## Stig Bojesen

List of Publications by Year in descending order

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6124 6686 30,638 294 83 161 citations h-index g-index papers 326 326 326 36046 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Risk of ulcerative colitis and Crohn's disease in smokers lacks causal evidence. European Journal of Epidemiology, 2022, 37, 735-745.	2.5	5
2	Chronic lymphocytic leukaemia clones are detectable decades before diagnosis. British Journal of Haematology, 2022, 196, 784-787.	1.2	3
3	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
4	AHRR (cg5575921) methylation safely improves specificity of lung cancer screening eligibility criteria: A cohort study. Cancer Epidemiology Biomarkers and Prevention, 2022, , cebp.1059.2021.	1.1	10
5	Epigenetic Regulation of <i>F2RL3</i> Associates With Myocardial Infarction and Platelet Function. Circulation Research, 2022, 130, 384-400.	2.0	10
6	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. Human Molecular Genetics, 2022, 31, 2831-2843.	1.4	4
7	Gene–gene interaction of AhRwith and within the Wntcascade affects susceptibility to lung cancer. European Journal of Medical Research, 2022, 27, 14.	0.9	1
8	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
9	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
10	Development and validation of a model to predict incident chronic liver disease in the general population: The CLivD score. Journal of Hepatology, 2022, 77, 302-311.	1.8	21
11	Self-reported and genetically predicted coffee consumption and smoking in dementia: A Mendelian randomization study. Atherosclerosis, 2022, 348, 36-43.	0.4	8
12	Pre- and Perioperative Inflammatory Biomarkers in Older Patients Resected for Localized Colorectal Cancer: Associations with Complications and Prognosis. Cancers, 2022, 14, 161.	1.7	9
13	A Large-Scale Genome-Wide Gene-Gene Interaction Study of Lung Cancer Susceptibility in Europeans With a Trans-Ethnic Validation in Asians. Journal of Thoracic Oncology, 2022, 17, 974-990.	0.5	18
14	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	3.6	19
15	Allostatic load as predictor of mortality: a cohort study from Lolland-Falster, Denmark. BMJ Open, 2022, 12, e057136.	0.8	5
16	Associations of a breast cancer polygenic risk score with tumor characteristics and survival Journal of Clinical Oncology, 2022, 40, 563-563.	0.8	1
17	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	3.0	45
18	Common Susceptibility Loci for Male Breast Cancer. Journal of the National Cancer Institute, 2021, 113, 453-461.	3.0	12

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19	Evaluating the role of alcohol consumption in breast and ovarian cancer susceptibility using populationâ€based cohort studies and twoâ€sample Mendelian randomization analyses. International Journal of Cancer, 2021, 148, 1338-1350.	2.3	9
20	Integration of multiomic annotation data to prioritize and characterize inflammation and immuneâ€related risk variants in squamous cell lung cancer. Genetic Epidemiology, 2021, 45, 99-114.	0.6	7
21	Causal relationships between body mass index, smoking and lung cancer: Univariable and multivariable Mendelian randomization. International Journal of Cancer, 2021, 148, 1077-1086.	2.3	73
22	Myocardial Ischemia Induced by 5-Fluorouracil: A Prospective Electrocardiographic and Cardiac Biomarker Study. Oncologist, 2021, 26, e403-e413.	1.9	18
23	Comprehensive functional annotation of susceptibility variants identifies genetic heterogeneity between lung adenocarcinoma and squamous cell carcinoma. Frontiers of Medicine, 2021, 15, 275-291.	1.5	21
24	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	2.9	5
25	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
26	Assessing Lung Cancer Absolute Risk Trajectory Based on a Polygenic Risk Model. Cancer Research, 2021, 81, 1607-1615.	0.4	50
27	Reference intervals for 12 clinical laboratory tests in a Danish population: The Lolland-Falster Health Study. Scandinavian Journal of Clinical and Laboratory Investigation, 2021, 81, 104-111.	0.6	2
28	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
29	Breast Cancer Risk Genes — Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
30	Pre-treatment serum vitamin D deficiency is associated with increased inflammatory biomarkers and short overall survival in patients with pancreatic cancer. European Journal of Cancer, 2021, 144, 72-80.	1.3	17
31	Circulating Protein Biomarkers for Use in Pancreatic Ductal Adenocarcinoma Identification. Clinical Cancer Research, 2021, 27, 2592-2603.	3.2	14
32	Heterogeneous contributions of change in population distribution of body mass index to change in obesity and underweight. ELife, $2021, 10, \ldots$	2.8	41
33	Genome-wide association meta-analysis identifies pleiotropic risk loci for aerodigestive squamous cell cancers. PLoS Genetics, 2021, 17, e1009254.	1.5	19
34	Genetic predisposition to long telomeres is associated with increased mortality after melanoma: A study of 2101 melanoma patients from hospital clinics and the general population. Pigment Cell and Melanoma Research, 2021, 34, 946-954.	1.5	4
35	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	1.7	4
36	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	2.6	6

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37	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. Breast Cancer Research, 2021, 23, 86.	2.2	7
38	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
39	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
40	Detection and characterization of lung cancer using cell-free DNA fragmentomes. Nature Communications, 2021, 12, 5060.	5 <b>.</b> 8	161
41	Inflammatory Biomarker Score Identifies Patients with Six-Fold Increased Risk of One-Year Mortality after Pancreatic Cancer. Cancers, 2021, 13, 4599.	1.7	5
42	Worldwide trends in hypertension prevalence and progress in treatment and control from 1990 to 2019: a pooled analysis of 1201 population-representative studies with 104 million participants. Lancet, The, 2021, 398, 957-980.	6.3	1,289
43	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	1.1	19
44	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
45	Response to the letter entitled: Re: Pre-treatment serum vitamin D deficiency is associated with increased inflammatory biomarkers and short overall survival in patients with pancreatic cancer. European Journal of Cancer, 2021, 158, 248-250.	1.3	0
46	Observational and genetic studies of short telomeres and Alzheimer's disease in 67,000 and 152,000 individuals: a Mendelian randomization study. European Journal of Epidemiology, 2020, 35, 147-156.	2.5	36
47	Clinical value of serum hyaluronan and propeptide of type III collagen in patients with pancreatic cancer. International Journal of Cancer, 2020, 146, 2913-2922.	2.3	41
48	Transcriptomeâ€wide association study reveals candidate causal genes for lung cancer. International Journal of Cancer, 2020, 146, 1862-1878.	2.3	33
49	Prognostic Value of Combined Detection of Serum IL6, YKL-40, and C-reactive Protein in Patients with Unresectable Pancreatic Cancer. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 176-184.	1.1	12
50	Genomeâ€wide association study of INDELs identified four novel susceptibility loci associated with lung cancer risk. International Journal of Cancer, 2020, 146, 2855-2864.	2.3	7
51	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
52	Immune-mediated genetic pathways resulting in pulmonary function impairment increase lung cancer susceptibility. Nature Communications, 2020, $11$ , $27$ .	5.8	23
53	Smoking, blood cells and myeloproliferative neoplasms: metaâ€analysis and Mendelian randomization of 2·3 million people. British Journal of Haematology, 2020, 189, 323-334.	1.2	27
54	Low high-density lipoprotein and increased risk of several cancers: 2 population-based cohort studies including 116,728 individuals. Journal of Hematology and Oncology, 2020, 13, 129.	6.9	46

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55	AHRR hypomethylation as an epigenetic marker of smoking history predicts risk of myocardial infarction in former smokers. Atherosclerosis, 2020, 312, 8-15.	0.4	7
56	Loss-of-function polymorphism in IL6R reduces risk of JAK2V617F somatic mutation and myeloproliferative neoplasm: A Mendelian randomization study. EClinicalMedicine, 2020, 21, 100280.	3.2	19
57	Breast cancer risk factors and their effects on survival: a Mendelian randomisation study. BMC Medicine, 2020, 18, 327.	2.3	40
58	Burden of prediabetes, undiagnosed, and poorly or potentially sub-controlled diabetes: Lolland-Falster health study. BMC Public Health, 2020, 20, 1711.	1.2	8
59	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
60	Height and body-mass index trajectories of school-aged children and adolescents from 1985 to 2019 in 200 countries and territories: a pooled analysis of 2181 population-based studies with 65 million participants. Lancet, The, 2020, 396, 1511-1524.	6.3	219
61	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
62	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	5.8	31
63	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2
64	Reply to: Clinical impact of high platelet count and high hematocrit, by Marc Sorigue. Journal of Thrombosis and Haemostasis, 2020, 18, 522-523.	1.9	0
65	Two-fold risk of pneumonia and respiratory mortality in individuals with myeloproliferative neoplasm: A population-based cohort study. EClinicalMedicine, 2020, 21, 100295.	3.2	5
66	Tocilizumab and soluble interleukin-6 receptor in JAK2V617F somatic mutation and myeloproliferative neoplasm. EClinicalMedicine, 2020, 22, 100337.	3.2	2
67	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
68	Incidental lymphopenia and mortality: a prospective cohort study. Cmaj, 2020, 192, E25-E33.	0.9	34
69	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
70	Elevated plasma YKL-40 and risk of infectious disease: a prospective study of 94665 individuals from the general population. Clinical Microbiology and Infection, 2020, 26, 1411.e1-1411.e9.	2.8	8
71	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	1.1	14
72	Association Analysis of Driver Gene–Related Genetic Variants Identified Novel Lung Cancer Susceptibility Loci with 20,871 Lung Cancer Cases and 15,971 Controls. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1423-1429.	1.1	6

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73	Arterial and venous thrombosis by high platelet count and high hematocrit: 108Â521 individuals from the Copenhagen General Population Study. Journal of Thrombosis and Haemostasis, 2019, 17, 1898-1911.	1.9	46
74	Lung Cancer Risk in Never-Smokers of European Descent is Associated With Genetic Variation in the 5p15.33 TERT-CLPTM1Ll Region. Journal of Thoracic Oncology, 2019, 14, 1360-1369.	0.5	27
75	Investigation of Leukocyte Telomere Length and Genetic Variants in Chromosome 5p15.33 as Prognostic Markers in Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1228-1237.	1.1	11
76	Measured and genetically predicted plasma YKL-40 levels and melanoma mortality. European Journal of Cancer, 2019, 121, 74-84.	1.3	3
77	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
78	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
79	Appraising the causal relevance of DNA methylation for risk of lung cancer. International Journal of Epidemiology, 2019, 48, 1493-1504.	0.9	53
80	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
81	Germline <i>BRCA2</i> K3326X and <i>CHEK2</i> I157T mutations increase risk for sporadic pancreatic ductal adenocarcinoma. International Journal of Cancer, 2019, 145, 686-693.	2.3	20
82	Elevated Platelet Count Appears to Be Causally Associated with Increased Risk of Lung Cancer: A Mendelian Randomization Analysis. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 935-942.	1.1	21
83	Physical activity and risk of instant and 28-day case-fatality in myocardial infarction. PLoS ONE, 2019, 14, e0217398.	1.1	6
84	Smoking does not accelerate leucocyte telomere attrition: a meta-analysis of 18 longitudinal cohorts. Royal Society Open Science, 2019, 6, 190420.	1.1	33
85	Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development. Oncotarget, 2019, 10, 1760-1774.	0.8	25
86	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
87	Smoking and Increased White and Red Blood Cells. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 965-977.	1.1	98
88	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
89	AHRR (cg05575921) methylation extent of leukocyte DNA and lung cancer survival. PLoS ONE, 2019, 14, e0211745.	1.1	9
90	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	2.2	24

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91	JAK2-tree: a simple CBC-based decision rule to guide appropriate JAK2 V617F mutation testing. Journal of Clinical Pathology, 2019, 72, 172-176.	1.0	8
92	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
93	Bone marrow mononuclear cell telomere length in acute myeloid leukaemia and highâ€risk myelodysplastic syndrome. European Journal of Haematology, 2019, 102, 218-226.	1.1	6
94	Systematic analyses of regulatory variants in DNase I hypersensitive sites identified two novel lung cancer susceptibility loci. Carcinogenesis, 2019, 40, 432-440.	1.3	5
95	Mononuclear Cell Telomere Attrition Is Associated with Overall Survival after Nonmyeloablative Allogeneic Hematopoietic Cell Transplantation for Hematologic Malignancies. Biology of Blood and Marrow Transplantation, 2019, 25, 496-504.	2.0	4
96	Mendelian Randomization and mediation analysis of leukocyte telomere length and risk of lung and head and neck cancers. International Journal of Epidemiology, 2019, 48, 751-766.	0.9	32
97	Is high vitamin B12 status a cause of lung cancer?. International Journal of Cancer, 2019, 145, 1499-1503.	2.3	58
98	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	0.9	81
99	Secular trends in smoking in relation to prevalent and incident smoking-related disease: A prospective population-based study. Tobacco Induced Diseases, 2019, 17, 72.	0.3	39
100	The <i>BRCA2</i> c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	1.1	19
101	Is smoking heaviness causally associated with alcohol use? A Mendelian randomization study in four European cohorts. International Journal of Epidemiology, 2018, 47, 1098-1105.	0.9	17
102	Genome-wide interaction study of smoking behavior and non-small cell lung cancer risk in Caucasian population. Carcinogenesis, 2018, 39, 336-346.	1.3	29
103	<i>AHRR</i> hypomethylation, lung function, lung function decline and respiratory symptoms. European Respiratory Journal, 2018, 51, 1701512.	3.1	35
104	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.	0.9	88
105	Serum Biomarker Signature-Based Liquid Biopsy for Diagnosis of Early-Stage Pancreatic Cancer. Journal of Clinical Oncology, 2018, 36, 2887-2894.	0.8	108
106	Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. Nature Communications, 2018, 9, 3927.	5.8	43
107	Lymphopenia and risk of infection and infection-related death in 98,344 individuals from a prospective Danish population-based study. PLoS Medicine, 2018, 15, e1002685.	3.9	119
108	Genetic modifiers of radon-induced lung cancer risk: a genome-wide interaction study in former uranium miners. International Archives of Occupational and Environmental Health, 2018, 91, 937-950.	1.1	27

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109	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	5.8	60
110	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
111	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	<b>7</b> 5
112	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	9.4	426
113	TP53 Arg72Pro, mortality after cancer, and all-cause mortality in 105,200 individuals. Scientific Reports, 2017, 7, 336.	1.6	8
114	Shorter leukocyte telomere length is associated with higher risk of infections: a prospective study of 75,309 individuals from the general population. Haematologica, 2017, 102, 1457-1465.	1.7	63
115	Asthma, other atopic conditions and risk of infections in 105 519 general population never and ever smokers. Journal of Internal Medicine, 2017, 282, 254-267.	2.7	25
116	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	9.4	472
117	<i>AHRR</i> (cg05575921) hypomethylation marks smoking behaviour, morbidity and mortality. Thorax, 2017, 72, 646-653.	2.7	147
118	Telomere length and depression: Prospective cohort study and Mendelian randomisation study in 67 306 individuals. British Journal of Psychiatry, 2017, 210, 31-38.	1.7	26
119	Kringle IV Type 2, Not Low Lipoprotein(a), as a Cause of Diabetes: A Novel Genetic Approach Using SNPs Associated Selectively with Lipoprotein(a) Concentrations or with Kringle IV Type 2 Repeats. Clinical Chemistry, 2017, 63, 1866-1876.	1.5	28
120	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
121	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
122	Gene–environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	2.3	20
123	Common breast cancer risk alleles and risk assessment: a study on 35Â441 individuals from the Danish general population. Annals of Oncology, 2017, 28, 175-181.	0.6	6
124	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
125	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	1.1	278
126	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45

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127	Pleiotropy of genetic variants on obesity and smoking phenotypes: Results from the Oncoarray Project of The International Lung Cancer Consortium. PLoS ONE, 2017, 12, e0185660.	1.1	11
128	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	2.2	43
129	The prognostic value of serum CA 19-9 in patients with metastatic colorectal cancer Journal of Clinical Oncology, 2017, 35, e15131-e15131.	0.8	1
130	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. PLoS ONE, 2017, 12, e0177875.	1.1	79
131	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on $6q14.1$ . Oncotarget, 2017, 8, $102769-102782$ .	0.8	9
132	The prognostic value of serum IL-6 and YKL-40 in patients with metastatic colorectal cancer Journal of Clinical Oncology, 2017, 35, e15060-e15060.	0.8	0
133	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.	0.8	31
134	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.	3.9	118
135	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
136	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
137	Inflammatory biomarkers and risk of cancer in 84,000 individuals from the general population. International Journal of Cancer, 2016, 139, 1493-1500.	2.3	73
138	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
139	Patient survival and tumor characteristics associated with CHEK2:p.I157T – findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	2.2	39
140	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	2.2	31
141	Role of inflammatory marker YKL-40 in the diagnosis, prognosis and cause of cardiovascular and liver diseases. Critical Reviews in Clinical Laboratory Sciences, 2016, 53, 396-408.	2.7	50
142	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
143	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.	0.8	21
144	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59

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145	The potential diagnostic value of serum microRNA signature in patients with pancreatic cancer. International Journal of Cancer, 2016, 139, 2312-2324.	2.3	33
146	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	1.4	33
147	Long telomeres and cancer risk among 95 568 individuals from the general population. International Journal of Epidemiology, 2016, 45, 1634-1643.	0.9	90
148	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	1.6	2
149	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.	7.7	157
150	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
151	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast–ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
152	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.	1.6	19
153	Short Telomere Length and Ischemic Heart Disease: Observational and Genetic Studies in 290 022 Individuals. Clinical Chemistry, 2016, 62, 1140-1149.	1.5	93
154	Age- and Tumor Subtype–Specific Breast Cancer Risk Estimates for ⟨i⟩CH⟨/i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩²1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
155	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	1.6	62
156	Observationally and Genetically High YKL-40 and Risk of Venous Thromboembolism in the General Population. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 1030-1036.	1.1	18
157	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.	1.4	106
158	Increased Risk for Other Cancers in Addition to Breast Cancer for <i>CHEK2</i> *1100delC Heterozygotes Estimated From the Copenhagen General Population Study. Journal of Clinical Oncology, 2016, 34, 1208-1216.	0.8	97
159	No evidence that protein truncating variants in <i>BRIP1</i> ii>are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
160	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
161	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.	1.8	8
162	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	3.0	77

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163	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
164	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
165	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.	2.3	34
166	Observational and genetic plasma <scp>YKL</scp> â€40 and cancer in 96,099 individuals from the general population. International Journal of Cancer, 2015, 137, 2696-2704.	2.3	20
167	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
168	SNP-SNP interaction analysis of NF-κB signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
169	lgE and risk of cancer in 37 747 individuals from the general population. Annals of Oncology, 2015, 26, 1784-1790.	0.6	37
170	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
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