

Andreas Engert

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8553849/publications.pdf>

Version: 2024-02-01

43
papers

8,470
citations

172457

29
h-index

254184

43
g-index

44
all docs

44
docs citations

44
times ranked

11401
citing authors

#	ARTICLE	IF	CITATIONS
1	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	5.0	15
2	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
3	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
4	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
5	Common Susceptibility Loci for Male Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2021, 113, 453-461.	6.3	12
6	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021, 124, 842-854.	6.4	5
7	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203.	6.2	6
8	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. <i>Breast Cancer Research</i> , 2021, 23, 86.	5.0	7
9	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. <i>Journal of the National Cancer Institute</i> , 2020, 112, 278-285.	6.3	61
10	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
11	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	21.4	265
12	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	12.8	30
13	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. <i>Nature Genetics</i> , 2020, 52, 494-504.	21.4	138
14	Epigenome-wide association study for lifetime estrogen exposure identifies an epigenetic signature associated with breast cancer risk. <i>Clinical Epigenetics</i> , 2019, 11, 66.	4.1	21
15	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
16	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
17	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. <i>Blood</i> , 2018, 132, 2040-2052.	1.4	17
18	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	21.4	356

#	ARTICLE	IF	CITATIONS
19	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
20	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
21	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. <i>Nature Communications</i> , 2017, 8, 1892.	12.8	40
22	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	2.5	12
23	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	5.1	51
24	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016, 25, 3863-3876.	2.9	33
25	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	12.8	78
26	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). <i>Scientific Reports</i> , 2016, 6, 32512.	3.3	19
27	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	21.4	125
28	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	2.9	40
29	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015, 96, 5-20.	6.2	76
30	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
31	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. <i>Nature Genetics</i> , 2015, 47, 987-995.	21.4	218
32	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	2.5	24
33	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 285-298.	2.9	38
34	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
35	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	6.2	98
36	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	21.4	493

#	ARTICLE	IF	CITATIONS
37	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	6.2	201
38	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	21.4	374
39	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	21.4	960
40	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003173.	3.5	105
41	Variation at 3p24.1 and 6q23.3 influences the risk of Hodgkin's lymphoma. <i>Nature Communications</i> , 2013, 4, 2549.	12.8	62
42	A genome-wide association study of Hodgkin's lymphoma identifies new susceptibility loci at 2p16.1 (REL), 8q24.21 and 10p14 (GATA3). <i>Nature Genetics</i> , 2010, 42, 1126-1130.	21.4	177
43	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. <i>Nature Genetics</i> , 2007, 39, 870-874.	21.4	1,370