

Sara Lindström

List of Publications by Year in descending order

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Version: 2024-02-01

164
papers

18,691
citations

20815

60
h-index

16650

123
g-index

171
all docs

171
docs citations

171
times ranked

24784
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic variants associated with circulating C-reactive protein levels and colorectal cancer survival: Sex-specific and lifestyle factors specific associations. <i>International Journal of Cancer</i> , 2022, 150, 1447-1454.	5.1	2
2	Oral postmenopausal hormone therapy and genetic risk on venous thromboembolism: gene-hormone interaction results from a large prospective cohort study. <i>Menopause</i> , 2022, 29, 293-303.	2.0	4
3	Cross-ancestry Genome-wide Association Studies of Sex Hormone Concentrations in Pre- and Postmenopausal Women. <i>Endocrinology</i> , 2022, 163, .	2.8	10
4	A Genome-Wide Gene-Based Gene-Environment Interaction Study of Breast Cancer in More than 90,000 Women. <i>Cancer Research Communications</i> , 2022, 2, 211-219.	1.7	6
5	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. <i>Breast Cancer Research</i> , 2022, 24, 27.	5.0	15
6	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. <i>Scientific Reports</i> , 2022, 12, 6199.	3.3	2
7	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021, 113, 329-337.	6.3	45
8	Association of Interactions Between Mammographic Density Phenotypes and Established Risk Factors With Breast Cancer Risk, by Tumor Subtype and Menopausal Status. <i>American Journal of Epidemiology</i> , 2021, 190, 44-58.	3.4	4
9	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. <i>Nature Genetics</i> , 2021, 53, 65-75.	21.4	264
10	A Genome-Wide Association Study of Childhood Body Fatness. <i>Obesity</i> , 2021, 29, 446-453.	3.0	8
11	Genetically Predicted Circulating C-Reactive Protein Concentration and Colorectal Cancer Survival: A Mendelian Randomization Consortium Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1349-1358.	2.5	6
12	Association between post-treatment circulating biomarkers of inflammation and survival among stage II-III colorectal cancer patients. <i>British Journal of Cancer</i> , 2021, 125, 806-815.	6.4	12
13	Risk of Late-Onset Breast Cancer in Genetically Predisposed Women. <i>Journal of Clinical Oncology</i> , 2021, 39, 3430-3440.	1.6	21
14	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100041.	1.7	6
15	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. <i>Journal of Clinical Oncology</i> , 2021, 39, 2564-2573.	1.6	47
16	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
17	Germline Pathogenic Variants in Cancer Predisposition Genes Among Women With Invasive Lobular Carcinoma of the Breast. <i>Journal of Clinical Oncology</i> , 2021, 39, 3918-3926.	1.6	22
18	Association Between Genetic Predictors for C-Reactive Protein and Venous Thromboembolism With Severe Adverse Coronavirus Disease 2019 Outcomes. , 2021, 3, e0602.		0

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19	Assessment of interactions between 205 breast cancer susceptibility loci and 13 established risk factors in relation to breast cancer risk, in the Breast Cancer Association Consortium. <i>International Journal of Epidemiology</i> , 2020, 49, 216-232.	1.9	21
20	Association Between Chronic Hepatitis C Virus Infection and Myocardial Infarction Among People Living With HIV in the United States. <i>American Journal of Epidemiology</i> , 2020, 189, 554-563.	3.4	4
21	The Use of Genetic Correlation and Mendelian Randomization Studies to Increase Our Understanding of Relationships between Complex Traits. <i>Current Epidemiology Reports</i> , 2020, 7, 104-112.	2.4	21
22	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	1.3	32
23	Allergy, asthma, and the risk of breast and prostate cancer: a Mendelian randomization study. <i>Cancer Causes and Control</i> , 2020, 31, 273-282.	1.8	14
24	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	1.4	162
25	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. <i>Nature Genetics</i> , 2019, 51, 1574-1579.	21.4	152
26	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	3.3	5
27	A large-scale exome array analysis of venous thromboembolism. <i>Genetic Epidemiology</i> , 2019, 43, 449-457.	1.3	22
28	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
29	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. <i>Breast Cancer Research</i> , 2019, 21, 68.	5.0	31
30	Association between genetically predicted polycystic ovary syndrome and ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2019, 48, 822-830.	1.9	22
31	Genetic associations of breast and prostate cancer are enriched for regulatory elements identified in disease-related tissues. <i>Human Genetics</i> , 2019, 138, 1091-1104.	3.8	7
32	Evaluation of significant genome-wide association studies risk SNPs in young breast cancer patients. <i>PLoS ONE</i> , 2019, 14, e0216997.	2.5	4
33	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	12.8	90
34	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	6.4	52
35	Efficient cross-trait penalized regression increases prediction accuracy in large cohorts using secondary phenotypes. <i>Nature Communications</i> , 2019, 10, 569.	12.8	50
36	Genetic Determinants of Lipids and Cardiovascular Disease Outcomes. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002711.	3.6	83

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37	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	6.2	711
38	Is Schizophrenia a Risk Factor for Breast Cancer? Evidence From Genetic Data. <i>Schizophrenia Bulletin</i> , 2019, 45, 1251-1256.	4.3	24
39	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 795-806.	1.9	81
40	A comprehensive analysis of polymorphic variants in steroid hormone and insulin-like growth factor metabolism and risk of <i>in situ</i> breast cancer: Results from the Breast and Prostate Cancer Cohort Consortium. <i>International Journal of Cancer</i> , 2018, 142, 1182-1188.	5.1	0
41	Metabolites Associated With the Risk of Incident Venous Thromboembolism: A Metabolomic Analysis. <i>Journal of the American Heart Association</i> , 2018, 7, e010317.	3.7	15
42	Adiposity throughout the life course and risk of venous thromboembolism. <i>Thrombosis Research</i> , 2018, 172, 67-73.	1.7	9
43	Addition of a polygenic risk score, mammographic density, and endogenous hormones to existing breast cancer risk prediction models: A nested case-control study. <i>PLoS Medicine</i> , 2018, 15, e1002644.	8.4	91
44	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , 2018, 50, 928-936.	21.4	652
45	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. <i>Nature Communications</i> , 2018, 9, 2256.	12.8	88
46	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.	21.4	184
47	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
48	Assessing the causal relationship between obesity and venous thromboembolism through a Mendelian Randomization study. <i>Human Genetics</i> , 2017, 136, 897-902.	3.8	46
49	Interactions Between Genome-Wide Significant Genetic Variants and Circulating Concentrations of 25-Hydroxyvitamin D in Relation to Prostate Cancer Risk in the National Cancer Institute BPC3. <i>American Journal of Epidemiology</i> , 2017, 185, 452-464.	3.4	11
50	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
51	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
52	Investigating the genetic relationship between Alzheimer's disease and cancer using GWAS summary statistics. <i>Human Genetics</i> , 2017, 136, 1341-1351.	3.8	46
53	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1427-1435.	2.5	48
54	Improved methods for multi-trait fine mapping of pleiotropic risk loci. <i>Bioinformatics</i> , 2017, 33, 248-255.	4.1	119

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55	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 126-135.	2.5	278
56	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	1.9	45
57	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. <i>BMJ: British Medical Journal</i> , 2017, 359, j4761.	2.3	126
58	Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. <i>PLoS Genetics</i> , 2017, 13, e1006945.	3.5	3
59	A comprehensive survey of genetic variation in 20,691 subjects from four large cohorts. <i>PLoS ONE</i> , 2017, 12, e0173997.	2.5	52
60	Interactions of established risk factors and a GWAS-based genetic risk score on the risk of venous thromboembolism. <i>Thrombosis and Haemostasis</i> , 2016, 116, 705-713.	3.4	15
61	<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.	3.2	174
62	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. <i>JAMA Oncology</i> , 2016, 2, 1295.	7.1	285
63	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.	1.8	21
64	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.9	100
65	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , 2016, 139, 2655-2670.	5.1	43
66	Meta-Analysis of Rare Variant Association Tests in Multiethnic Populations. <i>Genetic Epidemiology</i> , 2016, 40, 57-65.	1.3	9
67	Mendelian randomization study of adiposity-related traits and risk of breast, ovarian, prostate, lung and colorectal cancer. <i>International Journal of Epidemiology</i> , 2016, 45, 896-908.	1.9	124
68	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.	9.4	157
69	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93
70	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016, 7, 10979.	12.8	50
71	Deep targeted sequencing of 12 breast cancer susceptibility regions in 4611 women across four different ethnicities. <i>Breast Cancer Research</i> , 2016, 18, 109.	5.0	6
72	Interactions between breast cancer susceptibility loci and menopausal hormone therapy in relationship to breast cancer in the Breast and Prostate Cancer Cohort Consortium. <i>Breast Cancer Research and Treatment</i> , 2016, 155, 531-540.	2.5	2

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73	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. <i>Human Molecular Genetics</i> , 2016, 25, 1203-1214.	2.9	38
74	Variants in 6q25.1 Are Associated with Mammographic Density in Malaysian Chinese Women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 327-333.	2.5	10
75	Association between Adult Height and Risk of Colorectal, Lung, and Prostate Cancer: Results from Meta-analyses of Prospective Studies and Mendelian Randomization Analyses. <i>PLoS Medicine</i> , 2016, 13, e1002118.	8.4	69
76	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	5.0	26
77	ABO blood group alleles and prostate cancer risk: Results from the breast and prostate cancer cohort consortium (BPC3). <i>Prostate</i> , 2015, 75, 1677-1681.	2.3	14
78	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv279.	6.3	152
79	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	428
80	Association of breast cancer risk <i>loci</i> with breast cancer survival. <i>International Journal of Cancer</i> , 2015, 137, 2837-2845.	5.1	33
81	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	2.9	40
82	A Genome-wide Pleiotropy Scan for Prostate Cancer Risk. <i>European Urology</i> , 2015, 67, 649-657.	1.9	21
83	Vitamin D-Associated Genetic Variation and Risk of Breast Cancer in the Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 627-630.	2.5	20
84	Circulating vitamin D, vitamin D-related genetic variation, and risk of fatal prostate cancer in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. <i>Cancer</i> , 2015, 121, 1949-1956.	4.1	50
85	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	21.4	513
86	Circadian clock genes and risk of fatal prostate cancer. <i>Cancer Causes and Control</i> , 2015, 26, 25-33.	1.8	39
87	Genetic risk variants associated with in situ breast cancer. <i>Breast Cancer Research</i> , 2015, 17, 82.	5.0	25
88	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2015, 24, 5356-5366.	2.9	128
89	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. <i>Human Molecular Genetics</i> , 2015, 24, 5603-5618.	2.9	50
90	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	56

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91	Premenopausal plasma carotenoids, fluorescent oxidation products, and subsequent breast cancer risk in the nurses' health studies. <i>Breast Cancer Research and Treatment</i> , 2015, 151, 415-425.	2.5	21
92	Two susceptibility loci identified for prostate cancer aggressiveness. <i>Nature Communications</i> , 2015, 6, 6889.	12.8	88
93	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. <i>American Journal of Human Genetics</i> , 2015, 96, 532-542.	6.2	222
94	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. <i>Cancer Research</i> , 2015, 75, 2457-2467.	0.9	55
95	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	6.2	1,098
96	Partitioning heritability by functional annotation using genome-wide association summary statistics. <i>Nature Genetics</i> , 2015, 47, 1228-1235.	21.4	2,045
97	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.	21.4	357
98	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	6.3	99
99	Cross Cancer Genomic Investigation of Inflammation Pathway for Five Common Cancers: Lung, Ovary, Prostate, Breast, and Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv246.	6.3	63
100	Genome-Wide Association Study of Prostate Cancer-Specific Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1796-1800.	2.5	27
101	A Genome-Wide Pleiotropy Scan Does Not Identify New Susceptibility Loci for Estrogen Receptor Negative Breast Cancer. <i>PLoS ONE</i> , 2014, 9, e85955.	2.5	8
102	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. <i>PLoS Genetics</i> , 2014, 10, e1004722.	3.5	475
103	Fine-Mapping the HOXB Region Detects Common Variants Tagging a Rare Coding Allele: Evidence for Synthetic Association in Prostate Cancer. <i>PLoS Genetics</i> , 2014, 10, e1004129.	3.5	34
104	Additive Interactions Between Susceptibility Single-Nucleotide Polymorphisms Identified in Genome-Wide Association Studies and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. <i>American Journal of Epidemiology</i> , 2014, 180, 1018-1027.	3.4	36
105	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. <i>Human Molecular Genetics</i> , 2014, 23, 6616-6633.	2.9	90
106	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.	2.9	37
107	Premenopausal Plasma Ferritin Levels, HFE Polymorphisms, and Risk of Breast Cancer in the Nurses' Health Study II. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 516-524.	2.5	11
108	Genome-wide interaction study of smoking and bladder cancer risk. <i>Carcinogenesis</i> , 2014, 35, 1737-1744.	2.8	50

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109	Genome-wide association study identifies multiple loci associated with bladder cancer risk. <i>Human Molecular Genetics</i> , 2014, 23, 1387-1398.	2.9	137
110	Prostate Cancer (PCa) Risk Variants and Risk of Fatal PCa in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. <i>European Urology</i> , 2014, 65, 1069-1075.	1.9	75
111	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. <i>Cancer Research</i> , 2014, 74, 5808-5818.	0.9	24
112	Androgen Receptor CAG Repeat Polymorphism and Risk of TMPRSS2:ERG-Positive Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 2027-2031.	2.5	28
113	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. <i>Nature Communications</i> , 2014, 5, 5260.	12.8	123
114	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. <i>Nature Communications</i> , 2014, 5, 5303.	12.8	109
115	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	21.4	408
116	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. <i>Human Molecular Genetics</i> , 2013, 22, 4239-4239.	2.9	2
117	Insulin-like growth factor pathway genes and blood concentrations, dietary protein and risk of prostate cancer in the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). <i>International Journal of Cancer</i> , 2013, 133, 495-504.	5.1	28
118	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	21.4	374
119	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. <i>Nature Genetics</i> , 2013, 45, 385-391.	21.4	492
120	A genome-wide association study to identify genetic susceptibility loci that modify ductal and lobular postmenopausal breast cancer risk associated with menopausal hormone therapy use: a two-stage design with replication. <i>Breast Cancer Research and Treatment</i> , 2013, 138, 529-542.	2.5	18
121	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.	3.1	26
122	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. <i>Human Molecular Genetics</i> , 2013, 22, 408-415.	2.9	118
123	Plasma Carotenoid- and Retinol-Weighted Multi-SNP Scores and Risk of Breast Cancer in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 927-936.	2.5	15
124	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. <i>Human Molecular Genetics</i> , 2013, 22, 2520-2528.	2.9	100
125	Genetic Variation in the Vitamin D Pathway in Relation to Risk of Prostate Cancer—Results from the Breast and Prostate Cancer Cohort Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 688-696.	2.5	36
126	A Nonparametric Test to Detect Quantitative Trait Loci Where the Phenotypic Distribution Differs by Genotypes. <i>Genetic Epidemiology</i> , 2013, 37, 323-333.	1.3	26

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127	An Absolute Risk Model to Identify Individuals at Elevated Risk for Pancreatic Cancer in the General Population. <i>PLoS ONE</i> , 2013, 8, e72311.	2.5	120
128	Informed Conditioning on Clinical Covariates Increases Power in Case-Control Association Studies. <i>PLoS Genetics</i> , 2012, 8, e1003032.	3.5	78
129	Common Breast Cancer Susceptibility Variants in <i>LSP1</i> and <i>RAD51L1</i> Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1156-1166.	2.5	101
130	Association of Type 2 Diabetes Susceptibility Variants With Advanced Prostate Cancer Risk in the Breast and Prostate Cancer Cohort Consortium. <i>American Journal of Epidemiology</i> , 2012, 176, 1121-1129.	3.4	67
131	Identification of a novel percent mammographic density locus at 12q24. <i>Human Molecular Genetics</i> , 2012, 21, 3299-3305.	2.9	31
132	Replication of Five Prostate Cancer Loci Identified in an Asian Population—Results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 212-216.	2.5	23
133	Prediction of breast cancer risk by genetic risk factors, overall and by hormone receptor status. <i>Journal of Medical Genetics</i> , 2012, 49, 601-608.	3.2	58
134	Mammographic Breast Density and Breast Cancer: Evidence of a Shared Genetic Basis. <i>Cancer Research</i> , 2012, 72, 1478-1484.	0.9	54
135	Interactions Between Genome-wide Significant Genetic Variants and Circulating Concentrations of Insulin-like Growth Factor 1, Sex Hormones, and Binding Proteins in Relation to Prostate Cancer Risk in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. <i>American Journal of Epidemiology</i> , 2012, 175, 926-935.	3.4	16
136	Common Genetic Variants in Prostate Cancer Risk Prediction—Results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 437-444.	2.5	51
137	Vitamin D-Related Genetic Variation, Plasma Vitamin D, and Risk of Lethal Prostate Cancer: A Prospective Nested Case-Control Study. <i>Journal of the National Cancer Institute</i> , 2012, 104, 690-699.	6.3	196
138	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012, 21, 5373-5384.	2.9	168
139	Genetic variation in the toll-like receptor 4 and prostate cancer incidence and mortality. <i>Prostate</i> , 2012, 72, 209-216.	2.3	22
140	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptor-Positive, Lower Grade Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 2222-2231.	2.5	27
141	Interactions Between Genetic Variants and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. <i>Journal of the National Cancer Institute</i> , 2011, 103, 1252-1263.	6.3	147
142	A common variant at the <i>TERT-CLPTM1L</i> locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	21.4	279
143	<i>N-Acetyltransferase 2</i> Polymorphisms, Tobacco Smoking, and Breast Cancer Risk in the Breast and Prostate Cancer Cohort Consortium. <i>American Journal of Epidemiology</i> , 2011, 174, 1316-1322.	3.4	31
144	Common variants in <i>ZNF365</i> are associated with both mammographic density and breast cancer risk. <i>Nature Genetics</i> , 2011, 43, 185-187.	21.4	109

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145	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. <i>Nature Genetics</i> , 2011, 43, 785-791.	21.4	265
146	Genome-wide association study identifies new prostate cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2011, 20, 3867-3875.	2.9	160
147	Commentary: Averaged or Stratified Measures of Risk Profile Discrimination. <i>Epidemiology</i> , 2011, 22, 813-814.	2.7	0
148	Characterizing Associations and SNP-Environment Interactions for GWAS-Identified Prostate Cancer Risk Markers—Results from BPC3. <i>PLoS ONE</i> , 2011, 6, e17142.	2.5	57
149	Sequence Variants in the TLR4 and TLR6-1-10 Genes and Prostate Cancer Risk. Results Based on Pooled Analysis from Three Independent Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 873-876.	2.5	32
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