Manuel R. Teixeira

List of Publications by Year
in descending order

319	16,465	18436 62	26548 107
papers	citations	h-index	g-index

340	340	340	22829
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
2	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	9.4	492
3	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
4	The MLL recombinome of acute leukemias in 2013. Leukemia, 2013, 27, 2165-2176.	3.3	393
5	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
6	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
7	SMARCB1/INI1 Tumor Suppressor Gene Is Frequently Inactivated in Epithelioid Sarcomas. Cancer Research, 2005, 65, 4012-4019.	0.4	316
8	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
9	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
10	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
11	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. Nature, 2014, 508, 98-102.	13.7	261
12	Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2017, 109, .	3.0	242
13	A Quantitative Promoter Methylation Profile of Prostate Cancer. Clinical Cancer Research, 2004, 10, 8472-8478.	3.2	234
14	TMPRSS2-ERG Gene Fusion Causing ERG Overexpression Precedes Chromosome Copy Number Changes in Prostate Carcinomas, Paired HGPIN Lesions. Neoplasia, 2006, 8, 826-832.	2.3	225
15	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	1.1	224
16	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
17	Targeted Prostate Cancer Screening in BRCA1 and BRCA2 Mutation Carriers: Results from the Initial Screening Round of the IMPACT Study. European Urology, 2014, 66, 489-499.	0.9	195
18	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174

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19	Genetic basis of PD-L1 overexpression in diffuse large B-cell lymphomas. Blood, 2016, 127, 3026-3034.	0.6	168
20	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
21	Three Epigenetic Biomarkers, GDF15, TMEFF2, and VIM, Accurately Predict Bladder Cancer from DNA-Based Analyses of Urine Samples. Clinical Cancer Research, 2010, 16, 5842-5851.	3.2	155
22	Polygenic hazard score to guide screening for aggressive prostate cancer: development and validation in large scale cohorts. BMJ: British Medical Journal, 2018, 360, j5757.	2.4	153
23	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.	0.8	152
24	Intratumor genomic heterogeneity in breast cancer with clonal divergence between primary carcinomas and lymph node metastases. Breast Cancer Research and Treatment, 2007, 102, 143-155.	1.1	150
25	Association of ERBB2 gene status with histopathological parameters and disease-specific survival in gastric carcinoma patients. British Journal of Cancer, 2009, 100, 487-493.	2.9	149
26	Interim Results from the IMPACT Study: Evidence for Prostate-specific Antigen Screening in BRCA2 Mutation Carriers. European Urology, 2019, 76, 831-842.	0.9	148
27	The order of genetic events associated with colorectal cancer progression inferred from meta-analysis of copy number changes. Genes Chromosomes and Cancer, 2006, 45, 31-41.	1.5	143
28	Distinct patterns of KRAS mutations in colorectal carcinomas according to germline mismatch repair defects and hMLH1 methylation status. Human Molecular Genetics, 2004, 13, 2303-2311.	1.4	127
29	Gene amplification of the histone methyltransferase SETDB1 contributes to human lung tumorigenesis. Oncogene, 2014, 33, 2807-2813.	2.6	126
30	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
31	High Promoter Methylation Levels of APC Predict Poor Prognosis in Sextant Biopsies from Prostate Cancer Patients. Clinical Cancer Research, 2007, 13, 6122-6129.	3.2	122
32	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
33	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. Human Molecular Genetics, 2013, 22, 408-415.	1.4	118
34	Quantitative RARÎ²2 Hypermethylation. Clinical Cancer Research, 2004, 10, 4010-4014.	3.2	117
35	Exome sequencing reveals novel mutation targets in diffuse large B-cell lymphomas derived from Chinese patients. Blood, 2014, 124, 2544-2553.	0.6	102
36	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	1.4	100

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37	TCF21andPCDH17methylation: An innovative panel of biomarkers for a simultaneous detection of urological cancers. Epigenetics, 2011, 6, 1120-1130.	1.3	99
38	Germline Mutations in PALB2, BRCA1, and RAD51C, Which Regulate DNA Recombination Repair, in Patients With Gastric Cancer. Gastroenterology, 2017, 152, 983-986.e6.	0.6	98
39	Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. Nature Communications, 2015, 6, 10131.	5.8	93
40	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
41	Cytogenetic and molecular genetic analyses of endometrial stromal sarcoma: nonrandom involvement of chromosome arms 6p and 7p and confirmation of JAZF1/JJAZ1 gene fusion in t(7;17). Cancer Genetics and Cytogenetics, 2003, 144, 119-124.	1.0	92
42	ADAMTS1, CRABP1, and NR3C1 Identified as Epigenetically Deregulated Genes in Colorectal Tumorigenesis. Analytical Cellular Pathology, 2006, 28, 259-272.	0.7	92
43	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
44	Chromosome abnormalities in benign hyperproliferative disorders of epithelial and stromal breast tissue. International Journal of Cancer, 1995, 60, 49-53.	2.3	89
45	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.	2.2	88
46	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
47	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
48	DNA repair genes are selectively mutated in diffuse large B cell lymphomas. Journal of Experimental Medicine, 2013, 210, 1729-1742.	4.2	87
49	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. The Lancet Gastroenterology and Hepatology, 2018, 3, 489-498.	3.7	87
50	Epigenetic Heterogeneity of High-Grade Prostatic Intraepithelial Neoplasia: Clues for Clonal Progression in Prostate Carcinogenesis. Molecular Cancer Research, 2006, 4, 1-8.	1.5	85
51	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.	1.1	82
52	Clonal heterogeneity in breast cancer: Karyotypic comparisons of multiple intraâ€"and extraâ€"tumorous samples from 3 patients. International Journal of Cancer, 1995, 63, 63-68.	2.3	80
53	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€"ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
54	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. Cancer Causes and Control, 2015, 26, 1603-1616.	0.8	77

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55	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	3.0	77
56	Chromosome abnormalities in bilateral breast carcinomas. Cytogenetic evaluation of the clonal origin of multiple primary tumors. Cancer, 1995, 76, 250-258.	2.0	76
57	Distinct high resolution genome profiles of early onset and late onset colorectal cancer integrated with gene expression data identify candidate susceptibility loci. Molecular Cancer, 2010, 9, 100.	7.9	75
58	FLI1 is a novel ETS transcription factor involved in gene fusions in prostate cancer. Genes Chromosomes and Cancer, 2012, 51, 240-249.	1.5	73
59	Blood lipids and prostate cancer: a Mendelian randomization analysis. Cancer Medicine, 2016, 5, 1125-1136.	1.3	68
60	Molecular cytogenetic characterization of proximal-type epithelioid sarcoma. Genes Chromosomes and Cancer, 2004, 41, 283-290.	1.5	67
61	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	1.4	67
62	MT1G Hypermethylation Is Associated with Higher Tumor Stage in Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 1274-1278.	1.1	65
63	8q Gain Is an Independent Predictor of Poor Survival in Diagnostic Needle Biopsies from Prostate Cancer Suspects. Clinical Cancer Research, 2006, 12, 3961-3970.	3.2	65
64	Genomic aberrations in carcinomas of the uterine corpus. Genes Chromosomes and Cancer, 2004, 40, 229-246.	1.5	63
65	Molecular Subtyping of Primary Prostate Cancer Reveals Specific and Shared Target Genes of Different ETS Rearrangements. Neoplasia, 2012, 14, 600-IN15.	2.3	63
66	Array CGH and gene-expression profiling reveals distinct genomic instability patterns associated with DNA repair and cell-cycle checkpoint pathways in Ewing's sarcoma. Oncogene, 2008, 27, 2084-2090.	2.6	62
67	Cytogenetic clues to breast carcinogenesis. Genes Chromosomes and Cancer, 2002, 33, 1-16.	1.5	61
68	Frequency of NUP98-NSD1 fusion transcript in childhood acute myeloid leukaemia. Leukemia, 2003, 17, 2244-2247.	3.3	61
69	Hyperdiploidy with 58-66 chromosomes in childhood B-acute lymphoblastic leukemia is highly curable: 58951 CLG-EORTC results. Blood, 2013, 121, 2415-2423.	0.6	61
70	Frequent 14-3-3 Ïƒ Promoter Methylation in Benign and Malignant Prostate Lesions. DNA and Cell Biology, 2005, 24, 264-269.	0.9	60
71	8q24 Copy number gains and expression of the c-myc mRNA stabilizing proteinCRD-BP in primary breast carcinomas. International Journal of Cancer, 2003, 104, 54-59.	2.3	58
72	Genome signatures of colon carcinoma cell lines. Cancer Genetics and Cytogenetics, 2004, 155, 119-131.	1.0	58

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73	Quantitative promoter methylation analysis of multiple cancer-related genes in renal cell tumors. BMC Cancer, 2007, 7, 133.	1.1	58
74	Cytogenetic analysis of multifocal breast carcinomas: detection of karyotypically unrelated clones as well as clonal similarities between tumour foci. British Journal of Cancer, 1994, 70, 922-927.	2.9	57
75	<scp>FOXE1</scp> polymorphisms are associated with familial and sporadic nonmedullary thyroid cancer susceptibility. Clinical Endocrinology, 2012, 77, 926-933.	1.2	57
76	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.	2.2	57
77	Molecular circuit involving KLK4 integrates androgen and mTOR signaling in prostate cancer. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2572-81.	3.3	56
78	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. Cancer Discovery, 2015, 5, 368-379.	7.7	56
79	Hypermethylation of Cyclin D2 is associated with loss of mRNA expression and tumor development in prostate cancer. Journal of Molecular Medicine, 2006, 84, 911-918.	1.7	54
80	Genomic Changes in Chromosomes 10, 16, and X in Malignant Peripheral Nerve Sheath Tumors Identify a High-Risk Patient Group. Journal of Clinical Oncology, 2010, 28, 1573-1582.	0.8	54
81	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	1.2	54
82	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.	0.4	54
83	Detection of gene promoter hypermethylation in fine needle washings from breast lesions. Clinical Cancer Research, 2003, 9, 3413-7.	3.2	54
84	Cytogenetic polyclonality in tumors of the breast. Cancer Genetics and Cytogenetics, 1997, 95, 16-19.	1.0	52
85	Cytogenetic analysis shows that carcinosarcomas of the breast are of monoclonal origin. Genes Chromosomes and Cancer, 1998, 22, 145-151.	1.5	52
86	The c.156_157insAlu BRCA2 rearrangement accounts for more than one-fourth of deleterious BRCA mutations in northern/central Portugal. Breast Cancer Research and Treatment, 2009, 114, 31-38.	1.1	52
87	MLL-SEPTIN gene fusions in hematological malignancies. Biological Chemistry, 2011, 392, 713-724.	1.2	52
88	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
89	Cytogenetic comparison of primary tumors and lymph node metastases in breast cancer patients. , 1998, 22, 122-129.		50
90	Aberrant cellular retinol binding protein 1 (CRBP1) gene expression and promoter methylation in prostate cancer. Journal of Clinical Pathology, 2004, 57, 872-876.	1.0	50

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91	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50
92	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
93	Targeted next generation sequencing identifies functionally deleterious germline mutations in novel genes in early-onset/familial prostate cancer. PLoS Genetics, 2018, 14, e1007355.	1.5	50
94	Relative Copy Number Gain of MYC in Diagnostic Needle Biopsies is an Independent Prognostic Factor for Prostate Cancer Patients. European Urology, 2007, 52, 116-125.	0.9	49
95	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
96	A prospective prostate cancer screening programme for men with pathogenic variants in mismatch repair genes (IMPACT): initial results from an international prospective study. Lancet Oncology, The, 2021, 22, 1618-1631.	5.1	48
97	Quantitative hypermethylation of a small panel of genes augments the diagnostic accuracy in fine-needle aspirate washings of breast lesions. Breast Cancer Research and Treatment, 2008, 109, 27-34.	1.1	47
98	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	1.5	47
99	Characterization of supernumerary rings and giant marker chromosomes in well-differentiated lipomatous tumors by a combination of G-banding, CGH, M-FISH, and chromosome- and locus-specific FISH. Cytogenetic and Genome Research, 2002, 97, 13-19.	0.6	45
100	Recurrent Fusion Oncogenes in Carcinomas. Critical Reviews in Oncogenesis, 2006, 12, 257-271.	0.2	45
101	Statistical dissection of genetic pathways involved in prostate carcinogenesis. Genes Chromosomes and Cancer, 2006, 45, 154-163.	1.5	44
102	Heterogeneous genetic profiles in soft tissue myoepitheliomas. Modern Pathology, 2008, 21, 1311-1319.	2.9	44
103	Cernunnos influences human immunoglobulin class switch recombination and may be associated with B cell lymphomagenesis. Journal of Experimental Medicine, 2012, 209, 291-305.	4.2	44
104	High resolution melting analysis of KRAS, BRAF and PIK3CA in KRASexon 2 wild-type metastatic colorectal cancer. BMC Cancer, 2013, 13, 169.	1.1	44
105	<scp>POLE</scp> somatic mutations in advanced colorectal cancer. Cancer Medicine, 2017, 6, 2966-2971.	1.3	43
106	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	5.8	43
107	Genome characteristics of primary carcinomas, local recurrences, carcinomatoses, and liver metastases from colorectal cancer patients. Molecular Cancer, 2004, 3, 6.	7.9	42
108	SEPT2 is a new fusion partner of MLL in acute myeloid leukemia with t(2;11)(q37;q23). Oncogene, 2006, 25, 6147-6152.	2.6	42

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109	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	2.2	42
110	Pubertal development and prostate cancer risk: Mendelian randomization study in a population-based cohort. BMC Medicine, 2016, 14, 66.	2.3	42
111	Discrimination between multicentric and multifocal breast carcinoma by cytogenetic investigation of macroscopically distinct ipsilateral lesions. , 1997, 18, 170-174.		41
112	Feasibility of differential diagnosis of kidney tumors by comparative genomic hybridization of fine needle aspiration biopsies. Genes Chromosomes and Cancer, 2010, 49, 935-947.	1.5	41
113	Familial vs sporadic papillary thyroid carcinoma: a matched-case comparative study showing similar clinical/prognostic behaviour. European Journal of Endocrinology, 2014, 170, 321-327.	1.9	40
114	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	5.8	40
115	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. Nature Communications, 2021, 12, 1236.	5.8	40
116	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
117	Cyclin D1 A870G polymorphism and amplification in laryngeal squamous cell carcinoma: implications of tumor localization and tobacco exposure. Cancer Detection and Prevention, 2004, 28, 237-243.	2.1	38
118	Adenomas and follicular carcinomas of the thyroid display two major patterns of chromosomal changes. Journal of Pathology, 2005, 206, 305-311.	2.1	38
119	Hereditary Predisposition to Prostate Cancer: From Genetics to Clinical Implications. International Journal of Molecular Sciences, 2020, 21, 5036.	1.8	38
120	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	2.6	38
121	Genetic profiling of colorectal cancer liver metastases by combined comparative genomic hybridization and G-banding analysis. Genes Chromosomes and Cancer, 2003, 36, 189-197.	1.5	37
122	Detailed analysis of expression and promoter methylation status of apoptosis-related genes in prostate cancer. Apoptosis: an International Journal on Programmed Cell Death, 2010, 15, 956-965.	2.2	37
123	Comparison of methodologies for KRAS mutation detection in metastatic colorectal cancer. Cancer Genetics, 2011, 204, 439-446.	0.2	37
124	Multiple numerical chromosome aberrations in cancer: what are their causes and what are their consequences?. Seminars in Cancer Biology, 2005, 15, 3-12.	4.3	36
125	Cysteine-Rich Secretory Protein-3 (CRISP3) Is Strongly Up-Regulated in Prostate Carcinomas with the TMPRSS2-ERG Fusion Gene. PLoS ONE, 2011, 6, e22317.	1.1	36
126	Frequent copy number gains at 1q21 and 1q32 are associated with overexpression of the ETS transcription factors ETV3 and ELF3 in breast cancer irrespective of molecular subtypes. Breast Cancer Research and Treatment, 2013, 138, 37-45.	1.1	36

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127	Novel 5â€² Fusion Partners of ETV1 and ETV4 in Prostate Cancer. Neoplasia, 2013, 15, 720-IN6.	2.3	36
128	Overexpression of the mitotic checkpoint genes BUB1 and BUBR1 is associated with genomic complexity in clear cell kidney carcinomas. Cellular Oncology, 2008, 30, 389-95.	1.9	36
129	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. Scientific Reports, 2015, 5, 17369.	1.6	35
130	Conventional and molecular cytogenetics of human non-medullary thyroid carcinoma: characterization of eight cell line models and review of the literature on clinical samples. BMC Cancer, 2008, 8, 371.	1.1	34
131	Epigenetic regulation of Wnt signaling pathway in urological cancer. Epigenetics, 2010, 5, 343-351.	1.3	34
132	Fine-Mapping the HOXB Region Detects Common Variants Tagging a Rare Coding Allele: Evidence for Synthetic Association in Prostate Cancer. PLoS Genetics, 2014, 10, e1004129.	1.5	34
133	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34
134	Identification of Two Novel HOXB13 Germline Mutations in Portuguese Prostate Cancer Patients. PLoS ONE, 2015, 10, e0132728.	1.1	34
135	Evaluation of Breast Cancer Polyclonality by Combined Chromosome Banding and Comparative Genomic Hybridization Analysis. Neoplasia, 2001, 3, 204-214.	2.3	33
136	Immunohistochemical molecular phenotypes of gastric cancer based on SOX2 and CDX2 predict patient outcome. BMC Cancer, 2014, 14, 753.	1.1	33
137	Mutations in exon 14 of dihydropyrimidine dehydrogenase and 5-Fluorouracil toxicity in Portuguese colorectal cancer patients. Genetics in Medicine, 2004, 6, 102-107.	1.1	32
138	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
139	No significant role for beta tubulin mutations and mismatch repair defects in ovarian cancer resistance to paclitaxel/cisplatin. BMC Cancer, 2005, 5, 101.	1.1	31
140	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.	2.2	31
141	Chromosome banding analysis of gynecomastias and breast carcinomas in men. , 1998, 23, 16-20.		30
142	Cross-species color banding characterization of chromosomal rearrangements in leukemias with incomplete G-band karyotypes. , 1999, 26, 13-19.		30
143	Combined classical and molecular cytogenetic analysis of cancer. European Journal of Cancer, 2002, 38, 1580-1584.	1.3	30
144	BRCA1 and BRCA2 germline mutational spectrum and evidence for genetic anticipation in Portuguese breast/ovarian cancer families. Familial Cancer, 2006, 5, 379-387.	0.9	30

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145	EGFR exon mutation distribution and outcome in non-small-cell lung cancer: a Portuguese retrospective study. Tumor Biology, 2012, 33, 2061-2068.	0.8	30
146	Target gene mutational pattern in Lynch syndrome colorectal carcinomas according to tumour location and germline mutation. British Journal of Cancer, 2015, 113, 686-692.	2.9	30
147	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.	3.0	30
148	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
149	Cytogenetic abnormalities in anin situ ductal carcinoma and five prophylactically removed breasts from members of a family with hereditary breast cancer. Breast Cancer Research and Treatment, 1996, 38, 177-182.	1.1	29
150	Common Fusion Transcripts Identified in Colorectal Cancer Cell Lines by High-Throughput RNA Sequencing. Translational Oncology, 2013, 6, 546-IN5.	1.7	29
151	Detailed Genome-Wide Screening for Inter- and Intrachromosomal Abnormalities by Sequential G-Banding and RxFISH Color Banding of the Same Metaphase Cells. Cancer Genetics and Cytogenetics, 2000, 119, 94-101.	1.0	28
152	Genomic analysis of prostate carcinoma specimens obtained via ultrasound-guided needle biopsy may be of use in preoperative decision-making. Cancer, 2004, 101, 1786-1793.	2.0	28
153	Colorectal carcinomas with microsatellite instability display a different pattern of target gene mutations according to large bowel site of origin. BMC Cancer, 2010, 10, 587.	1.1	28
154	Alcohol consumption and prostate cancer incidence and progression: A Mendelian randomisation study. International Journal of Cancer, 2017, 140, 75-85.	2.3	28
155	Contribution of <scp>MLH</scp>1 constitutional methylation for Lynch syndrome diagnosis in patients with tumor <scp>MLH</scp>1 downregulation. Cancer Medicine, 2018, 7, 433-444.	1.3	28
156	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
157	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	5.8	28
158	Altered Expression of MGMT in High-Grade Gliomas Results from the Combined Effect of Epigenetic and Genetic Aberrations. PLoS ONE, 2013, 8, e58206.	1.1	28
159	Karyotypic changes in phyllodes tumors of the breast. Cancer Genetics and Cytogenetics, 1994, 78, 200-206.	1.0	27
160	Highly sensitive detection of the MGB1 transcript (mammaglobin) in the peripheral blood of breast cancer patients. International Journal of Cancer, 2004, 108, 592-595.	2.3	27
161	International distribution and age estimation of the Portuguese BRCA2 c.156_157insAlu founder mutation. Breast Cancer Research and Treatment, 2011, 127, 671-679.	1.1	27
162	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	1.1	27

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163	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1731-1738.	1.1	27
164	Karyotypic Evolution in Breast Carcinomas with i(1)(q10) and der(1;16)(q10;p10) as the Primary Chromosome Abnormality. Cancer Genetics and Cytogenetics, 1999, 113, 156-161.	1.0	26
165	Cytogenetic characterization of tumors of the vulva and vagina. Genes Chromosomes and Cancer, 2003, 38, 137-148.	1.5	26
166	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.	2.2	26
167	Assessing the role of insulinâ€like growth factors and binding proteins in prostate cancer using Mendelian randomization: Genetic variants as instruments for circulating levels. International Journal of Cancer, 2016, 139, 1520-1533.	2.3	26
168	The role of germline mutations in the BRCA1/2 and mismatch repair genes in men ascertained for early-onset and/or familial prostate cancer. Familial Cancer, 2016, 15, 111-121.	0.9	26
169	Bromodomain protein 4 discriminates tissue-specific super-enhancers containing disease-specific susceptibility loci in prostate and breast cancer. BMC Genomics, 2017, 18, 270.	1.2	26
170	Combined RxFISH/G-banding allows refined karyotyping of solid tumors. Human Genetics, 1999, 104, 370-375.	1.8	25
171	A universal assay for detection of oncogenic fusion transcripts by oligo microarray analysis. Molecular Cancer, 2009, 8, 5.	7.9	25
172	Li-Fraumeni-like syndrome associated with a large BRCA1 intragenic deletion. BMC Cancer, 2012, 12, 237.	1.1	25
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