Sofia Khan

List of Publications by Year
in descending order

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66 papers	6,496 citations	159358 30 h-index	102304 66 g-index
68 all docs	68 docs citations	68 times ranked	11114 citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
2	Breast-Cancer Risk in Families with Mutations in PALB2. New England Journal of Medicine, 2014, 371, 497-506.	13.9	745
3	Copy number analysis indicates monoclonal origin of lethal metastatic prostate cancer. Nature Medicine, 2009, 15, 559-565.	15.2	596
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.	9.4	513
5	Association of BRCA1 and BRCA2 Mutations With Survival, Chemotherapy Sensitivity, and Gene Mutator Phenotype in Patients With Ovarian Cancer. JAMA - Journal of the American Medical Association, 2011, 306, 1557.	3.8	466
6	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
7	Performance of protein stability predictors. Human Mutation, 2010, 31, 675-684.	1.1	275
8	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
9	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.	2.6	201
10	Exome sequencing identifies FANCM as a susceptibility gene for triple-negative breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15172-15177.	3.3	162
11	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
12	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
13	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
14	Spectrum of disease-causing mutations in protein secondary structures. BMC Structural Biology, 2007, 7, 56.	2.3	85
15	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
16	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
17	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
18	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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19	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	2.2	57
20	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
21	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
22	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
23	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
24	Computational strategies for single-cell multi-omics integration. Computational and Structural Biotechnology Journal, 2021, 19, 2588-2596.	1.9	46
25	Identification of Inherited Genetic Variations Influencing Prognosis in Early-Onset Breast Cancer. Cancer Research, 2013, 73, 1883-1891.	0.4	42
26	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. PLoS ONE, 2014, 9, e101488.	1.1	42
27	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
28	Integrative omics approaches provide biological and clinical insights: examples from mitochondrial diseases. Journal of Clinical Investigation, 2020, 130, 20-28.	3.9	39
29	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.	1.4	38
30	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	2.6	37
31	Metagenomics analysis of gut microbiota in response to diet intervention and gestational diabetes in overweight and obese women: a randomised, double-blind, placebo-controlled clinical trial. Gut, 2021, 70, gutjnl-2020-321643.	6.1	37
32	COMPLEXO: identifying the missing heritability of breast cancer via next generation collaboration. Breast Cancer Research, 2013, 15, 402.	2.2	36
33	Eukaryotic translation initiation factor 4E (eIF4E) expression is associated with breast cancer tumor phenotype and predicts survival after anthracycline chemotherapy treatment. Breast Cancer Research and Treatment, 2013, 141, 79-88.	1.1	33
34	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
35	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
36	Identification of differentially expressed genes after PPM1D silencing in breast cancer. Cancer Letters, 2008, 259, 61-70.	3.2	28

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37	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
38	FANCM mutation c.5791C>T is a risk factor for triple-negative breast cancer in the Finnish population. Breast Cancer Research and Treatment, 2017, 166, 217-226.	1.1	26
39	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
40	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.	1.1	24
41	Polygenic risk score is associated with increased disease risk in 52 Finnish breast cancer families. Breast Cancer Research and Treatment, 2016, 158, 463-469.	1.1	24
42	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
43	A survey of localized sequence rearrangements in human DNA. Nucleic Acids Research, 2018, 46, 1661-1673.	6.5	21
44	SNP-SNP interaction analysis of NF-Î¹B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
45	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
46	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. Nature Communications, 2017, 8, 1632.	5.8	18
47	Differences in definitive endoderm induction approaches using growth factors and small molecules. Journal of Cellular Physiology, 2018, 233, 3578-3589.	2.0	18
48	Gene Expression Profiles in Human and Mouse Primary Cells Provide New Insights into the Differential Actions of Vitamin D3 Metabolites. PLoS ONE, 2013, 8, e75338.	1.1	16
49	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	0.8	15
50	SNPs in lncRNA Regions and Breast Cancer Risk. Frontiers in Genetics, 2020, 11, 550.	1.1	14
51	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. Oncotarget, 2017, 8, 18381-18398.	0.8	14
52	FANCM c.5101C>T mutation associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2016, 139, 2760-2770.	2.3	13
53	Polymorphism at 19q13.41 Predicts Breast Cancer Survival Specifically after Endocrine Therapy. Clinical Cancer Research, 2015, 21, 4086-4096.	3.2	12
54	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12

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55	Adult-Onset Anti-Citrullinated Peptide Antibody-Negative Destructive Rheumatoid Arthritis Is Characterized by a Disease-Specific CD8+ T Lymphocyte Signature. Frontiers in Immunology, 2020, 11, 578848.	2.2	11
56	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	1.1	10
57	INPP4B and RAD50 have an interactive effect on survival after breast cancer. Breast Cancer Research and Treatment, 2015, 149, 363-371.	1.1	8
58	Meta-analysis of three genome-wide association studies identifies two loci that predict survival and treatment outcome in breast cancer. Oncotarget, 2018, 9, 4249-4257.	0.8	8
59	Screening of HELQ in breast and ovarian cancer families. Familial Cancer, 2016, 15, 19-23.	0.9	7
60	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. Npj Breast Cancer, 2020, 6, 44.	2.3	5
61	Critical evaluation of the subcutaneous engraftments of hormone naÃ¯ve primary prostate cancer. Translational Andrology and Urology, 2020, 9, 1120-1134.	0.6	3
62	High miR-30 Expression Associates with Improved Breast Cancer Patient Survival and Treatment Outcome. Cancers, 2021, 13, 2907.	1.7	3
63	Deep learning tools are top performers in long non-coding RNA prediction. Briefings in Functional Genomics, 2022, 21, 230-241.	1.3	3
64	Evaluation of Accuracy and Applicability of Protein Models: Retrospective Analysis of Biological and Biomedical Predictions. In Silico Biology, 2009, 9, 307-331.	0.4	1
65	Breast-Cancer Risk in Families With Mutations in PALB2. Obstetrical and Gynecological Survey, 2014, 69, 659-660.	0.2	1
66	Evaluation of the RHINO gene for breast cancer predisposition in Finnish breast cancer families. Breast Cancer Research and Treatment, 2014, 144, 437-441.	1.1	1