

Diana Maria Torres Lopez

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

4,971
citations

186265
28
h-index

189892
50
g-index

51
all docs

51
docs citations

51
times ranked

8011
citing authors

#	ARTICLE	IF	CITATIONS
1	Prevalence of <i>BRCA1</i> and <i>BRCA2</i> Germline Mutations in Patients of African Descent with Early-Onset and Familial Colombian Breast Cancer. <i>Oncologist</i> , 2022, 27, e151-e157.	3.7	0
2	Cancer Risks Associated With <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>Journal of Clinical Oncology</i> , 2022, 40, 1529-1541.	1.6	90
3	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	2.8	23
4	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	5.0	15
5	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	7.1	51
6	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	8.2	19
7	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 623-642.	2.5	19
8	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020, 80, 624-638.	0.9	39
9	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
10	Genetic Variability in the microRNA Binding Sites of <i>BMPR1B</i> , <i>TGFBR1</i> , <i>IQGAP1</i> , <i>KRAS</i> , <i>SETD8</i> and <i>RYR3</i> and Risk of Breast Cancer in Colombian Women. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 12281-12287.	2.0	2
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	Germline <i>HOXB13</i> mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	3.3	2
13	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	1.3	32
14	The <i>FANCM</i> :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	5.2	28
15	Two truncating variants in <i>FANCC</i> and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	3.3	5
16	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
17	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
18	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

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19	Low Prevalence of the Four Common Colombian Founder Mutations in <i>BRCA1</i> and <i>BRCA2</i> in Early-Onset and Familial Afro-Colombian Patients with Breast Cancer. <i>Oncologist</i> , 2019, 24, e475-e479.	3.7	4
20	Interaction between genetic ancestry and common breast cancer susceptibility variants in Colombian women. <i>International Journal of Cancer</i> , 2019, 144, 2181-2191.	5.1	9
21	Mutational spectrum in a worldwide study of 29,700 families with <i>BRCA1</i> or <i>BRCA2</i> mutations. <i>Human Mutation</i> , 2018, 39, 593-620.	2.5	224
22	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
23	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.9	75
24	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
25	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
26	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016, 7, 80140-80163.	1.8	31
27	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016, 13, e1002105.	8.4	118
28	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	2.5	12
29	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
30	<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
31	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
32	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , 2016, 99, 903-911.	6.2	59
33	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. <i>Scientific Reports</i> , 2016, 6, 36874.	3.3	2
34	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
35	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
36	Founder and Recurrent Mutations in <i>BRCA1</i> and <i>BRCA2</i> Genes in Latin American Countries: State of the Art and Literature Review. <i>Oncologist</i> , 2016, 21, 832-839.	3.7	73

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37	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	3.2	94
38	Breast cancer risk variants at 6q25 display different phenotype associations and regulate <i>ESR1</i> , <i>RMND1</i> and <i>CCDC170</i> . <i>Nature Genetics</i> , 2016, 48, 374-386.	21.4	125
39	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. <i>Human Genetics</i> , 2016, 135, 137-154.	3.8	8
40	<i>RAD51B</i> in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	2.5	26
41	A polymorphism in the base excision repair gene <i>PARP2</i> is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. <i>BMC Cancer</i> , 2015, 15, 978.	2.6	6
42	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating <i>MAP3K1</i> . <i>American Journal of Human Genetics</i> , 2015, 96, 5-20.	6.2	76
43	Inherited variants in the inner centromere protein (<i>INCENP</i>) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. <i>Carcinogenesis</i> , 2015, 36, 256-271.	2.8	14
44	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
45	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate <i>NRBF2</i> Expression. <i>American Journal of Human Genetics</i> , 2015, 97, 22-34.	6.2	37
46	Association of Type and Location of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Risk of Breast and Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1347.	7.4	390
47	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014, 5, 4051.	12.8	16
48	Evidence that breast cancer risk at the 2q35 locus is mediated through <i>IGFBP5</i> regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
49	High proportion of <i>BRCA1/2</i> founder mutations in Hispanic breast/ovarian cancer families from Colombia. <i>Breast Cancer Research and Treatment</i> , 2007, 103, 225-232.	2.5	86