

Anja Rudolph

List of Publications by Year in descending order

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Version: 2024-02-01

132
papers

12,106
citations

41627

51
h-index

34195

103
g-index

132
all docs

132
docs citations

132
times ranked

18745
citing authors

#	ARTICLE	IF	CITATIONS
1	Real-World Therapy with Pembrolizumab: Outcomes and Surrogate Endpoints for Predicting Survival in Advanced Melanoma Patients in Germany. <i>Cancers</i> , 2022, 14, 1804.	1.7	4
2	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.	2.3	19
3	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
4	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.	1.1	4
5	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
6	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	75
7	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
8	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
9	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
10	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
11	Genistein and enterolactone in relation to Ki67 expression and HER2 status in postmenopausal breast cancer patients. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1700449.	1.5	13
12	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	1.1	67
13	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
14	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017, 19, 119.	2.2	43
15	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
16	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
17	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	1.1	12
18	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 884-895.	0.9	71

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19	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
20	Plasma hyaluronic acid level as a prognostic and monitoring marker of metastatic breast cancer. <i>International Journal of Cancer</i> , 2016, 138, 2499-2509.	2.3	31
21	<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
22	Patient survival and tumor characteristics associated with <i>CHEK2</i> :p.I157T findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98.	2.2	39
23	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
24	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.	1.2	33
25	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016, 135, 741-756.	1.8	19
26	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	2.2	43
27	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
28	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 1619-1630.	0.9	111
29	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through <i>FGF10</i> and <i>MRPS30</i> Regulation. <i>American Journal of Human Genetics</i> , 2016, 99, 903-911.	2.6	59
30	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating <i>IGFBP5</i> expression. <i>Human Molecular Genetics</i> , 2016, 25, 3863-3876.	1.4	33
31	A splicing variant of <i>TERT</i> identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. <i>International Journal of Cancer</i> , 2016, 139, 2646-2654.	2.3	7
32	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
33	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
34	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
35	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
36	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.	2.2	56

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37	Relationship between menopausal hormone therapy and mortality after breast cancer The MARIE study, a prospective case cohort. <i>International Journal of Cancer</i> , 2016, 138, 2098-2108.	2.3	10
38	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016, 34, 2750-2760.	0.8	152
39	Gene-environment interaction and risk of breast cancer. <i>British Journal of Cancer</i> , 2016, 114, 125-133.	2.9	147
40	CYP24A1 variant modifies the association between use of oestrogen plus progestogen therapy and colorectal cancer risk. <i>British Journal of Cancer</i> , 2016, 114, 221-229.	2.9	18
41	Circulating miRNAs with prognostic value in metastatic breast cancer and for early detection of metastasis. <i>Carcinogenesis</i> , 2016, 37, 461-470.	1.3	122
42	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, 780-790.	1.1	10
43	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, 138-153.	1.3	19
44	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
45	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.	1.5	94
46	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
47	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
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	Evidence of a genetic link between endometriosis and ovarian cancer. <i>Fertility and Sterility</i> , 2016, 105, 35-43.e10.	0.5	37
50	Genome-Wide Interaction Analyses between Genetic Variants and Alcohol Consumption and Smoking for Risk of Colorectal Cancer. <i>PLoS Genetics</i> , 2016, 12, e1006296.	1.5	38
51	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	1.1	26
52	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.	0.8	5
53	Association of circulating inflammatory biomarkers and dietary inflammation potential with postmenopausal breast cancer prognosis.. <i>Journal of Clinical Oncology</i> , 2016, 34, 1566-1566.	0.8	0
54	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.	2.3	34

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55	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
56	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
57	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. Breast Cancer Research, 2015, 17, 110.	2.2	19
58	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
59	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
60	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
61	Dietary inflammation potential and postmenopausal breast cancer risk in a German case-control study. Breast, 2015, 24, 491-496.	0.9	61
62	Mendelian randomization study of height and risk of colorectal cancer. International Journal of Epidemiology, 2015, 44, 662-672.	0.9	55
63	Mendelian Randomization Study of Body Mass Index and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1024-1031.	1.1	67
64	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	1.4	40
65	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
66	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
67	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
68	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
69	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
70	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1574-1584.	1.1	28
71	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
72	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56

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73	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. <i>Gynecologic Oncology</i> , 2015, 136, 542-548.	0.6	15
74	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
75	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.	2.2	20
76	Statin Use and Survival After Colorectal Cancer: The Importance of Comprehensive Confounder Adjustment. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv045.	3.0	91
77	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.	3.8	171
78	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015, 6, 8234.	5.8	63
79	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
80	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. <i>Human Genetics</i> , 2015, 134, 1249-1262.	1.8	28
81	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, 1341-1353.	1.3	24
82	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015, 24, 5955-5964.	1.4	68
83	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
84	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
85	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
86	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
87	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 308-316.	1.1	22
88	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). <i>Journal of Genetics and Genome Research</i> , 2015, 2, .	0.3	25
89	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	1.1	49
90	Gene-Environment Interaction Involving Recently Identified Colorectal Cancer Susceptibility Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1824-1833.	1.1	48

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91	No Evidence of Gene–Calcium Interactions from Genome-Wide Analysis of Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 2971-2976.	1.1	9
92	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	1.5	39
93	Genome-Wide Diet-Gene Interaction Analyses for Risk of Colorectal Cancer. <i>PLoS Genetics</i> , 2014, 10, e1004228.	1.5	81
94	Variation in NF- κ B Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1421-1427.	1.1	13
95	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
96	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
97	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, 5260-5270.	1.4	37
98	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, 1125-1128.	1.1	3
99	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.	1.1	16
100	Risk of Ovarian Cancer and the NF- κ B Pathway: Genetic Association with <i>IL1A</i> and <i>TNFSF10</i> . <i>Cancer Research</i> , 2014, 74, 852-861.	0.4	48
101	Large-Scale Evaluation of Common Variation in Regulatory T Cell–Related Genes and Ovarian Cancer Outcome. <i>Cancer Immunology Research</i> , 2014, 2, 332-340.	1.6	21
102	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
103	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. <i>Human Genetics</i> , 2014, 133, 481-497.	1.8	23
104	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Gene–Environment Interactions. <i>Genetic Epidemiology</i> , 2014, 38, 84-93.	0.6	28
105	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. <i>Carcinogenesis</i> , 2014, 35, 1012-1019.	1.3	145
106	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, 2023-2035.	1.5	16
107	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, 934-945.	1.1	37
108	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548

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109	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	5.8	105
110	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
111	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
112	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.	0.8	0
113	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	9.4	326
114	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, 1046-1060.	2.6	98
115	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
116	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, 543-548.	1.1	10
117	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
118	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	374
119	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	9.4	960
120	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genome-wide interaction study. <i>Endocrine-Related Cancer</i> , 2013, 20, 875-887.	1.6	26
121	Colorectal Cancer Risk Associated with Hormone Use Varies by Expression of Estrogen Receptor- β . <i>Cancer Research</i> , 2013, 73, 3306-3315.	0.4	45
122	Evidence of Gene-Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. <i>PLoS Genetics</i> , 2013, 9, e1003284.	1.5	136
123	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
124	Tubal ligation and risk of ovarian cancer subtypes: a pooled analysis of case-control studies. <i>International Journal of Epidemiology</i> , 2013, 42, 579-589.	0.9	146
125	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, 987-992.	1.1	20
126	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	5.8	98

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127	The UGT1A6_19_GG genotype is a breast cancer risk factor. <i>Frontiers in Genetics</i> , 2013, 4, 104.	1.1	8
128	Effect of Type 2 Diabetes Predisposing Genetic Variants on Colorectal Cancer Risk. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2012, 97, E845-E851.	1.8	56
129	Shared ancestral susceptibility to colorectal cancer and other nutrition related diseases. <i>BMC Medical Genetics</i> , 2012, 13, 94.	2.1	6
130	Copy number variations of <i>GSTT1</i> and <i>GSTM1</i> , colorectal cancer risk and possible effect modification of cigarette smoking and menopausal hormone therapy. <i>International Journal of Cancer</i> , 2012, 131, E841-8.	2.3	10
131	A Comprehensive Investigation on Common Polymorphisms in the MDR1/ABCB1 Transporter Gene and Susceptibility to Colorectal Cancer. <i>PLoS ONE</i> , 2012, 7, e32784.	1.1	30
132	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, 371-384.	1.6	23