

Marta Cardoso

List of Publications by Year in descending order

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Version: 2024-02-01

96
papers

5,995
citations

87723

38
h-index

85405

71
g-index

101
all docs

101
docs citations

101
times ranked

11297
citing authors

#	ARTICLE	IF	CITATIONS
1	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	9.4	408
2	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.	3.8	390
3	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
4	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
5	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.	9.4	265
6	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. <i>Nature</i> , 2014, 508, 98-102.	13.7	261
7	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	9.4	221
8	Targeted Prostate Cancer Screening in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Results from the Initial Screening Round of the IMPACT Study. <i>European Urology</i> , 2014, 66, 489-499.	0.9	195
9	<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.	1.5	174
10	Genetic basis of PD-L1 overexpression in diffuse large B-cell lymphomas. <i>Blood</i> , 2016, 127, 3026-3034.	0.6	168
11	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	7.7	157
12	Polygenic hazard score to guide screening for aggressive prostate cancer: development and validation in large scale cohorts. <i>BMJ: British Medical Journal</i> , 2018, 360, j5757.	2.4	153
13	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.	9.4	125
14	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
15	Exome sequencing reveals novel mutation targets in diffuse large B-cell lymphomas derived from Chinese patients. <i>Blood</i> , 2014, 124, 2544-2553.	0.6	102
16	Germline Mutations in <i>PALB2</i> , <i>BRCA1</i> , and <i>RAD51C</i> , Which Regulate DNA Recombination Repair, in Patients With Gastric Cancer. <i>Gastroenterology</i> , 2017, 152, 983-986.e6.	0.6	98
17	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
18	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	5.8	90

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19	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
20	Germline pathogenic variants in PALB2 and other cancer-predisposing genes in families with hereditary diffuse gastric cancer without CDH1 mutation: a whole-exome sequencing study. <i>The Lancet Gastroenterology and Hepatology</i> , 2018, 3, 489-498.	3.7	87
21	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	1.1	82
22	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
23	The effects of height and BMI on prostate cancer incidence and mortality: a Mendelian randomization study in 20,848 cases and 20,214 controls from the PRACTICAL consortium. <i>Cancer Causes and Control</i> , 2015, 26, 1603-1616.	0.8	77
24	Blood lipids and prostate cancer: a Mendelian randomization analysis. <i>Cancer Medicine</i> , 2016, 5, 1125-1136.	1.3	68
25	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. <i>Human Molecular Genetics</i> , 2015, 24, 5589-5602.	1.4	67
26	Cytogenetic clues to breast carcinogenesis. <i>Genes Chromosomes and Cancer</i> , 2002, 33, 1-16.	1.5	61
27	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. <i>Cancer Discovery</i> , 2015, 5, 368-379.	7.7	56
28	Prediction of individual genetic risk to prostate cancer using a polygenic score. <i>Prostate</i> , 2015, 75, 1467-1474.	1.2	54
29	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	0.4	54
30	The c.156_157insAlu BRCA2 rearrangement accounts for more than one-fourth of deleterious BRCA mutations in northern/central Portugal. <i>Breast Cancer Research and Treatment</i> , 2009, 114, 31-38.	1.1	52
31	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	2.9	52
32	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 1478-1492.	1.4	50
33	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016, 7, 10979.	5.8	50
34	Targeted next generation sequencing identifies functionally deleterious germline mutations in novel genes in early-onset/familial prostate cancer. <i>PLoS Genetics</i> , 2018, 14, e1007355.	1.5	50
35	Characterization of the Cancer Spectrum in Men With Germline BRCA1 and BRCA2 Pathogenic Variants. <i>JAMA Oncology</i> , 2020, 6, 1218.	3.4	48
36	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. <i>PLoS Genetics</i> , 2014, 10, e1004256.	1.5	47

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37	Recurrent Fusion Oncogenes in Carcinomas. <i>Critical Reviews in Oncogenesis</i> , 2006, 12, 257-271.	0.2	45
38	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. <i>Breast Cancer Research</i> , 2016, 18, 112.	2.2	42
39	Pubertal development and prostate cancer risk: Mendelian randomization study in a population-based cohort. <i>BMC Medicine</i> , 2016, 14, 66.	2.3	42
40	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.	0.4	39
41	Hereditary Predisposition to Prostate Cancer: From Genetics to Clinical Implications. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5036.	1.8	38
42	Multiple numerical chromosome aberrations in cancer: what are their causes and what are their consequences?. <i>Seminars in Cancer Biology</i> , 2005, 15, 3-12.	4.3	36
43	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. <i>Scientific Reports</i> , 2015, 5, 17369.	1.6	35
44	Fine-Mapping the HOXB Region Detects Common Variants Tagging a Rare Coding Allele: Evidence for Synthetic Association in Prostate Cancer. <i>PLoS Genetics</i> , 2014, 10, e1004129.	1.5	34
45	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020.	1.1	34
46	Identification of Two Novel HOXB13 Germline Mutations in Portuguese Prostate Cancer Patients. <i>PLoS ONE</i> , 2015, 10, e0132728.	1.1	34
47	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
48	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	2.2	31
49	Target gene mutational pattern in Lynch syndrome colorectal carcinomas according to tumour location and germline mutation. <i>British Journal of Cancer</i> , 2015, 113, 686-692.	2.9	30
50	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
51	Genomic analysis of prostate carcinoma specimens obtained via ultrasound-guided needle biopsy may be of use in preoperative decision-making. <i>Cancer</i> , 2004, 101, 1786-1793.	2.0	28
52	Alcohol consumption and prostate cancer incidence and progression: A Mendelian randomisation study. <i>International Journal of Cancer</i> , 2017, 140, 75-85.	2.3	28
53	International distribution and age estimation of the Portuguese BRCA2 c.156_157insAlu founder mutation. <i>Breast Cancer Research and Treatment</i> , 2011, 127, 671-679.	1.1	27
54	Genome-Wide Association Study of Prostate Cancer-Specific Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1796-1800.	1.1	27

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55	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1731-1738.	1.1	27
56	Assessing the role of insulin-like growth factors and binding proteins in prostate cancer using Mendelian randomization: Genetic variants as instruments for circulating levels. <i>International Journal of Cancer</i> , 2016, 139, 1520-1533.	2.3	26
57	The role of germline mutations in the BRCA1/2 and mismatch repair genes in men ascertained for early-onset and/or familial prostate cancer. <i>Familial Cancer</i> , 2016, 15, 111-121.	0.9	26
58	Pathogenicity Evaluation of BRCA1 and BRCA2 Unclassified Variants Identified in Portuguese Breast/Ovarian Cancer Families. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 324-334.	1.2	24
59	Full in-frame exon 3 skipping of <i>BRCA2</i> confers high risk of breast and/or ovarian cancer. <i>Oncotarget</i> , 2018, 9, 17334-17348.	0.8	24
60	Specific and redundant activities of <i>ETV1</i> and <i>ETV4</i> in prostate cancer aggressiveness revealed by co-overexpression cellular contexts. <i>Oncotarget</i> , 2015, 6, 5217-5236.	0.8	24
61	Polyunsaturated fatty acids and prostate cancer risk: a Mendelian randomisation analysis from the PRACTICAL consortium. <i>British Journal of Cancer</i> , 2016, 115, 624-631.	2.9	23
62	Implementation of next-generation sequencing for molecular diagnosis of hereditary breast and ovarian cancer highlights its genetic heterogeneity. <i>Breast Cancer Research and Treatment</i> , 2016, 159, 245-256.	1.1	23
63	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	1.4	23
64	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 308-316.	1.1	22
65	Cytogenetic Analysis of Tumor Clonality. <i>Advances in Cancer Research</i> , 2011, 112, 127-149.	1.9	21
66	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. <i>British Journal of Cancer</i> , 2019, 121, 180-192.	2.9	19
67	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122.	3.0	19
68	Carcinoma of the Thyroid With Ewing/PNET Family Tumor Elements. <i>International Journal of Surgical Pathology</i> , 2014, 22, 579-581.	0.4	18
69	Association of breast cancer risk in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. <i>Breast Cancer Research and Treatment</i> , 2017, 161, 117-134.	1.1	18
70	Investigating the possible causal role of coffee consumption with prostate cancer risk and progression using Mendelian randomization analysis. <i>International Journal of Cancer</i> , 2017, 140, 322-328.	2.3	17
71	The CHEK2 Variant C.349A>G Is Associated with Prostate Cancer Risk and Carriers Share a Common Ancestor. <i>Cancers</i> , 2020, 12, 3254.	1.7	16
72	The predictive ability of the 313 variant-based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous <i>BRCA1</i> or <i>BRCA2</i> pathogenic variant. <i>Genetics in Medicine</i> , 2021, 23, 1726-1737.	1.1	16

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73	Analysis of Founder Mutations in Rare Tumors Associated With Hereditary Breast/Ovarian Cancer Reveals a Novel Association of BRCA2 Mutations with Ampulla of Vater Carcinomas. <i>PLoS ONE</i> , 2016, 11, e0161438.	1.1	15
74	Discontinuation of tyrosine kinase inhibitors in CML patients in real-world clinical practice at a single institution. <i>BMC Cancer</i> , 2018, 18, 1245.	1.1	15
75	Validation of a Next-Generation Sequencing Pipeline for the Molecular Diagnosis of Multiple Inherited Cancer Predisposing Syndromes. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 502-513.	1.2	13
76	Prostate Cancer Prognosis Defined by the Combined Analysis of 8q, PTEN and ERG. <i>Translational Oncology</i> , 2016, 9, 575-582.	1.7	12
77	Prostate-specific antigen velocity in a prospective prostate cancer screening study of men with genetic predisposition. <i>British Journal of Cancer</i> , 2018, 118, 266-276.	2.9	12
78	Identification of previously unrecognized FAP in children with Gardner fibroma. <i>European Journal of Human Genetics</i> , 2015, 23, 715-718.	1.4	11
79	SNP interaction pattern identifier (SIPI): an intensive search for SNP-SNP interaction patterns. <i>Bioinformatics</i> , 2017, 33, 822-833.	1.8	11
80	Ponatinib induces a sustained deep molecular response in a chronic myeloid leukaemia patient with an early relapse with a T315I mutation following allogeneic hematopoietic stem cell transplantation: a case report. <i>BMC Cancer</i> , 2018, 18, 1229.	1.1	11
81	Tumor Testing for Somatic and Germline BRCA1/BRCA2 Variants in Ovarian Cancer Patients in the Context of Strong Founder Effects. <i>Frontiers in Oncology</i> , 2020, 10, 1318.	1.3	11
82	Uncovering potential downstream targets of oncogenic GRPR overexpression in prostate carcinomas harboring ETS rearrangements. <i>Oncoscience</i> , 2015, 2, 497-507.	0.9	11
83	Portuguese c.156_157insAlu BRCA2 founder mutation: gastrointestinal and tongue neoplasias may be part of the phenotype. <i>Familial Cancer</i> , 2012, 11, 657-660.	0.9	10
84	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. <i>PLoS ONE</i> , 2016, 11, e0158801.	1.1	10
85	Haplotype analysis of the internationally distributed BRCA1 c.3331_3334delCAAG founder mutation reveals a common ancestral origin in Iberia. <i>Breast Cancer Research</i> , 2020, 22, 108.	2.2	9
86	Prostate cancer risk regions at 8q24 and 17q24 are differentially associated with somatic Tmprss2:ERG fusion status. <i>Human Molecular Genetics</i> , 2016, 25, ddw349.	1.4	8
87	Co-occurrence of nonsense mutations in MSH6 and MSH2 in Lynch syndrome families evidencing that not all truncating mutations are equal. <i>Journal of Human Genetics</i> , 2016, 61, 151-156.	1.1	8
88	Screening and characterization of BRCA2 c.156_157insAlu in Brazil: Results from 1380 individuals from the South and Southeast. <i>Cancer Genetics</i> , 2018, 228-229, 93-97.	0.2	6
89	Karyotypic divergence and convergence in two synchronous lung metastases of a clear cell sarcoma of tendons and aponeuroses with t(12;22)(q13;q12) and type 1 EWS/ATF1. <i>Cancer Genetics and Cytogenetics</i> , 2003, 145, 121-125.	1.0	5
90	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 44.	2.3	5

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91	AA9int: SNP interaction pattern search using non-hierarchical additive model set. <i>Bioinformatics</i> , 2018, 34, 4141-4150.	1.8	3
92	Overexpression of the Mitotic Checkpoint Genes <i>BUB1</i> and <i>BUBR1</i> is Associated with Genomic Complexity in Clear Cell Kidney Carcinomas. <i>Analytical Cellular Pathology</i> , 2008, 30, 389-395.	0.7	3
93	Multi-Gene Panel Testing in Gastroenterology: Are We Ready for the Results?. <i>GE Portuguese Journal of Gastroenterology</i> , 2021, 28, 1-7.	0.3	2
94	Pathogenicity reclassification of two BRCA1/BRCA2 exonic duplications after identification of genomic breakpoints and tandem orientation. <i>Cancer Genetics</i> , 2020, 248-249, 18-24.	0.2	0
95	Genetic and Clinical Characterization of 45 Acute Leukemia Patients with MLL Gene Rearrangements From a Single Institution.. <i>Blood</i> , 2012, 120, 2477-2477.	0.6	0
96	Prognostic Impact of High Hematogones in Acute Myeloid Leukemia. <i>Blood</i> , 2012, 120, 1435-1435.	0.6	0