Jamie Allen

List of Publications by Year in descending order

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Version: 2024-02-01

27 papers	6,843 citations	516710 16 h-index	526287 27 g-index
27 all docs	27 docs citations	27 times ranked	12136 citing authors

#	Article	IF	Citations
1	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	14.5	1,231
2	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	14.5	1,103
3	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
4	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	14.5	1,076
5	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
6	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	27.0	532
7	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
8	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	1.6	270
9	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
10	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
11	Rare, protein-truncating variants inATM,CHEK2andPALB2, but notXRCC2, are associated with increased breast cancer risks. Journal of Medical Genetics, 2017, 54, 732-741.	3.2	68
12	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
13	Inherited mutations in BRCA1 and BRCA2 in an unselected multiethnic cohort of Asian patients with breast cancer and healthy controls from Malaysia. Journal of Medical Genetics, 2018, 55, 97-103.	3.2	34
14	Prevalence of BRCA1 and BRCA2 pathogenic variants in a large, unselected breast cancer cohort. International Journal of Cancer, 2019, 144, 1195-1204.	5.1	31
15	Use of deep whole-genome sequencing data to identify structure risk variants in breast cancer susceptibility genes. Human Molecular Genetics, 2018, 27, 853-859.	2.9	20
16	Differential Burden of Rare and Common Variants on Tumor Characteristics, Survival, and Mode of Detection in Breast Cancer. Cancer Research, 2018, 78, 6329-6338.	0.9	19
17	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
18	Splicing predictions, minigene analyses, and <scp>ACMG</scp>â€<scp>AMP</scp> clinical classification of 42 germline <scp>PALB2</scp> spliceâ€site variants. Journal of Pathology, 2022, 256, 321-334.	4.5	16

#	Article	IF	Citations
19	Predicting the Likelihood of Carrying a BRCA1 or BRCA2 Mutation in Asian Patients With Breast Cancer. Journal of Clinical Oncology, 2022, 40, 1542-1551.	1.6	14
20	Comprehensive Functional Characterization and Clinical Interpretation of 20 Splice-Site Variants of the RAD51C Gene. Cancers, 2020, 12, 3771.	3.7	10
21	RAD51D Aberrant Splicing in Breast Cancer: Identification of Splicing Regulatory Elements and Minigene-Based Evaluation of 53 DNA Variants. Cancers, 2021, 13, 2845.	3.7	10
22	Targeted Resequencing of the Coding Sequence of 38 Genes Near Breast Cancer GWAS Loci in a Large Caseâ€“Control Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 822-825.	2.5	7
23	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. Npj Breast Cancer, 2021, 7, 52.	5.2	7
24	Minigeneâ€based splicing analysis and <scp>ACMG</scp>/<scp>AMP</scp>â€based tentative classification of 56 <scp>ATM</scp> variants. Journal of Pathology, 2022, 258, 83-101.	4.5	5
25	Breast Cancer Risk in Women from Ghana Carrying Rare Germline Pathogenic Mutations. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1593-1601.	2.5	3
26	VEXOR: an integrative environment for prioritization of functional variants in fine-mapping analysis. Bioinformatics, 2017, 33, 1389-1391.	4.1	2
27	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. Cancers, 2022, 14, 3363.	3.7	2