Anja Rudolph

List of Publications by Year
in descending order

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132	12,106	36303	30087
papers	citations	51 h-index	103 g-index

132	132	132	17225
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
3	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
4	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
5	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
6	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
7	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
8	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
9	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
10	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
11	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
12	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
13	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	6.2	201
14	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
15	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
16	Association of Aspirin and NSAID Use With Risk of Colorectal Cancer According to Genetic Variants. JAMA - Journal of the American Medical Association, 2015, 313, 1133.	7.4	171
17	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
18	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152

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19	Geneâ€“environment interaction and risk of breast cancer. British Journal of Cancer, 2016, 114, 125-133.	6.4	147
20	Tubal ligation and risk of ovarian cancer subtypes: a pooled analysis of case-control studies. International Journal of Epidemiology, 2013, 42, 579-589.	1.9	146
21	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. Carcinogenesis, 2014, 35, 1012-1019.	2.8	145
22	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
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. Human Molecular Genetics, 2013, 22, 5056-5064.	2.9	130
24	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
25	Circulating miRNAs with prognostic value in metastatic breast cancer and for early detection of metastasis. Carcinogenesis, 2016, 37, 461-470.	2.8	122
26	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	8.4	118
27	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	1.9	111
28	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. Human Molecular Genetics, 2016, 25, 2256-2268.	2.9	106
29	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
30	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
31	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98
32	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
33	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
34	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
35	Statin Use and Survival After Colorectal Cancer: The Importance of Comprehensive Confounder Adjustment. Journal of the National Cancer Institute, 2015, 107, djv045.	6.3	91
36	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2018, 47, 526-536.	1.9	88

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37	Genome-Wide Diet-Gene Interaction Analyses for Risk of Colorectal Cancer. PLoS Genetics, 2014, 10, e1004228.	3.5	81
38	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
39	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
40	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.	6.2	76
41	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
42	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	1.9	71
43	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
44	Mendelian Randomization Study of Body Mass Index and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1024-1031.	2.5	67
45	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
46	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
47	Dietary inflammation potential and postmenopausal breast cancer risk in a German case-control study. Breast, 2015, 24, 491-496.	2.2	61
48	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.	6.2	59
49	Effect of Type 2 Diabetes Predisposing Genetic Variants on Colorectal Cancer Risk. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E845-E851.	3.6	56
50	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
51	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. Breast Cancer Research, 2016, 18, 104.	5.0	56
52	Mendelian randomization study of height and risk of colorectal cancer. International Journal of Epidemiology, 2015, 44, 662-672.	1.9	55
53	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
54	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51

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55	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
56	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
57	Geneâ€“Environment Interaction Involving Recently Identified Colorectal Cancer Susceptibility Loci. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1824-1833.	2.5	48
58	Risk of Ovarian Cancer and the NF-ÎºB Pathway: Genetic Association with IL1A and TNFSF10. Cancer Research, 2014, 74, 852-861.	0.9	48
59	Colorectal Cancer Risk Associated with Hormone Use Varies by Expression of Estrogen Receptor-Î². Cancer Research, 2013, 73, 3306-3315.	0.9	45
60	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
61	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
62	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
63	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
64	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
65	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
66	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
67	Patient survival and tumor characteristics associated with CHEK2:p.I157T â€“ findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	5.0	39
68	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	2.9	38
69	Genome-Wide Interaction Analyses between Genetic Variants and Alcohol Consumption and Smoking for Risk of Colorectal Cancer. PLoS Genetics, 2016, 12, e1006296.	3.5	38
70	Post-GWAS geneâ€“environment interplay in breast cancer: results from the Breast and Prostate Cancer Cohort Consortium and a meta-analysis on 79 000 women. Human Molecular Genetics, 2014, 23, 5260-5270.	2.9	37
71	Alcohol Consumption and Survival after a Breast Cancer Diagnosis: A Literature-Based Meta-analysis and Collaborative Analysis of Data for 29,239 Cases. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 934-945.	2.5	37
72	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.	6.2	37

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73	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	1.0	37
74	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	5.1	34
75	Candidate locus analysis of the TERTâ€“CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	3.8	34
76	Phyto-oestrogens and colorectal cancer risk: a systematic review and doseâ€“response meta-analysis of observational studies. British Journal of Nutrition, 2016, 116, 2115-2128.	2.3	33
77	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.	2.9	33
78	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	2.9	32
79	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	1.8	31
80	Plasma hyaluronic acid level as a prognostic and monitoring marker of metastatic breast cancer. International Journal of Cancer, 2016, 138, 2499-2509.	5.1	31
81	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.	5.0	31
82	A Comprehensive Investigation on Common Polymorphisms in the MDR1/ABCB1 Transporter Gene and Susceptibility to Colorectal Cancer. PLoS ONE, 2012, 7, e32784.	2.5	30
83	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28
84	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.	2.5	28
85	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. Human Genetics, 2015, 134, 1249-1262.	3.8	28
86	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genomeâ€“wide interaction study. Endocrine-Related Cancer, 2013, 20, 875-887.	3.1	26
87	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
88	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
89	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
90	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24

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91	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	2.5	24
92	Modification of menopausal hormone therapy-associated colorectal cancer risk by polymorphisms in sex steroid signaling, metabolism and transport related genes. Endocrine-Related Cancer, 2011, 18, 371-384.	3.1	23
93	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	3.8	23
94	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
95	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	2.5	22
96	Large-Scale Evaluation of Common Variation in Regulatory T Cellâ€"Related Genes and Ovarian Cancer Outcome. Cancer Immunology Research, 2014, 2, 332-340.	3.4	21
97	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	1.8	21
98	Analysis of Over 10,000 Cases Finds No Association between Previously Reported Candidate Polymorphisms and Ovarian Cancer Outcome. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 987-992.	2.5	20
99	SNP-SNP interaction analysis of NF-Î¹B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
100	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. Breast Cancer Research, 2015, 17, 18.	5.0	20
101	Geneâ€"environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	5.1	20
102	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. Breast Cancer Research, 2015, 17, 110.	5.0	19
103	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
104	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	3.3	19
105	Highâ€throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. Journal of Pathology: Clinical Research, 2016, 2, 138-153.	3.0	19
106	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. International Journal of Cancer, 2018, 143, 746-757.	5.1	19
107	CYP24A1 variant modifies the association between use of oestrogen plus progestogen therapy and colorectal cancer risk. British Journal of Cancer, 2016, 114, 221-229.	6.4	18
108	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	12.8	16

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109	Repeat polymorphisms in ESR2 and ARand colorectal cancer risk and prognosis: results from a German population-based case-control study. BMC Cancer, 2014, 14, 817.	2.6	16
110	Consortium analysis of gene and geneâ€“folate interactions in purine and pyrimidine metabolism pathways with ovarian carcinoma risk. Molecular Nutrition and Food Research, 2014, 58, 2023-2035.	3.3	16
111	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	1.4	15
112	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
113	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.	2.8	14
114	Variation in NF-ÎºB Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1421-1427.	2.5	13
115	Genistein and enterolactone in relation to Kiâ€67 expression and HER2 status in postmenopausal breast cancer patients. Molecular Nutrition and Food Research, 2017, 61, 1700449.	3.3	13
116	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
117	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
118	Copy number variations of GSTT1 and GSTM1, colorectal cancer risk and possible effect modification of cigarette smoking and menopausal hormone therapy. International Journal of Cancer, 2012, 131, E841-8.	5.1	10
119	Confirmation of the reduction of hormone replacement therapy-related breast cancer risk for carriers of the HSD17B1_937_G variant. Breast Cancer Research and Treatment, 2013, 138, 543-548.	2.5	10
120	Relationship between menopausal hormone therapy and mortality after breast cancer The MARIEplusstudy, a prospective case cohort. International Journal of Cancer, 2016, 138, 2098-2108.	5.1	10
121	Assessment of Multifactor Geneâ€“Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 780-790.	2.5	10
122	No Evidence of Geneâ€“Calcium Interactions from Genome-Wide Analysis of Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2971-2976.	2.5	9
123	The UGT1A6_19_GG genotype is a breast cancer risk factor. Frontiers in Genetics, 2013, 4, 104.	2.3	8
124	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. Human Genetics, 2016, 135, 137-154.	3.8	8
125	A splicing variant of TERT identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. International Journal of Cancer, 2016, 139, 2646-2654.	5.1	7
126	Shared ancestral susceptibility to colorectal cancer and other nutrition related diseases. BMC Medical Genetics, 2012, 13, 94.	2.1	6

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127	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	1.8	5
128	Prognostic impact of surgery for early-stage invasive breast cancer on breast cancer-specific survival, overall survival, and recurrence risk: a population-based analysis. Breast Cancer Research and Treatment, 2018, 170, 381-390.	2.5	4
129	Real-World Therapy with Pembrolizumab: Outcomes and Surrogate Endpoints for Predicting Survival in Advanced Melanoma Patients in Germany. Cancers, 2022, 14, 1804.	3.7	4
130	GWAS-Identified Common Variants for Obesity Are Not Associated with the Risk of Developing Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1125-1128.	2.5	3
131	Diagnostic, prognostic, and treatment monitoring value of plasma X in patients with metastatic breast cancer.. Journal of Clinical Oncology, 2014, 32, 37-37.	1.6	0
132	Association of circulating inflammatory biomarkers and dietary inflammation potential with postmenopausal breast cancer prognosis.. Journal of Clinical Oncology, 2016, 34, 1566-1566.	1.6	0