Trinidad Caldes

List of Publications by Year
in descending order

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94 papers	10,355 citations	61984 43 h-index	37204 96 g-index
98 all docs	98 docs citations	98 times ranked	13419 citing authors

#	Article	IF	Citations
1	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	6.3	19
2	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in BRCA1 and BRCA2 compared with those harboring protein truncating variants. Genetics in Medicine, 2022, 24, 119-129.	2.4	10
3	BRIP1, a Gene Potentially Implicated in Familial Colorectal Cancer Type X. Cancer Prevention Research, 2021, 14, 185-194.	1.5	7
4	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	12.8	19
5	The predictive ability of the 313 variantâ€“based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	2.4	16
6	Oral contraceptive use and ovarian cancer risk for BRCA1/2 mutation carriers: an international cohort study. American Journal of Obstetrics and Gynecology, 2021, 225, 51.e1-51.e17.	1.3	34
7	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.9	39
8	Using linkage studies combined with wholeâ€exome sequencing to identify novel candidate genes for familial colorectal cancer. International Journal of Cancer, 2020, 146, 1568-1577.	5.1	8
9	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
10	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	2.4	82
11	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
12	Germline Mutations in FAF1 Are Associated With Hereditary Colorectal Cancer. Gastroenterology, 2020, 159, 227-240.e7.	1.3	18
13	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	7.1	48
14	Alcohol Consumption, Cigarette Smoking, and Risk of Breast Cancer for BRCA1 and BRCA2 Mutation Carriers: Results from The BRCA1 and BRCA2 Cohort Consortium. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 368-378.	2.5	24
15	Risk-reducing salpingo-oophorectomy, natural menopause, and breast cancer risk: an international prospective cohort of BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2020, 22, 8.	5.0	41
16	Contribution of New Adenomatous Polyposis Predisposition Genes in an Unexplained Attenuated Spanish Cohort by Multigene Panel Testing. Scientific Reports, 2019, 9, 9814.	3.3	9
17	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
18	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88

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19	Large scale multifactorial likelihood quantitative analysis of BRCA1 and BRCA2 variants: An ENIGMA resource to support clinical variant classification. Human Mutation, 2019, 40, 1557-1578.	2.5	102
20	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. British Journal of Cancer, 2019, 121, 180-192.	6.4	19
21	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
22	Update on genetic predisposition to colorectal cancer and polyposis. Molecular Aspects of Medicine, 2019, 69, 10-26.	6.4	113
23	Alternative splicing and ACMG-AMP-2015-based classification of PALB2 genetic variants: an ENIGMA report. Journal of Medical Genetics, 2019, 56, 453-460.	3.2	30
24	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
25	RECQL5 : Another DNA helicase potentially involved in hereditary breast cancer susceptibility. Human Mutation, 2019, 40, 566-577.	2.5	16
26	Height and Body Mass Index as Modifiers of Breast Cancer Risk in BRCA1/2 Mutation Carriers: A Mendelian Randomization Study. Journal of the National Cancer Institute, 2019, 111, 350-364.	6.3	30
27	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	2.5	224
28	Rare germline copy number variants in colorectal cancer predisposition characterized by exome sequencing analysis. Journal of Genetics and Genomics, 2018, 45, 41-45.	3.9	11
29	Association Between Germline Mutations in BRF1, a Subunit of the RNA Polymerase III Transcription Complex, and Hereditary Colorectal Cancer. Gastroenterology, 2018, 154, 181-194.e20.	1.3	32
30	The Influence of Number and Timing of Pregnancies on Breast Cancer Risk for Women With BRCA1 or BRCA2 Mutations. JNCI Cancer Spectrum, 2018, 2, pky078.	2.9	21
31	Novel genetic mutations detected by multigene panel are associated with hereditary colorectal cancer predisposition. PLoS ONE, 2018, 13, e0203885.	2.5	24
32	Oral Contraceptive Use and Breast Cancer Risk: Retrospective and Prospective Analyses From a BRCA1 and BRCA2 Mutation Carrier Cohort Study. JNCI Cancer Spectrum, 2018, 2, pky023.	2.9	33
33	Differential distribution and enrichment of non-coding RNAs in exosomes from normal and Cancer-associated fibroblasts in colorectal cancer. Molecular Cancer, 2018, 17, 114.	19.2	61
34	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.9	54
35	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
36	Evaluation of copy-number variants as modifiers of breast and ovarian cancer risk for BRCA1 pathogenic variant carriers. European Journal of Human Genetics, 2017, 25, 432-438.	2.8	26

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37	Risks of Breast, Ovarian, and Contralateral Breast Cancer for BRCA1 and BRCA2 Mutation Carriers. JAMA - Journal of the American Medical Association, 2017, 317, 2402.	7.4	1,898
38	Tumor burden monitoring using cell-free tumor DNA could be limited by tumor heterogeneity in advanced breast cancer and should be evaluated together with radiographic imaging. BMC Cancer, 2017, 17, 210.	2.6	59
39	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
40	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
41	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
42	Characterisation of the novel deleterious RAD51C p.Arg312Trp variant and prioritisation criteria for functional analysis of RAD51C missense changes. British Journal of Cancer, 2017, 117, 1048-1062.	6.4	12
43	SETD6 dominant negative mutation in familial colorectal cancer type X. Human Molecular Genetics, 2017, 26, 4481-4493.	2.9	23
44	Role of GALNT12 in the genetic predisposition to attenuated adenomatous polyposis syndrome. PLoS ONE, 2017, 12, e0187312.	2.5	10
45	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.	1.6	152
46	A novel TP53 germline inframe deletion identified in a Spanish series of Li-fraumeni syndrome suspected families. Familial Cancer, 2017, 16, 567-575.	1.9	5
47	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.	2.5	10
48	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.	5.0	31
49	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	5.0	88
50	The Fanconi anemia DNA damage repair pathway in the spotlight for germline predisposition to colorectal cancer. European Journal of Human Genetics, 2016, 24, 1501-1505.	2.8	59
51	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	5.0	42
52	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
53	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
54	Association of a let-7 miRNA binding region ofTGFBR1with hereditary mismatch repair proficient colorectal cancer (MSS HNPCC). Carcinogenesis, 2016, 37, 751-758.	2.8	16

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55	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
56	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	5.0	26
57	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	2.5	34
58	BRCA1 and BRCA2 mutations in males with familial breast and ovarian cancer syndrome. Results of a Spanish multicenter study. Familial Cancer, 2015, 14, 505-513.	1.9	15
59	Identification of E545k mutation in plasma from a PIK3CA wild-type metastatic breast cancer patient by array-based digital polymerase chain reaction. Translational Research, 2015, 166, 783-787.	5.0	7
60	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
61	Germline Mutations in FAN1 Cause Hereditary Colorectal Cancer by Impairing DNA Repair. Gastroenterology, 2015, 149, 563-566.	1.3	94
62	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	7.4	390
63	BRCA1 Alternative splicing landscape in breast tissue samples. BMC Cancer, 2015, 15, 219.	2.6	17
64	Prognostic Value of BRAF, PI3K, PTEN, EGFR Copy Number, Amphiregulin and Epiregulin Status in Patients with KRAS Codon 12 Wild-Type Metastatic Colorectal Cancer Receiving First-Line Chemotherapy with Anti-EGFR Therapy. Molecular Diagnosis and Therapy, 2015, 19, 397-408.	3.8	24
65	Whole-exome sequencing identifies rare pathogenic variants in new predisposition genes for familial colorectal cancer. Genetics in Medicine, 2015, 17, 131-142.	2.4	82
66	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	3.5	47
67	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
68	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.	5.0	57
69	Comprehensive annotation of splice junctions supports pervasive alternative splicing at the BRCA1 locus: a report from the ENIGMA consortium. Human Molecular Genetics, 2014, 23, 3666-3680.	2.9	96
70	Cancer risk and overall survival in mismatch repair proficient hereditary non-polyposis colorectal cancer, Lynch syndrome and sporadic colorectal cancer. Familial Cancer, 2014, 13, 109-119.	1.9	14
71	Capillary Electrophoresis Analysis of Conventional Splicing Assays: IARC Analytical and Clinical Classification of 31BRCA2Genetic Variants. Human Mutation, 2014, 35, 53-57.	2.5	25
72	Comparison of mRNA Splicing Assay Protocols across Multiple Laboratories: Recommendations for Best Practice in Standardized Clinical Testing. Clinical Chemistry, 2014, 60, 341-352.	3.2	95

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73	New genes emerging for colorectal cancer predisposition. World Journal of Gastroenterology, 2014, 20, 1961.	3.3	34
74	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
75	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
76	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	3.5	244
77	Frequency and Variability of Genomic Rearrangements on MSH2 in Spanish Lynch Syndrome Families. PLoS ONE, 2013, 8, e72195.	2.5	7
78	Pathology of Breast and Ovarian Cancers among BRCA1 and BRCA2 Mutation Carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 134-147.	2.5	513
79	Study of KRAS new predictive marker in a clinical laboratory. Clinical and Translational Oncology, 2012, 14, 937-942.	2.4	4
80	Topoisomerase 2 alpha: a real predictor of anthracycline efficacy?. Clinical and Translational Oncology, 2012, 14, 163-168.	2.4	22
81	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. Breast Cancer Research, 2012, 14, R33.	5.0	78
82	Common alleles at 6q25.1 and 1p11.2 are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2011, 20, 3304-3321.	2.9	68
83	Analysis of the Oxidative Damage Repair GenesNUDT1,OGG1, andMUTYHin Patients from Mismatch Repair Proficient HNPCC Families (MSS-HNPCC). Clinical Cancer Research, 2011, 17, 1701-1712.	7.0	34
84	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptorâ€“negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	21.4	309
85	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2009, 18, 4442-4456.	2.9	99
86	Common Breast Cancer-Predisposition Alleles Are Associated with Breast Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. American Journal of Human Genetics, 2008, 82, 937-948.	6.2	257
87	Molecular Analysis of Colorectal Cancer Tumors from Patients with Mismatch Repairâ€“Proficient Hereditary Nonpolyposis Colorectal Cancer Suggests Novel Carcinogenic Pathways. Clinical Cancer Research, 2007, 13, 5729-5735.	7.0	43
88	Screening for large rearrangements of the BRCA2 gene in Spanish families with breast/ovarian cancer. Breast Cancer Research and Treatment, 2007, 103, 103-107.	2.5	43
89	Genomic Rearrangements at the BRCA1 Locus in Spanish Families with Breast/Ovarian Cancer. Clinical Chemistry, 2006, 52, 1480-1485.	3.2	60
90	TGFBR1â˜†6A May Contribute to Hereditary Colorectal Cancer. Journal of Clinical Oncology, 2005, 23, 3074-3078.	1.6	45

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91	Low prevalence of germline hMSH6 mutations in colorectal cancer families from Spain. World Journal of Gastroenterology, 2005, 11, 5770.	3.3	17
92	Immunohistochemistry and microsatellite instability testing for selecting MLH1, MSH2 and MSH6 mutation carriers in hereditary non-polyposis colorectal cancer. Oncology Reports, 2004, 12, 621-9.	2.6	33
93	Prevalence of germline mutations ofMLH1 andMSH2 in hereditary nonpolyposis colorectal cancer families from Spain. International Journal of Cancer, 2002, 98, 774-779.	5.1	41
94	Eight novel germlineMLH1andMSH2mutations in hereditary non-polyposis colorectal cancer families from Spain. Human Mutation, 2001, 18, 549-549.	2.5	10