Breast and Prostate Cancer Cohort Consortium and a meta-analysis on 79,000 women. <i>Human Molecular Genetics</i> , 2014 , 23, 5260-70	5.6	30
25	GWAS-identified common variants for obesity are not associated with the risk of developing colorectal cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 1125-8	4	3

24	Repeat polymorphisms in ESR2 and AR and colorectal cancer risk and prognosis: results from a German population-based case-control study. <i>BMC Cancer</i> , 2014 , 14, 817	4.8	13
23	Risk of ovarian cancer and the NF- κ B pathway: genetic association with IL1A and TNFSF10. <i>Cancer Research</i> , 2014 , 74, 852-61	10.1	36
22	Large-scale evaluation of common variation in regulatory T cell-related genes and ovarian cancer outcome. <i>Cancer Immunology Research</i> , 2014 , 2, 332-40	12.5	20
21	Diagnostic, prognostic, and treatment monitoring value of plasma X in patients with metastatic breast cancer.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 37-37	2.2	
20	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013 , 45, 362-70, 370e1-2	36.3	267
19	Fine-scale mapping of the FGFR2 breast cancer risk locus: putative functional variants differentially bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013 , 93, 1046-60	11	80
18	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, 371-84, 384e1-2	36.3	422
17	Confirmation of the reduction of hormone replacement therapy-related breast cancer risk for carriers of the HSD17B1_937_G variant. <i>Breast Cancer Research and Treatment</i> , 2013 , 138, 543-8	4.4	9
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	11	167
15	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013 , 45, 392-8, 398e1-2	36.3	327
14	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013 , 45, 353-61, 361e1-2	36.3	813
13	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genome-wide interaction study. <i>Endocrine-Related Cancer</i> , 2013 , 20, 875-87	5.7	19
12	Colorectal cancer risk associated with hormone use varies by expression of estrogen receptor- β . <i>Cancer Research</i> , 2013 , 73, 3306-15	10.1	36
11	Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors. <i>PLoS Genetics</i> , 2013 , 9, e1003284	6	112
10	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, 5056-64	5.6	107
9	Tubal ligation and risk of ovarian cancer subtypes: a pooled analysis of case-control studies. <i>International Journal of Epidemiology</i> , 2013 , 42, 579-89	7.8	122
8	Analysis of over 10,000 Cases finds no association between previously reported candidate polymorphisms and ovarian cancer outcome. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013 , 22, 987-92	4	20
7	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013 , 4, 1627	17.4	85

6	The UGT1A6_19_GG genotype is a breast cancer risk factor. <i>Frontiers in Genetics</i> , 2013 , 4, 104	4.5	7
5	Effect of type 2 diabetes predisposing genetic variants on colorectal cancer risk. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2012 , 97, E845-51	5.6	43
4	Shared ancestral susceptibility to colorectal cancer and other nutrition related diseases. <i>BMC Medical Genetics</i> , 2012 , 13, 94	2.1	4
3	Copy number variations of GSTT1 and GSTM1, colorectal cancer risk and possible effect modification of cigarette smoking and menopausal hormone therapy. <i>International Journal of Cancer</i> , 2012 , 131, E841-8	7.5	10
2	A comprehensive investigation on common polymorphisms in the MDR1/ABCB1 transporter gene and susceptibility to colorectal cancer. <i>PLoS ONE</i> , 2012 , 7, e32784	3.7	27
1	Modification of menopausal hormone therapy-associated colorectal cancer risk by polymorphisms in sex steroid signaling, metabolism and transport related genes. <i>Endocrine-Related Cancer</i> , 2011 , 18, 371-84	5.7	21