Manuel R. Teixeira

List of Publications by Year
in descending order

319 papers	16,465 citations	21215 62 h-index	30277 107 g-index
340 all docs	340 docs citations	340 times ranked	24701 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.	3.0	19
2	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
3	Expression Profiling in Ovarian Cancer Reveals Coordinated Regulation of BRCA1/2 and Homologous Recombination Genes. Biomedicines, 2022, 10, 199.	1.4	3
4	Male gender as a poor prognostic factor in Medullary Thyroid Carcinoma: behaviour or biological difference?. Minerva Endocrinology, 2022, , .	0.6	1
5	Prostate cancer risk stratification improvement across multiple ancestries with new polygenic hazard score. Prostate Cancer and Prostatic Diseases, 2022, 25, 755-761.	2.0	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.	1.0	3
7	The role of TP53 pathogenic variants in early-onset HER2-positive breast cancer. Familial Cancer, 2021, 20, 173-180.	0.9	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.	9.4	264
9	Additional SNPs improve risk stratification of a polygenic hazard score for prostate cancer. Prostate Cancer and Prostatic Diseases, 2021, 24, 532-541.	2.0	16
10	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. Nature Communications, 2021, 12, 1236.	5.8	40
11	Multi-Gene Panel Testing in Gastroenterology: Are We Ready for the Results?. GE Portuguese Journal of Gastroenterology, 2021, 28, 1-7.	0.3	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.	1.5	4
13	KLK3 SNPâ€“SNP interactions for prediction of prostate cancer aggressiveness. Scientific Reports, 2021, 11, 9264.	1.6	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.	1.3	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.	1.1	16
16	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	2.6	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.	1.3	5
18	Identification of SPRY4 as a Novel Candidate Susceptibility Gene for Familial Nonmedullary Thyroid Cancer. Thyroid, 2021, 31, 1366-1375.	2.4	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.	5.1	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.	1.1	0
21	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
22	Widening the spectrum of Lynch syndrome: first report of testicular seminoma attributable to MSH2 loss. Histopathology, 2020, 76, 486-489.	1.6	5
23	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	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.	0.2	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.	2.2	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.	1.7	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.	1.1	82
28	Hereditary Predisposition to Prostate Cancer: From Genetics to Clinical Implications. International Journal of Molecular Sciences, 2020, 21, 5036.	1.8	38
29	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	5.8	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.	1.3	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.	2.3	5
32	The CHEK2 Variant C.349A>G Is Associated with Prostate Cancer Risk and Carriers Share a Common Ancestor. Cancers, 2020, 12, 3254.	1.7	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.	9.4	265
34	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	1.4	14
35	Surveillance of succinate dehydrogenase gene mutation carriers: Insights from a nationwide cohort. Clinical Endocrinology, 2020, 92, 545-553.	1.2	10
36	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

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37	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
38	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
39	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
40	The Spectrum of FANCM Protein Truncating Variants in European Breast Cancer Cases. Cancers, 2020, 12, 292.	1.7	11
41	Myeloid Disease with the CSF3R T618I Mutation after CLL. Case Reports in Hematology, 2020, 2020, 1-4.	0.3	1
42	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
43	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
44	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	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.	2.9	19
46	Negative MR4Â·0chronic myeloid leukaemia and its possible implications for treatmentâ€free remission. British Journal of Haematology, 2019, 186, e181-e184.	1.2	1
47	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	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.	1.5	3
49	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	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.	1.3	25
51	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 208-216.	1.1	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.	3.0	30
53	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	1.1	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.	1.3	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.	2.9	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.	2.4	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.	3.7	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.	1.5	19
59	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	5.8	43
60	Discontinuation of tyrosine kinase inhibitors in CML patients in real-world clinical practice at a single institution. BMC Cancer, 2018, 18, 1245.	1.1	15
61	Potential clinical applications of circulating cell-free DNA in ovarian cancer patients. Expert Reviews in Molecular Medicine, 2018, 20, e6.	1.6	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.	1.1	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.	0.2	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.	0.9	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.	1.5	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.	0.4	54
67	AA9int: SNP interaction pattern search using non-hierarchical additive model set. Bioinformatics, 2018, 34, 4141-4150.	1.8	3
68	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
69	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	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.	0.8	12
71	Full in-frame exon 3 skipping of BRCA2 confers high risk of breast and/or ovarian cancer. Oncotarget, 2018, 9, 17334-17348.	0.8	24
72	SNP interaction pattern identifier (SIPI): an intensive search for SNPâ€“SNP interaction patterns. Bioinformatics, 2017, 33, 822-833.	1.8	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.	1.2	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.	1.4	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.	1.2	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.	1.2	26
77	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	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.	0.6	98
79	<scp>POLE</scp> somatic mutations in advanced colorectal cancer. Cancer Medicine, 2017, 6, 2966-2971.	1.3	43
80	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
81	Height, selected genetic markers and prostate cancer risk: results from the PRACTICAL consortium. British Journal of Cancer, 2017, 117, 734-743.	2.9	7
82	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	5.8	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.	1.1	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.	2.3	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.	0.9	2
86	Alcohol consumption and prostate cancer incidence and progression: A Mendelian randomisation study. International Journal of Cancer, 2017, 140, 75-85.	2.3	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, .	3.0	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.	0.8	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.	0.6	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.	0.7	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.	1.1	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.	1.1	15
94	Oncogenic mechanisms of HOXB13 missense mutations in prostate carcinogenesis. Oncoscience, 2016, 3, 288-296.	0.9	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.	1.5	14
96	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	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.	2.2	31
98	Correspondence: SEMA4A variation and risk of colorectal cancer. Nature Communications, 2016, 7, 10611.	5.8	7
99	Prostate Cancer Prognosis Defined by the Combined Analysis of 8q, PTEN and ERG. Translational Oncology, 2016, 9, 575-582.	1.7	12
100	Pathologic Findings in Prophylactic and Nonprophylactic Hysterectomy Specimens of Patients With Lynch Syndrome. American Journal of Surgical Pathology, 2016, 40, 1177-1191.	2.1	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.	2.2	88
102	Genetic basis of PD-L1 overexpression in diffuse large B-cell lymphomas. Blood, 2016, 127, 3026-3034.	0.6	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.	2.9	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.	2.3	26
105	Blood lipids and prostate cancer: a Mendelian randomization analysis. Cancer Medicine, 2016, 5, 1125-1136.	1.3	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.	1.1	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.	1.5	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.	7.7	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.	2.2	42
110	Prostate cancer risk regions at 8q24 and 17q24 are differentially associated with somaticTMPRSS2:ERGfusion status. Human Molecular Genetics, 2016, 25, ddw349.	1.4	8
111	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
112	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
113	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
114	Pubertal development and prostate cancer risk: Mendelian randomization study in a population-based cohort. BMC Medicine, 2016, 14, 66.	2.3	42
115	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
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.	2.9	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.	3.0	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.	1.1	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.	0.9	26
120	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
121	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. Scientific Reports, 2015, 5, 16286.	1.6	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.	1.6	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.	2.2	26
124	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	1.2	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.	1.1	34
126	Identification of Two Novel HOXB13 Germline Mutations in Portuguese Prostate Cancer Patients. PLoS ONE, 2015, 10, e0132728.	1.1	34

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127	Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. Nature Communications, 2015, 6, 10131.	5.8	93
128	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. Cancer Discovery, 2015, 5, 368-379.	7.7	56
129	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	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.	3.8	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.	0.8	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.	1.4	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.	2.9	30
134	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	1.1	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.	1.0	24
136	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	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.	1.1	22
138	Identification of previously unrecognized FAP in children with Gardner fibroma. European Journal of Human Genetics, 2015, 23, 715-718.	1.4	11
139	Uncovering potential downstream targets of oncogenic GRPR overexpression in prostate carcinomas harboring ETS rearrangements. Oncoscience, 2015, 2, 497-507.	0.9	11
140	Specific and redundant activities ofETV1andETV4in prostate cancer aggressiveness revealed by co-overexpression cellular contexts. Oncotarget, 2015, 6, 5217-5236.	0.8	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.	1.5	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.	1.5	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.	0.7	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.	1.9	40
146	Carcinoma of the Thyroid With Ewing/PNET Family Tumor Elements. International Journal of Surgical Pathology, 2014, 22, 579-581.	0.4	18
147	Carcinoma of the Thyroid With Ewing Family Tumor Elements and Favorable Prognosis. International Journal of Surgical Pathology, 2014, 22, 260-265.	0.4	25
148	Immunohistochemical molecular phenotypes of gastric cancer based on SOX2 and CDX2 predict patient outcome. BMC Cancer, 2014, 14, 753.	1.1	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.	2.2	57
150	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. Nature, 2014, 508, 98-102.	13.7	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.	0.9	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.	1.2	24
153	PNET with neuroendocrine differentiation of the lung. International Journal of Surgical Pathology, 2014, 22, 427-433.	0.4	9
154	The Brazilian Founder MutationTP53p.R337H is Uncommon in Portuguese Women Diagnosed with Breast Cancer. Breast Journal, 2014, 20, 534-536.	0.4	6
155	Transcriptome instability as a molecular pan-cancer characteristic of carcinomas. BMC Genomics, 2014, 15, 672.	1.2	15
156	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
157	Re: Role of the Oxidative DNA Damage Repair Gene OGG1 in Colorectal Tumorigenesis. Journal of the National Cancer Institute, 2014, 106, .	3.0	9
158	Gene amplification of the histone methyltransferase SETDB1 contributes to human lung tumorigenesis. Oncogene, 2014, 33, 2807-2813.	2.6	126
159	Exome sequencing reveals novel mutation targets in diffuse large B-cell lymphomas derived from Chinese patients. Blood, 2014, 124, 2544-2553.	0.6	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.	1.6	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.	1.1	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.	7.9	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.	1.1	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.	1.0	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.	1.4	2
167	Novel 5â€² Fusion Partners of ETV1 and ETV4 in Prostate Cancer. Neoplasia, 2013, 15, 720-IN6.	2.3	36
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