Manuel R. Teixeira

List of Publications by Year
in descending order

319 papers	16,465 citations	18482 62 h-index	26613 107 g-index
340 all docs	340 docs citations	340 times ranked	22829 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	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	2.8	23
3	Expression Profiling in Ovarian Cancer Reveals Coordinated Regulation of BRCA1/2 and Homologous Recombination Genes. Biomedicines, 2022, 10, 199.	3.2	3
4	Male gender as a poor prognostic factor in Medullary Thyroid Carcinoma: behaviour or biological difference?. Minerva Endocrinology, 2022, , .	1.1	1
5	Prostate cancer risk stratification improvement across multiple ancestries with new polygenic hazard score. Prostate Cancer and Prostatic Diseases, 2022, 25, 755-761.	3.9	14
6	KRAS and NRAS mutational analysis in plasma ctDNA from patients with metastatic colorectal cancer by real-time PCR and digital PCR. International Journal of Colorectal Disease, 2022, 37, 895-905.	2.2	3
7	The role of TP53 pathogenic variants in early-onset HER2-positive breast cancer. Familial Cancer, 2021, 20, 173-180.	1.9	2
8	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.	21.4	264
9	Additional SNPs improve risk stratification of a polygenic hazard score for prostate cancer. Prostate Cancer and Prostatic Diseases, 2021, 24, 532-541.	3.9	16
10	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. Nature Communications, 2021, 12, 1236.	12.8	40
11	Multi-Gene Panel Testing in Gastroenterology: Are We Ready for the Results?. GE Portuguese Journal of Gastroenterology, 2021, 28, 1-7.	0.8	2
12	Case Report: Pheochromocytoma and Synchronous Neuroblastoma in a Family With Hereditary Pheochromocytoma Associated With a MAX Deleterious Variant. Frontiers in Endocrinology, 2021, 12, 609263.	3.5	4
13	KLK3 SNPâ€“SNP interactions for prediction of prostate cancer aggressiveness. Scientific Reports, 2021, 11, 9264.	3.3	5
14	When to Stop TKIs in Patients with Chronic Myeloid Leukemia and How to Follow Them Subsequently. Current Treatment Options in Oncology, 2021, 22, 49.	3.0	1
15	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
16	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	5.4	38
17	Next Generation Sequencing of Tumor and Matched Plasma Samples: Identification of Somatic Variants in ctDNA From Ovarian Cancer Patients. Frontiers in Oncology, 2021, 11, 754094.	2.8	5
18	Identification of SPRY4 as a Novel Candidate Susceptibility Gene for Familial Nonmedullary Thyroid Cancer. Thyroid, 2021, 31, 1366-1375.	4.5	9

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19	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.	10.7	48
20	Prognostic Value of Histone Modifying Enzyme EZH2 in RCHOP-Treated Diffuse Large B-Cell Lymphoma and High Grade B-Cell Lymphoma. Journal of Personalized Medicine, 2021, 11, 1384.	2.5	0
21	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.9	39
22	Widening the spectrum of Lynch syndrome: first report of testicular seminoma attributable to MSH2 loss. Histopathology, 2020, 76, 486-489.	2.9	5
23	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
24	Pathogenicity reclassification of two BRCA1/BRCA2 exonic duplications after identification of genomic breakpoints and tandem orientation. Cancer Genetics, 2020, 248-249, 18-24.	0.4	0
25	Haplotype analysis of the internationally distributed BRCA1 c.3331_3334delCAAG founder mutation reveals a common ancestral origin in Iberia. Breast Cancer Research, 2020, 22, 108.	5.0	9
26	Gene Panel Tumor Testing in Ovarian Cancer Patients Significantly Increases the Yield of Clinically Actionable Germline Variants beyond BRCA1/BRCA2. Cancers, 2020, 12, 2834.	3.7	6
27	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
28	Hereditary Predisposition to Prostate Cancer: From Genetics to Clinical Implications. International Journal of Molecular Sciences, 2020, 21, 5036.	4.1	38
29	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	12.8	28
30	Tumor Testing for Somatic and Germline BRCA1/BRCA2 Variants in Ovarian Cancer Patients in the Context of Strong Founder Effects. Frontiers in Oncology, 2020, 10, 1318.	2.8	11
31	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. Npj Breast Cancer, 2020, 6, 44.	5.2	5
32	The CHEK2 Variant C.349A>G Is Associated with Prostate Cancer Risk and Carriers Share a Common Ancestor. Cancers, 2020, 12, 3254.	3.7	16
33	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
34	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	2.8	14
35	Surveillance of succinate dehydrogenase gene mutation carriers: Insights from a nationwide cohort. Clinical Endocrinology, 2020, 92, 545-553.	2.4	10
36	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1731-1738.	2.5	27

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37	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	7.1	48
38	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
39	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
40	The Spectrum of FANCM Protein Truncating Variants in European Breast Cancer Cases. Cancers, 2020, 12, 292.	3.7	11
41	Myeloid Disease with the CSF3R T618I Mutation after CLL. Case Reports in Hematology, 2020, 2020, 1-4.	0.4	1
42	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
43	Interim Results from the IMPACT Study: Evidence for Prostate-specific Antigen Screening in BRCA2 Mutation Carriers. European Urology, 2019, 76, 831-842.	1.9	148
44	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
45	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
46	Negative MR4Â·0chronic myeloid leukaemia and its possible implications for treatmentâ€free remission. British Journal of Haematology, 2019, 186, e181-e184.	2.5	1
47	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
48	The nonsense mutation MSH2 c.2152C>T shows a founder effect in Portuguese Lynch syndrome families. Genes Chromosomes and Cancer, 2019, 58, 657-664.	2.8	3
49	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
50	Genetic counselling and testing of susceptibility genes for therapeutic decision-making in breast cancerâ€”an European consensus statement and expert recommendations. European Journal of Cancer, 2019, 106, 54-60.	2.8	25
51	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 208-216.	2.5	21
52	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
53	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	2.5	224
54	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.	2.8	28

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55	Prostate-specific antigen velocity in a prospective prostate cancer screening study of men with genetic predisposition. British Journal of Cancer, 2018, 118, 266-276.	6.4	12
56	Polygenic hazard score to guide screening for aggressive prostate cancer: development and validation in large scale cohorts. BMJ: British Medical Journal, 2018, 360, j5757.	2.3	153
57	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.	8.1	87
58	Genetic Testing and Clinical Management Practices for Variants in Non-BRCA1/2 Breast (and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 632 for the Interpretation of Germline Mutant Alleles (ENIGMA) Clinical Working Group. JCO Precision Oncology, 2018, 2, 1-42.	3.0	19
59	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	12.8	43
60	Discontinuation of tyrosine kinase inhibitors in CML patients in real-world clinical practice at a single institution. BMC Cancer, 2018, 18, 1245.	2.6	15
61	Potential clinical applications of circulating cell-free DNA in ovarian cancer patients. Expert Reviews in Molecular Medicine, 2018, 20, e6.	3.9	20
62	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. BMC Cancer, 2018, 18, 1229.	2.6	11
63	Screening and characterization of BRCA2 c.156_157insAlu in Brazil: Results from 1380 individuals from the South and Southeast. Cancer Genetics, 2018, 228-229, 93-97.	0.4	6
64	Hybrid oncocytic/chromophobe renal cell tumor: An integrated genetic and epigenetic characterization of a case. Experimental and Molecular Pathology, 2018, 105, 352-356.	2.1	3
65	Targeted next generation sequencing identifies functionally deleterious germline mutations in novel genes in early-onset/familial prostate cancer. PLoS Genetics, 2018, 14, e1007355.	3.5	50
66	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
67	AA9int: SNP interaction pattern search using non-hierarchical additive model set. Bioinformatics, 2018, 34, 4141-4150.	4.1	3
68	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
69	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
70	Detection of microsatellite instability (MSI) in colorectal cancer samples with a novel set of highly sensitive markers by means of the Idylla MSI Test prototype.. Journal of Clinical Oncology, 2018, 36, e15639-e15639.	1.6	12
71	Full in-frame exon 3 skipping of BRCA2 confers high risk of breast and/or ovarian cancer. Oncotarget, 2018, 9, 17334-17348.	1.8	24
72	SNP interaction pattern identifier (SIPI): an intensive search for SNPâ€“SNP interaction patterns. Bioinformatics, 2017, 33, 822-833.	4.1	11

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73	Identification of somatic <scp>TERT</scp> promoter mutations in familial nonmedullary thyroid carcinomas. Clinical Endocrinology, 2017, 87, 394-399.	2.4	23
74	Ovarian metastasis from uveal melanoma with MLH1/PMS2 protein loss in a patient with germline MLH1 mutated Lynch syndrome: consequence or coincidence?. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2017, 470, 347-352.	2.8	9
75	Validation of a Next-Generation Sequencing Pipeline for the Molecular Diagnosis of Multiple Inherited Cancer Predisposing Syndromes. Journal of Molecular Diagnostics, 2017, 19, 502-513.	2.8	13
76	Bromodomain protein 4 discriminates tissue-specific super-enhancers containing disease-specific susceptibility loci in prostate and breast cancer. BMC Genomics, 2017, 18, 270.	2.8	26
77	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
78	Germline Mutations in PALB2, BRCA1, and RAD51C, Which Regulate DNA Recombination Repair, in Patients With Gastric Cancer. Gastroenterology, 2017, 152, 983-986.e6.	1.3	98
79	<scp>POLE</scp> somatic mutations in advanced colorectal cancer. Cancer Medicine, 2017, 6, 2966-2971.	2.8	43
80	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
81	Height, selected genetic markers and prostate cancer risk: results from the PRACTICAL consortium. British Journal of Cancer, 2017, 117, 734-743.	6.4	7
82	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	12.8	40
83	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. Breast Cancer Research and Treatment, 2017, 161, 117-134.	2.5	18
84	Investigating the possible causal role of coffee consumption with prostate cancer risk and progression using Mendelian randomization analysis. International Journal of Cancer, 2017, 140, 322-328.	5.1	17
85	Performance of Lynch syndrome predictive models in quantifying the likelihood of germline mutations in patients with abnormal MLH1 immunoexpression. Familial Cancer, 2017, 16, 73-81.	1.9	2
86	Alcohol consumption and prostate cancer incidence and progression: A Mendelian randomisation study. International Journal of Cancer, 2017, 140, 75-85.	5.1	28
87	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, .	6.3	242
88	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
89	Abstract LB-158: Germline mutations inPALB2,BRCA1andRAD51Cobserved in gastric cancer cases. , 2017, , .		0
90	BRCA1 and BRCA2 rearrangements in Brazilian individuals with Hereditary Breast and Ovarian Cancer Syndrome. Genetics and Molecular Biology, 2016, 39, 223-231.	1.3	22

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91	Lapatinib-capecitabine versus capecitabine alone as radiosensitizers in RAS wild-type resectable rectal cancer, an adaptive randomized phase II trial (LaRRC trial): study protocol for a randomized controlled trial. Trials, 2016, 17, 459.	1.6	2
92	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
93	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. PLoS ONE, 2016, 11, e0161438.	2.5	15
94	Oncogenic mechanisms of HOXB13 missense mutations in prostate carcinogenesis. Oncoscience, 2016, 3, 288-296.	2.2	11
95	NCOA2 is a candidate target gene of 8q gain associated with clinically aggressive prostate cancer. Genes Chromosomes and Cancer, 2016, 55, 365-374.	2.8	14
96	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
97	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
98	Correspondence: SEMA4A variation and risk of colorectal cancer. Nature Communications, 2016, 7, 10611.	12.8	7
99	Prostate Cancer Prognosis Defined by the Combined Analysis of 8q, PTEN and ERG. Translational Oncology, 2016, 9, 575-582.	3.7	12
100	Pathologic Findings in Prophylactic and Nonprophylactic Hysterectomy Specimens of Patients With Lynch Syndrome. American Journal of Surgical Pathology, 2016, 40, 1177-1191.	3.7	23
101	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
102	Genetic basis of PD-L1 overexpression in diffuse large B-cell lymphomas. Blood, 2016, 127, 3026-3034.	1.4	168
103	Polyunsaturated fatty acids and prostate cancer risk: a Mendelian randomisation analysis from the PRACTICAL consortium. British Journal of Cancer, 2016, 115, 624-631.	6.4	23
104	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.	5.1	26
105	Blood lipids and prostate cancer: a Mendelian randomization analysis. Cancer Medicine, 2016, 5, 1125-1136.	2.8	68
106	Implementation of next-generation sequencing for molecular diagnosis of hereditary breast and ovarian cancer highlights its genetic heterogeneity. Breast Cancer Research and Treatment, 2016, 159, 245-256.	2.5	23
107	Truncating and missense PPM1D mutations in earlyâ€onset and/or familial/hereditary prostate cancer patients. Genes Chromosomes and Cancer, 2016, 55, 954-961.	2.8	15
108	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.	9.4	157

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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.	5.0	42
110	Prostate cancer risk regions at 8q24 and 17q24 are differentially associated with somaticTMPRSS2:ERGfusion status. Human Molecular Genetics, 2016, 25, ddw349.	2.9	8
111	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
112	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
113	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
114	Pubertal development and prostate cancer risk: Mendelian randomization study in a population-based cohort. BMC Medicine, 2016, 14, 66.	5.5	42
115	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
116	Gene and pathway level analyses of germline DNA-repair gene variants and prostate cancer susceptibility using the iCOGS-genotyping array. British Journal of Cancer, 2016, 114, 945-952.	6.4	17
117	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
118	Co-occurrence of nonsense mutations in MSH6 and MSH2 in Lynch syndrome families evidencing that not all truncating mutations are equal. Journal of Human Genetics, 2016, 61, 151-156.	2.3	8
119	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.	1.9	26
120	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
121	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	3.3	24
122	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.	3.3	35
123	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
124	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	2.3	54
125	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
126	Identification of Two Novel HOXB13 Germline Mutations in Portuguese Prostate Cancer Patients. PLoS ONE, 2015, 10, e0132728.	2.5	34

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127	Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. Nature Communications, 2015, 6, 10131.	12.8	93
128	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. Cancer Discovery, 2015, 5, 368-379.	9.4	56
129	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
130	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
131	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.	1.8	77
132	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	2.9	67
133	Target gene mutational pattern in Lynch syndrome colorectal carcinomas according to tumour location and germline mutation. British Journal of Cancer, 2015, 113, 686-692.	6.4	30
134	Genome-Wide Association Study of Prostate Cancerâ€"Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	2.5	27
135	The role of targeted <scp>BRCA1</scp><scp>BRCA2</scp> mutation analysis in hereditary breast/ovarian cancer families of Portuguese ancestry. Clinical Genetics, 2015, 88, 41-48.	2.0	24
136	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
137	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	2.5	22
138	Identification of previously unrecognized FAP in children with Gardner fibroma. European Journal of Human Genetics, 2015, 23, 715-718.	2.8	11
139	Uncovering potential downstream targets of oncogenic GRPR overexpression in prostate carcinomas harboring ETS rearrangements. Oncoscience, 2015, 2, 497-507.	2.2	11
140	Specific and redundant activities ofETV1andETV4in prostate cancer aggressiveness revealed by co-overexpression cellular contexts. Oncotarget, 2015, 6, 5217-5236.	1.8	24
141	Abstract 2739: Transcontinental characterization of the Hispanic BRCA1 3450del4 breast cancer founder mutation. , 2015, , .		0
142	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
143	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.	3.5	34
144	After Angelina and the Supreme Court Decision, where do we go from here? BRCA gene testing in Rhode Island's Portuguese population. American Journal of Medical Genetics, Part A, 2014, 164, 557-558.	1.2	0

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145	Familial vs sporadic papillary thyroid carcinoma: a matched-case comparative study showing similar clinical/prognostic behaviour. European Journal of Endocrinology, 2014, 170, 321-327.	3.7	40
146	Carcinoma of the Thyroid With Ewing/PNET Family Tumor Elements. International Journal of Surgical Pathology, 2014, 22, 579-581.	0.8	18
147	Carcinoma of the Thyroid With Ewing Family Tumor Elements and Favorable Prognosis. International Journal of Surgical Pathology, 2014, 22, 260-265.	0.8	25
148	Immunohistochemical molecular phenotypes of gastric cancer based on SOX2 and CDX2 predict patient outcome. BMC Cancer, 2014, 14, 753.	2.6	33
149	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
150	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. Nature, 2014, 508, 98-102.	27.8	261
151	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.	1.9	195
152	Pathogenicity Evaluation of BRCA1 and BRCA2 Unclassified Variants Identified in Portuguese Breast/Ovarian Cancer Families. Journal of Molecular Diagnostics, 2014, 16, 324-334.	2.8	24
153	PNET with neuroendocrine differentiation of the lung. International Journal of Surgical Pathology, 2014, 22, 427-433.	0.8	9
154	The Brazilian Founder MutationTP53p.R337H is Uncommon in Portuguese Women Diagnosed with Breast Cancer. Breast Journal, 2014, 20, 534-536.	1.0	6
155	Transcriptome instability as a molecular pan-cancer characteristic of carcinomas. BMC Genomics, 2014, 15, 672.	2.8	15
156	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
157	Re: Role of the Oxidative DNA Damage Repair Gene OGG1 in Colorectal Tumorigenesis. Journal of the National Cancer Institute, 2014, 106, .	6.3	9
158	Gene amplification of the histone methyltransferase SETDB1 contributes to human lung tumorigenesis. Oncogene, 2014, 33, 2807-2813.	5.9	126
159	Exome sequencing reveals novel mutation targets in diffuse large B-cell lymphomas derived from Chinese patients. Blood, 2014, 124, 2544-2553.	1.4	102
160	Epigenetic regulation of <scp>EFEMP</scp>1 in prostate cancer: biological relevance and clinical potential. Journal of Cellular and Molecular Medicine, 2014, 18, 2287-2297.	3.6	23
161	Abstract 1281: Identification of novel susceptibility genes in familial gastric cancer using next generation sequencing and identity-by-descent mapping. , 2014, , .		0
162	High resolution melting analysis of KRAS, BRAF and PIK3CA in KRASexon 2 wild-type metastatic colorectal cancer. BMC Cancer, 2013, 13, 169.	2.6	44

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163	POU1F1 is a novel fusion partner of NUP98 in acute myeloid leukemia with t(3;11)(p11;p15). Molecular Cancer, 2013, 12, 5.	19.2	12
164	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.	2.5	36
165	The <scp>MSH2</scp> c.388_389del mutation shows a founder effect in Portuguese Lynch syndrome families. Clinical Genetics, 2013, 84, 244-250.	2.0	13
166	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 4239-4239.	2.9	2
167	Novel 5â€² Fusion Partners of ETV1 and ETV4 in Prostate Cancer. Neoplasia, 2013, 15, 720-IN6.	5.3	36
168	The MLL recombinome of acute leukemias in 2013. Leukemia, 2013, 27, 2165-2176.	7.2	393
169	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	21.4	492
170	DNA repair genes are selectively mutated in diffuse large B cell lymphomas. Journal of Experimental Medicine, 2013, 210, 1729-1742.	8.5	87
171	Common Fusion Transcripts Identified in Colorectal Cancer Cell Lines by High-Throughput RNA Sequencing. Translational Oncology, 2013, 6, 546-IN5.	3.7	29
172	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.	2.9	118
173	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.	7.1	56
174	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	2.9	100
175	BMP2 / BMP4 colorectal cancer susceptibility loci in northern and southern European populations. Carcinogenesis, 2013, 34, 314-318.	2.8	14
176	Genomic characterization of two large Alu-mediated rearrangements of the BRCA1 gene. Journal of Human Genetics, 2013, 58, 78-83.	2.3	24
177	Deregulation of <scp>PAX</scp>2 expression in renal cell tumours: mechanisms and potential use in differential diagnosis. Journal of Cellular and Molecular Medicine, 2013, 17, 1048-1058.	3.6	16
178	Hyperdiploidy with 58-66 chromosomes in childhood B-acute lymphoblastic leukemia is highly curable: 58951 CLG-EORTC results. Blood, 2013, 121, 2415-2423.	1.4	61
179	Altered Expression of MGMT in High-Grade Gliomas Results from the Combined Effect of Epigenetic and Genetic Aberrations. PLoS ONE, 2013, 8, e58206.	2.5	28
180	Assessment of Fusion Gene Status in Sarcomas Using a Custom Made Fusion Gene Microarray. PLoS ONE, 2013, 8, e70649.	2.5	3

#	Article	IF	Citations
181	Carcinogenic ability of possibly through oncogenic mutation of gene. Advances in Cancer: Research & Treatment, 2013, 2013, .	0.0	12
182	Cernunnos influences human immunoglobulin class switch recombination and may be associated with B cell lymphomagenesis. Journal of Experimental Medicine, 2012, 209, 291-305.	8.5	44
183	Desmoplastic Small Round Cell Tumor: Diagnosis by Fine-Needle Aspiration Cytology. Acta Cytologica, 2012, 56, 576-580.	1.3	14
184	EGFR exon mutation distribution and outcome in non-small-cell lung cancer: a Portuguese retrospective study. Tumor Biology, 2012, 33, 2061-2068.	1.8	30
185	<scp>FOXE1</scp> polymorphisms are associated with familial and sporadic nonmedullary thyroid cancer susceptibility. Clinical Endocrinology, 2012, 77, 926-933.	2.4	57
186	Molecular Subtyping of Primary Prostate Cancer Reveals Specific and Shared Target Genes of Different ETS Rearrangements. Neoplasia, 2012, 14, 600-IN15.	5.3	63
187	Portuguese c.156_157insAlu BRCA2 founder mutation: gastrointestinal and tongue neoplasias may be part of the phenotype. Familial Cancer, 2012, 11, 657-660.	1.9	10
188	12q amplification defines a subtype of extraskeletal osteosarcoma with good prognosis that is the soft tissue homologue of parosteal osteosarcoma. Cancer Genetics, 2012, 205, 332-336.	0.4	16
189	Li-Fraumeni-like syndrome associated with a large BRCA1 intragenic deletion. BMC Cancer, 2012, 12, 237.	2.6	25
190	Genetic and clinical characterization of 45 acute leukemia patients with MLL gene rearrangements from a single institution. Molecular Oncology, 2012, 6, 553-564.	4.6	19
191	Variability of the paracrineâ€induced osteoclastogenesis by human breast cancer cell lines. Journal of Cellular Biochemistry, 2012, 113, 1069-1079.	2.6	8
192	FLI1 is a novel ETS transcription factor involved in gene fusions in prostate cancer. Genes Chromosomes and Cancer, 2012, 51, 240-249.	2.8	73
193	Potential Downstream Target Genes of Aberrant ETS Transcription Factors Are Differentially Affected in Ewingâ€™s Sarcoma and Prostate Carcinoma. PLoS ONE, 2012, 7, e49819.	2.5	21
194	Prognostic Impact of High Hematogones in Acute Myeloid Leukemia. Blood, 2012, 120, 1435-1435.	1.4	0
195	Cysteine-Rich Secretory Protein-3 (CRISP3) Is Strongly Up-Regulated in Prostate Carcinomas with the TMPRSS2-ERG Fusion Gene. PLoS ONE, 2011, 6, e22317.	2.5	36
196	Cytogenetic Analysis of Tumor Clonality. Advances in Cancer Research, 2011, 112, 127-149.	5.0	21
197	Comparison of methodologies for KRAS mutation detection in metastatic colorectal cancer. Cancer Genetics, 2011, 204, 439-446.	0.4	37
198	TCF21andPCDH17methylation: An innovative panel of biomarkers for a simultaneous detection of urological cancers. Epigenetics, 2011, 6, 1120-1130.	2.7	99

#	Article	IF	Citations
199	Intraepidermal epidermotropic metastatic melanoma: a clinical and histopathological mimicker of melanoma in situ occurring in multiplicity. Journal of Cutaneous Pathology, 2011, 38, 514-520.	1.3	14
200	International distribution and age estimation of the Portuguese BRCA2 c.156_157insAlu founder mutation. Breast Cancer Research and Treatment, 2011, 127, 671-679.	2.5	27
201	Endometrial endometrioid adenocarcinoma associated with primitive neuroectodermal tumour of the uterus: a poor prognostic subtype of uterine tumours. Medical Oncology, 2011, 28, 1488-1494.	2.5	5
202	Acute megakaryoblastic leukemia with a fourâ€way variant translocation originating the RBM15â€“MKL1 fusion gene. Pediatric Blood and Cancer, 2011, 56, 846-849.	1.5	16
203	Relative 8q gain predicts diseaseâ€specific survival irrespective of the TMPRSS2â€ERG fusion status in diagnostic biopsies of prostate cancer. Genes Chromosomes and Cancer, 2011, 50, 662-671.	2.8	24
204	MLL-SEPTIN gene fusions in hematological malignancies. Biological Chemistry, 2011, 392, 713-724.	2.5	52
205	A novel exonic rearrangement affecting MLH1 and the contiguous LRRFIP2 is a founder mutation in Portuguese Lynch syndrome families. Genetics in Medicine, 2011, 13, 895-902.	2.4	21
206	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.	4.9	37
207	Promoter methylation and large intragenic rearrangements of DPYD are not implicated in severe toxicity to 5-fluorouracil-based chemotherapy in gastrointestinal cancer patients. BMC Cancer, 2010, 10, 470.	2.6	17
208	A novel spliced fusion of MLL with CT45A2in a pediatric biphenotypic acute leukemia. BMC Cancer, 2010, 10, 518.	2.6	9
209	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.	2.6	28
210	Chromosome copy number changes carry prognostic information independent of KIT/PDGFRA point mutations in gastrointestinal stromal tumors. BMC Medicine, 2010, 8, 26.	5.5	15
211	Coexistence of alternative MLLâ€“SEPT9 fusion transcripts in an acute myeloid leukemia with t(11;17)(q23;q25). Cancer Genetics and Cytogenetics, 2010, 197, 60-64.	1.0	13
212	Hereditary gastrointestinal stromal tumors sharing the KIT Exon 17 germline mutation p.Asp820Tyr develop through different cytogenetic progression pathways. Genes Chromosomes and Cancer, 2010, 49, 91-98.	2.8	17
213	Genotypic and phenotypic classification of cancer: How should the impact of the two diagnostic approaches best be balanced?. Genes Chromosomes and Cancer, 2010, 49, 763-774.	2.8	5
214	Feasibility of differential diagnosis of kidney tumors by comparative genomic hybridization of fine needle aspiration biopsies. Genes Chromosomes and Cancer, 2010, 49, 935-947.	2.8	41
215	Expression pattern of the septin gene family in acute myeloid leukemias with and without MLL-SEPT fusion genes. Leukemia Research, 2010, 34, 615-621.	0.8	19
216	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.	7.0	155

#	Article	IF	Citations
217	Epigenetic regulation of Wnt signaling pathway in urological cancer. Epigenetics, 2010, 5, 343-351.	2.7	34
218	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.	19.2	75
219	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.	1.6	54
220	Both SEPT2 and MLL are down-regulated in MLL-SEPT2therapy-related myeloid neoplasia. BMC Cancer, 2009, 9, 147.	2.6	11
221	Molecular diagnosis of the Portuguese founder mutation BRCA2 c.156_157insAlu. Breast Cancer Research and Treatment, 2009, 117, 215-217.	2.5	8
222	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.	2.5	52
223	Haplotype and quantitative transcript analyses of Portuguese breast/ovarian cancer families with the BRCA1 R71G founder mutation of Galician origin. Familial Cancer, 2009, 8, 203-208.	1.9	11
224	TP53 germline mutations in Portugal and genetic modifiers of age at cancer onset. Familial Cancer, 2009, 8, 383-390.	1.9	14
225	CSF1R copy number changes, point mutations, and RNA and protein overexpression in renal cell carcinomas. Modern Pathology, 2009, 22, 744-752.	5.5	23
226	Association of ERBB2 gene status with histopathological parameters and disease-specific survival in gastric carcinoma patients. British Journal of Cancer, 2009, 100, 487-493.	6.4	149
227	Altered expression of key cell cycle regulators in renal cell carcinoma associated with Xp11.2 translocation. Pathology Research and Practice, 2009, 205, 466-472.	2.3	8
228	Mitochondrial genome alterations in rectal and sigmoid carcinomas. Cancer Letters, 2009, 280, 38-43.	7.2	20
229	A universal assay for detection of oncogenic fusion transcripts by oligo microarray analysis. Molecular Cancer, 2009, 8, 5.	19.2	25
230	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.	2.5	47
231	Genetic diagnosis of alveolar rhabdomyosarcoma in the bone marrow of a patient without evidence of primary tumor. Pediatric Blood and Cancer, 2008, 51, 554-557.	1.5	8
232	Heterogeneous genetic profiles in soft tissue myoepitheliomas. Modern Pathology, 2008, 21, 1311-1319.	5.5	44
233	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.	5.9	62
234	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.	2.6	34

#	Article	IF	Citations
235	A novel MLL-SEPT2 fusion variant in therapy-related myelodysplastic syndrome. Cancer Genetics and Cytogenetics, 2008, 185, 62-64.	1.0	4
236	Cryptic chromosome rearrangement resulting in SYT-SSX2 fusion gene in a monophasic synovial sarcoma. Cancer Genetics and Cytogenetics, 2008, 187, 45-49.	1.0	13
237	Molecular characterization of the MLL-SEPT6 fusion gene in acute myeloid leukemia: identification of novel fusion transcripts and cloning of genomic breakpoint junctions. Haematologica, 2008, 93, 1076-1080.	3.5	17
238	Chromosome Mechanisms Giving Rise to the TMPRSS2-ERG Fusion Oncogene in Prostate Cancer and HGPIN Lesions. American Journal of Surgical Pathology, 2008, 32, 640-644.	3.7	20
239	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
240	Array-Based Comparative Genomic Hybridization in Prostate Cancer: Research and Clinical Applications. , 2008, , 415-429.		0
241	High Promoter Methylation Levels of APC Predict Poor Prognosis in Sextant Biopsies from Prostate Cancer Patients. Clinical Cancer Research, 2007, 13, 6122-6129.	7.0	122
242	Quantitative promoter methylation analysis of multiple cancer-related genes in renal cell tumors. BMC Cancer, 2007, 7, 133.	2.6	58
243	Molecular characterization of a rare MLLâ€“AF4 (MLLâ€“AFF1) fusion rearrangement in infant leukemia. Cancer Genetics and Cytogenetics, 2007, 178, 61-64.	1.0	2
244	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.	1.9	49
245	Reply to AnnaMaria Cianciulli, Roberta Merola and Costantino Leonardoâ€™s Letter to the Editor re: Franclim R. Ribeiro, Rui Henrique, Ana T. Martins, Carmen JerÃ³nimo and Manuel R. Teixeira. Relative Copy Number Gain of MYC in Diagnostic Needle Biopsies is an Independent Prognostic Factor for Prostate Cancer Patients. Eur Urol 2007;52:116â€“25. European Urology, 2007, 52, 1539-1540.	1.9	0
246	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.	2.5	150
247	Expression changes of the MAD mitotic checkpoint gene family in renal cell carcinomas characterized by numerical chromosome changes. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2007, 450, 379-385.	2.8	17
248	TMPRSS2-ERG Gene Fusion Causing ERG Overexpression Precedes Chromosome Copy Number Changes in Prostate Carcinomas, Paired HGPIN Lesions. Neoplasia, 2006, 8, 826-832.	5.3	225
249	Comparison of chromosomal and array-based comparative genomic hybridization for the detection of genomic imbalances in primary prostate carcinomas. Molecular Cancer, 2006, 5, 33.	19.2	19
250	ADAMTS1, CRABP1, and NR3C1 Identified as Epigenetically Deregulated Genes in Colorectal Tumorigenesis. Analytical Cellular Pathology, 2006, 28, 259-272.	1.4	92
251	MSH6 germline mutations in early-onset colorectal cancer patients without family history of the disease. British Journal of Cancer, 2006, 95, 752-756.	6.4	21
252	SEPT2 is a new fusion partner of MLL in acute myeloid leukemia with t(2;11)(q37;q23). Oncogene, 2006, 25, 6147-6152.	5.9	42

#	Article	IF	Citations
253	BRCA1 and BRCA2 germline mutational spectrum and evidence for genetic anticipation in Portuguese breast/ovarian cancer families. Familial Cancer, 2006, 5, 379-387.	1.9	30
254	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.	3.9	54
255	Chromosome analysis and molecular cytogenetic investigations of an epithelioid hemangioendothelioma. Cancer Genetics and Cytogenetics, 2006, 169, 164-168.	1.0	22
256	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.	2.8	143
257	Statistical dissection of genetic pathways involved in prostate carcinogenesis. Genes Chromosomes and Cancer, 2006, 45, 154-163.	2.8	44
258	Epigenetic Heterogeneity of High-Grade Prostatic Intraepithelial Neoplasia: Clues for Clonal Progression in Prostate Carcinogenesis. Molecular Cancer Research, 2006, 4, 1-8.	3.4	85
259	8q Gain Is an Independent Predictor of Poor Survival in Diagnostic Needle Biopsies from Prostate Cancer Suspects. Clinical Cancer Research, 2006, 12, 3961-3970.	7.0	65
260	Recurrent Fusion Oncogenes in Carcinomas. Critical Reviews in Oncogenesis, 2006, 12, 257-271.	0.4	45
261	Multimodal genetic diagnosis of solid variant alveolar rhabdomyosarcoma. Cancer Genetics and Cytogenetics, 2005, 163, 138-143.	1.0	13
262	Multiple numerical chromosome aberrations in cancer: what are their causes and what are their consequences?. Seminars in Cancer Biology, 2005, 15, 3-12.	9.6	36
263	No significant role for beta tubulin mutations and mismatch repair defects in ovarian cancer resistance to paclitaxel/cisplatin. BMC Cancer, 2005, 5, 101.	2.6	31
264	Adenomas and follicular carcinomas of the thyroid display two major patterns of chromosomal changes. Journal of Pathology, 2005, 206, 305-311.	4.5	38
265	TP53mutations are associated with a particular pattern of genomic imbalances in breast carcinomas. Journal of Pathology, 2005, 207, 14-19.	4.5	7
266	SMARCB1/INI1 Tumor Suppressor Gene Is Frequently Inactivated in Epithelioid Sarcomas. Cancer Research, 2005, 65, 4012-4019.	0.9	316
267	Frequent 14-3-3 Ïƒ Promoter Methylation in Benign and Malignant Prostate Lesions. DNA and Cell Biology, 2005, 24, 264-269.	1.9	60
268	MT1G Hypermethylation Is Associated with Higher Tumor Stage in Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 1274-1278.	2.5	65
269	The loss of NKX3.1 expression in testicular--and prostate--cancers is not caused by promoter hypermethylation. Molecular Cancer, 2005, 4, 8.	19.2	8
270	QuantitativeRARÎ²2Hypermethylation. Clinical Cancer Research, 2004, 10, 4010-4014.	7.0	117

#	Article	IF	Citations
271	A Quantitative Promoter Methylation Profile of Prostate Cancer. Clinical Cancer Research, 2004, 10, 8472-8478.	7.0	234
272	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.	2.9	127
273	Mutations in exon 14 of dihydropyrimidine dehydrogenase and 5-Fluorouracil toxicity in Portuguese colorectal cancer patients. Genetics in Medicine, 2004, 6, 102-107.	2.4	32
274	Aberrant cellular retinol binding protein 1 (CRBP1) gene expression and promoter methylation in prostate cancer. Journal of Clinical Pathology, 2004, 57, 872-876.	2.0	50
275	Genome signatures of colon carcinoma cell lines. Cancer Genetics and Cytogenetics, 2004, 155, 119-131.	1.0	58
276	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
277	Genomic aberrations in carcinomas of the uterine corpus. Genes Chromosomes and Cancer, 2004, 40, 229-246.	2.8	63
278	Molecular cytogenetic characterization of proximalâ€type epithelioid sarcoma. Genes Chromosomes and Cancer, 2004, 41, 283-290.	2.8	67
279	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.	4.1	28
280	Highly sensitive detection of the MGB1 transcript (mammaglobin) in the peripheral blood of breast cancer patients. International Journal of Cancer, 2004, 108, 592-595.	5.1	27
281	Genome characteristics of primary carcinomas, local recurrences, carcinomatoses, and liver metastases from colorectal cancer patients. Molecular Cancer, 2004, 3, 6.	19.2	42
282	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
283	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. Cancer Genetics and Cytogenetics, 2003, 145, 121-125.	1.0	5
284	Genetic profiling of colorectal cancer liver metastases by combined comparative genomic hybridization and G-banding analysis. Genes Chromosomes and Cancer, 2003, 36, 189-197.	2.8	37
285	Cytogenetic characterization of tumors of the vulva and vagina. Genes Chromosomes and Cancer, 2003, 38, 137-148.	2.8	26
286	Multicentric mammary carcinoma. Cancer, 2003, 97, 715-717.	4.1	5
287	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.	5.1	58
288	Frequency of NUP98-NSD1 fusion transcript in childhood acute myeloid leukaemia. Leukemia, 2003, 17, 2244-2247.	7.2	61

#	Article	IF	Citations
289	Telomerase Activity and Genetic Alterations in Primary Breast Carcinomas. Neoplasia, 2003, 5, 170-178.	5.3	8
290	Detection of gene promoter hypermethylation in fine needle washings from breast lesions. Clinical Cancer Research, 2003, 9, 3413-7.	7.0	54
291	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.	1.1	45
292	Combined classical and molecular cytogenetic analysis of cancer. European Journal of Cancer, 2002, 38, 1580-1584.	2.8	30
293	Genome profiling of breast cancer cells selected against in vitro shows copy number changes. Genes Chromosomes and Cancer, 2002, 33, 304-309.	2.8	16
294	Cytogenetic clues to breast carcinogenesis. Genes Chromosomes and Cancer, 2002, 33, 1-16.	2.8	61
295	Evaluation of Breast Cancer Polyclonality by Combined Chromosome Banding and Comparative Genomic Hybridization Analysis. Neoplasia, 2001, 3, 204-214.	5.3	33
296	Complete cytogenetic characterization of the human breast cancer cell line MA11 combining G-banding, comparative genomic hybridization, multicolor fluorescence in situ hybridization, RxFISH, and chromosome-specific painting. Cancer Genetics and Cytogenetics, 2001, 131, 25-30.	1.0	23
297	High frequency of clonal chromosome abnormalities in prostatic neoplasms sampled by prostatectomy or ultrasound-guided needle biopsy. , 2000, 28, 211-219.		12
298	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
299	Acute Myeloid Leukemia with inv(8)(p11q13). Leukemia and Lymphoma, 2000, 39, 651-656.	1.3	19
300	Cytogenetic Approaches to Breast Cancer. , 1999, , 373-388.		0
301	Combined RxFISH/G-banding allows refined karyotyping of solid tumors. Human Genetics, 1999, 104, 370-375.	3.8	25
302	Karyotypic Findings in Tumors of the Vulva and Vagina. Cancer Genetics and Cytogenetics, 1999, 111, 87-91.	1.0	22
303	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
304	Cross-species color banding characterization of chromosomal rearrangements in leukemias with incomplete G-band karyotypes. Genes Chromosomes and Cancer, 1999, 26, 13-19.	2.8	30
305	Translocation (3;3)(p14;q29) as the Primary Chromosome Abnormality in a Peritoneal Mesothelioma. Cancer Genetics and Cytogenetics, 1998, 103, 73-75.	1.0	2
306	Cytogenetic comparison of primary tumors and lymph node metastases in breast cancer patients. Genes Chromosomes and Cancer, 1998, 22, 122-129.	2.8	50

#	Article	IF	Citations
307	Cytogenetic analysis shows that carcinosarcomas of the breast are of monoclonal origin. Genes Chromosomes and Cancer, 1998, 22, 145-151.	2.8	52
308	Chromosome banding analysis of gynecomastias and breast carcinomas in men. , 1998, 23, 16-20.		30
309	Cytogenetic analysis of several pseudomyxoma peritonei lesions originating from a mucinous cystadenoma of the appendix. Cancer Genetics and Cytogenetics, 1997, 93, 157-159.	1.0	18
310	Cytogenetic polyclonality in tumors of the breast. Cancer Genetics and Cytogenetics, 1997, 95, 16-19.	1.0	52
311	Fluorescence in situ hybridization of old G-banded and mounted chromosome preparations. Cancer Genetics and Cytogenetics, 1997, 98, 9-15.	1.0	6
312	Discrimination between multicentric and multifocal breast carcinoma by cytogenetic investigation of macroscopically distinct ipsilateral lesions. , 1997, 18, 170-174.		41
313	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.	2.5	29
314	Chromosome abnormalities in bilateral breast carcinomas. Cytogenetic evaluation of the clonal origin of multiple primary tumors. Cancer, 1995, 76, 250-258.	4.1	76
315	Chromosome abnormalities in benign hyperproliferative disorders of epithelial and stromal breast tissue. International Journal of Cancer, 1995, 60, 49-53.	5.1	89
316	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.	5.1	80
317	Karyotypic changes in phyllodes tumors of the breast. Cancer Genetics and Cytogenetics, 1994, 78, 200-206.	1.0	27
318	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.	6.4	57
319	Molecular classification of endometrial carcinoma: protocol for a cohort study (Preprint). JMIR Research Protocols, 0, , .	1.0	2