Sara LindstrÃ¶m

List of Publications by Year
in descending order

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164 papers	18,691 citations	23879 60 h-index	18944 123 g-index
171 all docs	171 docs citations	171 times ranked	27208 citing authors

#	Article	IF	Citations
1	Genetic variants associated with circulating Câ€reactive protein levels and colorectal cancer survival: Sexâ€specific and lifestyle factors specific associations. International Journal of Cancer, 2022, 150, 1447-1454.	2.3	2
2	Oral postmenopausal hormone therapy and genetic risk on venous thromboembolism: gene-hormone interaction results from a large prospective cohort study. Menopause, 2022, 29, 293-303.	0.8	4
3	Cross-ancestry Genome-wide Association Studies of Sex Hormone Concentrations in Pre- and Postmenopausal Women. Endocrinology, 2022, 163, .	1.4	10
4	A Genome-Wide Gene-Based Geneâ€"Environment Interaction Study of Breast Cancer in More than 90,000 Women. Cancer Research Communications, 2022, 2, 211-219.	0.7	6
5	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. Breast Cancer Research, 2022, 24, 27.	2.2	15
6	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199.	1.6	2
7	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
8	Association of Interactions Between Mammographic Density Phenotypes and Established Risk Factors With Breast Cancer Risk, by Tumor Subtype and Menopausal Status. American Journal of Epidemiology, 2021, 190, 44-58.	1.6	4
9	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
10	A Genomeâ€Wide Association Study of Childhood Body Fatness. Obesity, 2021, 29, 446-453.	1.5	8
11	Genetically Predicted Circulating C-Reactive Protein Concentration and Colorectal Cancer Survival: A Mendelian Randomization Consortium Study. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1349-1358.	1.1	6
12	Association between post-treatment circulating biomarkers of inflammation and survival among stage IIâ€"III colorectal cancer patients. British Journal of Cancer, 2021, 125, 806-815.	2.9	12
13	Risk of Late-Onset Breast Cancer in Genetically Predisposed Women. Journal of Clinical Oncology, 2021, 39, 3430-3440.	0.8	21
14	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.0	6
15	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. Journal of Clinical Oncology, 2021, 39, 2564-2573.	0.8	47
16	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
17	Germline Pathogenic Variants in Cancer Predisposition Genes Among Women With Invasive Lobular Carcinoma of the Breast. Journal of Clinical Oncology, 2021, 39, 3918-3926.	0.8	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. International Journal of Epidemiology, 2020, 49, 216-232.	0.9	21
20	Association Between Chronic Hepatitis C Virus Infection and Myocardial Infarction Among People Living With HIV in the United States. American Journal of Epidemiology, 2020, 189, 554-563.	1.6	4
21	The Use of Genetic Correlation and Mendelian Randomization Studies to Increase Our Understanding of Relationships between Complex Traits. Current Epidemiology Reports, 2020, 7, 104-112.	1.1	21
22	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
23	Allergy, asthma, and the risk of breast and prostate cancer: a Mendelian randomization study. Cancer Causes and Control, 2020, 31, 273-282.	0.8	14
24	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
25	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. Nature Genetics, 2019, 51, 1574-1579.	9.4	152
26	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
27	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
28	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
29	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. Breast Cancer Research, 2019, 21, 68.	2.2	31
30	Association between genetically predicted polycystic ovary syndrome and ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2019, 48, 822-830.	0.9	22
31	Genetic associations of breast and prostate cancer are enriched for regulatory elements identified in disease-related tissues. Human Genetics, 2019, 138, 1091-1104.	1.8	7
32	Evaluation of significant genome-wide association studies risk â€" SNPs in young breast cancer patients. PLoS ONE, 2019, 14, e0216997.	1.1	4
33	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
34	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
35	Efficient cross-trait penalized regression increases prediction accuracy in large cohorts using secondary phenotypes. Nature Communications, 2019, 10, 569.	5.8	50
36	Genetic Determinants of Lipids and Cardiovascular Disease Outcomes. Circulation Genomic and Precision Medicine, 2019, 12, e002711.	1.6	83

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37	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
38	Is Schizophrenia a Risk Factor for Breast Cancer?â€"Evidence From Genetic Data. Schizophrenia Bulletin, 2019, 45, 1251-1256.	2.3	24
39	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
40	A comprehensive analysis of polymorphic variants in steroid hormone and insulinâ€like growth factorâ€1 metabolism and risk of in situ breast cancer: Results from the Breast and Prostate Cancer Cohort Consortium. International Journal of Cancer, 2018, 142, 1182-1188.	2.3	0
41	Metabolites Associated With the Risk of Incident Venous Thromboembolism: A Metabolomic Analysis. Journal of the American Heart Association, 2018, 7, e010317.	1.6	15
42	Adiposity throughout the life course and risk of venous thromboembolism. Thrombosis Research, 2018, 172, 67-73.	0.8	9
43	Addition of a polygenic risk score, mammographic density, and endogenous hormones to existing breast cancer risk prediction models: A nested caseâ€"control study. PLoS Medicine, 2018, 15, e1002644.	3.9	91
44	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
45	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
46	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
47	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
48	Assessing the causal relationship between obesity and venous thromboembolism through a Mendelian Randomization study. Human Genetics, 2017, 136, 897-902.	1.8	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. American Journal of Epidemiology, 2017, 185, 452-464.	1.6	11
50	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
51	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
52	Investigating the genetic relationship between Alzheimerâ€™s disease and cancer using GWAS summary statistics. Human Genetics, 2017, 136, 1341-1351.	1.8	46
53	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	1.1	48
54	Improved methods for multi-trait fine mapping of pleiotropic risk loci. Bioinformatics, 2017, 33, 248-255.	1.8	119

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55	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
56	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
57	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. BMJ: British Medical Journal, 2017, 359, j4761.	2.4	126
58	Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. PLoS Genetics, 2017, 13, e1006945.	1.5	3
59	A comprehensive survey of genetic variation in 20,691 subjects from four large cohorts. PLoS ONE, 2017, 12, e0173997.	1.1	52
60	Interactions of established risk factors and a GWAS-based genetic risk score on the risk of venous thromboembolism. Thrombosis and Haemostasis, 2016, 116, 705-713.	1.8	15
61	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
62	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	3.4	285
63	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
64	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.4	100
65	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	2.3	43
66	Metaâ€Analysis of Rare Variant Association Tests in Multiethnic Populations. Genetic Epidemiology, 2016, 40, 57-65.	0.6	9
67	Mendelian randomization study of adiposity-related traits and risk of breast, ovarian, prostate, lung and colorectal cancer. International Journal of Epidemiology, 2016, 45, 896-908.	0.9	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. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
69	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
70	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
71	Deep targeted sequencing of 12 breast cancer susceptibility regions in 4611 women across four different ethnicities. Breast Cancer Research, 2016, 18, 109.	2.2	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. Breast Cancer Research and Treatment, 2016, 155, 531-540.	1.1	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. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
74	Variants in 6q25.1 Are Associated with Mammographic Density in Malaysian Chinese Women. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 327-333.	1.1	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. PLoS Medicine, 2016, 13, e1002118.	3.9	69
76	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
77	ABO blood group alleles and prostate cancer risk: Results from the breast and prostate cancer cohort consortium (BPC3). Prostate, 2015, 75, 1677-1681.	1.2	14
78	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	3.0	152
79	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
80	Association of breast cancer risk loci with breast cancer survival. International Journal of Cancer, 2015, 137, 2837-2845.	2.3	33
81	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
82	A Genome-wide Pleiotropy Scan for Prostate Cancer Risk. European Urology, 2015, 67, 649-657.	0.9	21
83	Vitamin Dâ€“Associated Genetic Variation and Risk of Breast Cancer in the Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 627-630.	1.1	20
84	Circulating vitamin D, vitamin Dâ€“related genetic variation, and risk of fatal prostate cancer in the <scp>N</scp>ational <scp>C</scp>ancer <scp>I</scp>nstitute <scp>B</scp>reast and <scp>P</scp>rostate <scp>C</scp>ancer <scp>C</scp>ohort <scp>C</scp>onsortium. Cancer, 2015, 121, 1949-1956.	2.0	50
85	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
86	Circadian clock genes and risk of fatal prostate cancer. Cancer Causes and Control, 2015, 26, 25-33.	0.8	39
87	Genetic risk variants associated with in situ breast cancer. Breast Cancer Research, 2015, 17, 82.	2.2	25
88	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	1.4	128
89	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618.	1.4	50
90	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56

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91	Premenopausal plasma carotenoids, fluorescent oxidation products, and subsequent breast cancer risk in the nursesâ€™ health studies. Breast Cancer Research and Treatment, 2015, 151, 415-425.	1.1	21
92	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	5.8	88
93	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	2.6	222
94	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.4	55
95	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
96	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045
97	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
98	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
99	Cross Cancer Genomic Investigation of Inflammation Pathway for Five Common Cancers: Lung, Ovary, Prostate, Breast, and Colorectal Cancer. Journal of the National Cancer Institute, 2015, 107, djv246.	3.0	63
100	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	1.1	27
101	A Genome-Wide â€œPleiotropy Scanâ€•Does Not Identify New Susceptibility Loci for Estrogen Receptor Negative Breast Cancer. PLoS ONE, 2014, 9, e85955.	1.1	8
102	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	1.5	475
103	Fine-Mapping the HOXB Region Detects Common Variants Tagging a Rare Coding Allele: Evidence for Synthetic Association in Prostate Cancer. PLoS Genetics, 2014, 10, e1004129.	1.5	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. American Journal of Epidemiology, 2014, 180, 1018-1027.	1.6	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. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
106	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.	1.4	37
107	Premenopausal Plasma Ferritin Levels, HFE Polymorphisms, and Risk of Breast Cancer in the Nurses' Health Study II. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 516-524.	1.1	11
108	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	1.3	50

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109	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	1.4	137
110	Prostate Cancer (PCa) Risk Variants and Risk of Fatal PCa in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. European Urology, 2014, 65, 1069-1075.	0.9	75
111	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.4	24
112	Androgen Receptor CAG Repeat Polymorphism and Risk of TMPRSS2:ERGâ€“Positive Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2027-2031.	1.1	28
113	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. Nature Communications, 2014, 5, 5260.	5.8	123
114	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	5.8	109
115	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
116	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 4239-4239.	1.4	2
117	Insulinâ€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). International Journal of Cancer, 2013, 133, 495-504.	2.3	28
118	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
119	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	9.4	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. Breast Cancer Research and Treatment, 2013, 138, 529-542.	1.1	18
121	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genomeâ€“wide interaction study. Endocrine-Related Cancer, 2013, 20, 875-887.	1.6	26
122	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. Human Molecular Genetics, 2013, 22, 408-415.	1.4	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. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 927-936.	1.1	15
124	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	1.4	100
125	Genetic Variation in the Vitamin D Pathway in Relation to Risk of Prostate Cancerâ€”Results from the Breast and Prostate Cancer Cohort Consortium. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 688-696.	1.1	36
126	A Nonparametric Test to Detect Quantitative Trait Loci Where the Phenotypic Distribution Differs by Genotypes. Genetic Epidemiology, 2013, 37, 323-333.	0.6	26

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127	An Absolute Risk Model to Identify Individuals at Elevated Risk for Pancreatic Cancer in the General Population. PLoS ONE, 2013, 8, e72311.	1.1	120
128	Informed Conditioning on Clinical Covariates Increases Power in Case-Control Association Studies. PLoS Genetics, 2012, 8, e1003032.	1.5	78
129	Common Breast Cancer Susceptibility Variants in LSP1 and RAD51L1 Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1156-1166.	1.1	101
130	Association of Type 2 Diabetes Susceptibility Variants With Advanced Prostate Cancer Risk in the Breast and Prostate Cancer Cohort Consortium. American Journal of Epidemiology, 2012, 176, 1121-1129.	1.6	67
131	Identification of a novel percent mammographic density locus at 12q24. Human Molecular Genetics, 2012, 21, 3299-3305.	1.4	31
132	Replication of Five Prostate Cancer Loci Identified in an Asian Populationâ€"Results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 212-216.	1.1	23
133	Prediction of breast cancer risk by genetic risk factors, overall and by hormone receptor status. Journal of Medical Genetics, 2012, 49, 601-608.	1.5	58
134	Mammographic Breast Density and Breast Cancer: Evidence of a Shared Genetic Basis. Cancer Research, 2012, 72, 1478-1484.	0.4	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. American Journal of Epidemiology, 2012, 175, 926-935.	1.6	16
136	Common Genetic Variants in Prostate Cancer Risk Predictionâ€"Results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 437-444.	1.1	51
137	Vitamin Dâ€"Related Genetic Variation, Plasma Vitamin D, and Risk of Lethal Prostate Cancer: A Prospective Nested Caseâ€"Control Study. Journal of the National Cancer Institute, 2012, 104, 690-699.	3.0	196
138	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	1.4	168
139	Genetic variation in the tollâ€like receptor 4 and prostate cancer incidence and mortality. Prostate, 2012, 72, 209-216.	1.2	22
140	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptorâ€"Positive, Lower Grade Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2222-2231.	1.1	27
141	Interactions Between Genetic Variants and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. Journal of the National Cancer Institute, 2011, 103, 1252-1263.	3.0	147
142	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€"negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	9.4	279
143	N-Acetyltransferase 2 Polymorphisms, Tobacco Smoking, and Breast Cancer Risk in the Breast and Prostate Cancer Cohort Consortium. American Journal of Epidemiology, 2011, 174, 1316-1322.	1.6	31
144	Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. Nature Genetics, 2011, 43, 185-187.	9.4	109

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145	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	9.4	265
146	Genome-wide association study identifies new prostate cancer susceptibility loci. Human Molecular Genetics, 2011, 20, 3867-3875.	1.4	160
147	Commentary: Averaged or Stratified Measures of Risk Profile Discrimination. Epidemiology, 2011, 22, 813-814.	1.2	0
148	Characterizing Associations and SNP-Environment Interactions for GWAS-Identified Prostate Cancer Risk Markersâ€"Results from BPC3. PLoS ONE, 2011, 6, e17142.	1.1	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. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 873-876.	1.1	32
150	A Large Study of Androgen Receptor Germline Variants and Their Relation to Sex Hormone Levels and Prostate Cancer Risk. Results from the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. Journal of Clinical Endocrinology and Metabolism, 2010, 95, E121-E127.	1.8	48
151	The Impact of Gene-Environment Dependence and Misclassification in Genetic Association Studies Incorporating Gene-Environment Interactions. Human Heredity, 2009, 68, 171-181.	0.4	38
152	Genetic variation in the upstream region of ERG and prostate cancer. Cancer Causes and Control, 2009, 20, 1173-1180.	0.8	3
153	Estimation of absolute risk for prostate cancer using genetic markers and family history. Prostate, 2009, 69, 1565-1572.	1.2	76
154	The UGT2B17 gene deletion is not associated with prostate cancer risk. Prostate, 2008, 68, 571-575.	1.2	38
155	Influence of MUC1 genetic variation on prostate cancer risk and survival. European Journal of Human Genetics, 2008, 16, 1521-1525.	1.4	9
156	Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. Nature Genetics, 2008, 40, 281-283.	9.4	357
157	A multigenic approach to evaluating prostate cancer risk in a systematic replication study. Cancer Genetics and Cytogenetics, 2008, 183, 94-98.	1.0	6
158	Y Chromosome Haplotypes and Prostate Cancer in Sweden. Clinical Cancer Research, 2008, 14, 6712-6716.	3.2	13
159	Inherited Variation in Hormone-Regulating Genes and Prostate Cancer Survival. Clinical Cancer Research, 2007, 13, 5156-5161.	3.2	25
160	Genetic variation in p53 and ATM haplotypes and risk of glioma and meningioma. Journal of Neuro-Oncology, 2007, 82, 229-237.	1.4	55
161	Systematic replication study of reported genetic associations in prostate cancer: Strong support for genetic variation in the androgen pathway. Prostate, 2006, 66, 1729-1743.	1.2	64
162	Estrogen Receptor Î² Polymorphism Is Associated with Prostate Cancer Risk. Clinical Cancer Research, 2006, 12, 1936-1941.	3.2	54

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163	Germ-Line Genetic Variation in the Key Androgen-Regulating Genes Androgen Receptor, Cytochrome P450, and Steroid-5-Î±-Reductase Type 2 Is Important for Prostate Cancer Development. Cancer Research, 2006, 66, 11077-11083.	0.4	43
164	Comprehensive genetic evaluation of common E-cadherin sequence variants and prostate cancer risk: strong confirmation of functional promoter SNP. Human Genetics, 2005, 118, 339-347.	1.8	29