

# Carlos Caldas

## List of Publications by Year in descending order

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Version: 2024-02-01

410  
papers

77,660  
citations

997

114  
h-index

568

263  
g-index

454  
all docs

454  
docs citations

454  
times ranked

84474  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.  | 27.8 | 8,060     |
| 2  | The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.                                   | 27.8 | 4,708     |
| 3  | International network of cancer genome projects. Nature, 2010, 464, 993-998.   | 27.8 | 2,114     |
| 4  | Analysis of Circulating Tumor DNA to Monitor Metastatic Breast Cancer. New England Journal of Medicine, 2013, 368, 1199-1209.                              | 27.0 | 1,884     |
| 5  | Liquid biopsies come of age: towards implementation of circulating tumour DNA. Nature Reviews Cancer, 2017, 17, 223-238.                                   | 28.4 | 1,786     |
| 6  | The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.  | 27.8 | 1,778     |
| 7  | Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.  | 27.8 | 1,760     |
| 8  | Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. Nature Genetics, 2005, 37, 391-400.           | 21.4 | 1,710     |
| 9  | Differential oestrogen receptor binding is associated with clinical outcome in breast cancer. Nature, 2012, 481, 389-393.                                  | 27.8 | 1,655     |
| 10 | The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.   | 27.8 | 1,535     |
| 11 | Non-invasive analysis of acquired resistance to cancer therapy by sequencing of plasma DNA. Nature, 2013, 497, 108-112.                                    | 27.8 | 1,443     |
| 12 | Patient-Derived Xenograft Models: An Emerging Platform for Translational Cancer Research. Cancer Discovery, 2014, 4, 998-1013.                             | 9.4  | 1,341     |
| 13 | The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. Nature Communications, 2016, 7, 11479.           | 12.8 | 1,221     |
| 14 | Noninvasive Identification and Monitoring of Cancer Mutations by Targeted Deep Sequencing of Plasma DNA. Science Translational Medicine, 2012, 4, 136ra68. | 12.4 | 1,086     |
| 15 | Frequent somatic mutations and homozygous deletions of the p16 (MTS1) gene in pancreatic adenocarcinoma. Nature Genetics, 1994, 8, 27-32.                  | 21.4 | 1,063     |
| 16 | Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.                                      | 27.8 | 984       |
| 17 | Genetic Unmasking of an Epigenetically Silenced microRNA in Human Cancer Cells. Cancer Research, 2007, 67, 1424-1429.                                      | 0.9  | 883       |
| 18 | MicroRNA expression profiling of human breast cancer identifies new markers of tumor subtype. Genome Biology, 2007, 8, R214.                               | 9.6  | 828       |

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|----|---|------|-----------|
| 19 | Molecular Classification and Molecular Forecasting of Breast Cancer: Ready for Clinical Application?. Journal of Clinical Oncology, 2005, 23, 7350-7360.  | 1.6  | 798       |
| 20 | Subtyping of Breast Cancer by Immunohistochemistry to Investigate a Relationship between Subtype and Short and Long Term Survival: A Collaborative Analysis of Data for 10,159 Cases from 12 Studies. PLoS Medicine, 2010, 7, e1000279. | 8.4  | 764       |
| 21 | Clinical validity of circulating tumour cells in patients with metastatic breast cancer: a pooled analysis of individual patient data. Lancet Oncology, The, 2014, 15, 406-414.   | 10.7 | 703       |
| 22 | Driver mutations in <i>TP53</i> are ubiquitous in high grade serous carcinoma of the ovary. Journal of Pathology, 2010, 221, 49-56.   | 4.5  | 617       |
| 23 | Association between CD8+ T-cell infiltration and breast cancer survival in 12 439 patients. Annals of Oncology, 2014, 25, 1536-1543.  | 1.2  | 610       |
| 24 | Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.  | 30.7 | 604       |
| 25 | Systematic comparison of microarray profiling, real-time PCR, and next-generation sequencing technologies for measuring differential microRNA expression. Rna, 2010, 16, 991-1006.  | 3.5  | 588       |
| 26 | Incidence of gastric cancer and breast cancer in CDH1 (E-cadherin) mutation carriers from hereditary diffuse gastric cancer families. Gastroenterology, 2001, 121, 1348-1353.   | 1.3  | 579       |
| 27 | Helicobacter pylori and Interleukin 1 Genotyping: An Opportunity to Identify High-Risk Individuals for Gastric Carcinoma. Journal of the National Cancer Institute, 2002, 94, 1680-1687.  | 6.3  | 563       |
| 28 | p300/CBP and cancer. Oncogene, 2004, 23, 4225-4231.   | 5.9  | 547       |
| 29 | Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. Nature, 2015, 518, 422-426.   | 27.8 | 545       |
| 30 | Mutations truncating the EP300 acetylase in human cancers. Nature Genetics, 2000, 24, 300-303.  | 21.4 | 543       |
| 31 | Hereditary Diffuse Gastric Cancer Syndrome. JAMA Oncology, 2015, 1, 23.   | 7.1  | 540       |
| 32 | Interrogating open issues in cancer precision medicine with patient-derived xenografts. Nature Reviews Cancer, 2017, 17, 254-268.   | 28.4 | 527       |
| 33 | Progesterone receptor modulates ER $\alpha$ action in breast cancer. Nature, 2015, 523, 313-317.  | 27.8 | 504       |
| 34 | Hereditary diffuse gastric cancer: updated consensus guidelines for clinical management and directions for future research. Journal of Medical Genetics, 2010, 47, 436-444.   | 3.2  | 495       |
| 35 | Hereditary diffuse gastric cancer: updated clinical guidelines with an emphasis on germline <i>CDH1</i> mutation carriers. Journal of Medical Genetics, 2015, 52, 361-374.  | 3.2  | 479       |
| 36 | Patterns of Immune Infiltration in Breast Cancer and Their Clinical Implications: A Gene-Expression-Based Retrospective Study. PLoS Medicine, 2016, 13, e1002194.   | 8.4  | 473       |

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|----|---|------|-----------|
| 37 | A proinflammatory genetic profile increases the risk for chronic atrophic gastritis and gastric carcinoma. <i>Gastroenterology</i> , 2003, 125, 364-371.          | 1.3  | 450       |
| 38 | An immune response gene expression module identifies a good prognosis subtype in estrogen receptor negative breast cancer. <i>Genome Biology</i> , 2007, 8, R157. | 9.6  | 433       |
| 39 | A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017, 49, 1476-1486.   | 21.4 | 427       |
| 40 | Prognostic and predictive value of PDL1 expression in breast cancer. <i>Oncotarget</i> , 2015, 6, 5449-5464.  | 1.8  | 424       |
| 41 | Early Gastric Cancer in Young, Asymptomatic Carriers of Germ-Line E-Cadherin Mutations. <i>New England Journal of Medicine</i> , 2001, 344, 1904-1909.            | 27.0 | 420       |
| 42 | Multifocal clonal evolution characterized using circulating tumour DNA in a case of metastatic breast cancer. <i>Nature Communications</i> , 2015, 6, 8760.       | 12.8 | 409       |
| 43 | Interleukin 1B and interleukin 1RN polymorphisms are associated with increased risk of gastric carcinoma. <i>Gastroenterology</i> , 2001, 121, 823-829.           | 1.3  | 402       |
| 44 | Molecular heterogeneity of breast carcinomas and the cancer stem cell hypothesis. <i>Nature Reviews Cancer</i> , 2007, 7, 791-799.                                | 28.4 | 397       |
| 45 | EMSY Links the BRCA2 Pathway to Sporadic Breast and Ovarian Cancer. <i>Cell</i> , 2003, 115, 523-535.   | 28.9 | 389       |
| 46 | MicroRNAâ€™implications for cancer. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2008, 452, 1-10.                | 2.8  | 386       |
| 47 | CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. <i>Nature Communications</i> , 2017, 8, 14432.                    | 12.8 | 379       |
| 48 | Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. <i>Cell Stem Cell</i> , 2015, 16, 712-724.      | 11.1 | 376       |
| 49 | A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. <i>Cell</i> , 2016, 167, 260-274.e22.                | 28.9 | 376       |
| 50 | The shaping and functional consequences of the microRNA landscape in breast cancer. <i>Nature</i> , 2013, 497, 378-382.   | 27.8 | 370       |
| 51 | Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. <i>Cell</i> , 2018, 173, 1398-1412.e22.  | 28.9 | 362       |
| 52 | Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. <i>Science Translational Medicine</i> , 2012, 4, 157ra143.  | 12.4 | 356       |
| 53 | Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251343.                             | 12.6 | 348       |
| 54 | Endogenous Purification Reveals GREB1 as a Key Estrogen Receptor Regulatory Factor. <i>Cell Reports</i> , 2013, 3, 342-349.                                       | 6.4  | 319       |

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|----|---|------|-----------|
| 55 | The Implications of Clonal Genome Evolution for Cancer Medicine. New England Journal of Medicine, 2013, 368, 842-851.   | 27.0 | 316       |
| 56 | Ordering of mutations in preinvasive disease stages of esophageal carcinogenesis. Nature Genetics, 2014, 46, 837-843.   | 21.4 | 302       |
| 57 | Shieldin complex promotes DNA end-joining and counters homologous recombination in BRCA1-null cells. Nature Cell Biology, 2018, 20, 954-965.  | 10.3 | 291       |
| 58 | Chromatin modifier enzymes, the histone code and cancer. European Journal of Cancer, 2005, 41, 2381-2402.   | 2.8  | 290       |
| 59 | PREDICT: a new UK prognostic model that predicts survival following surgery for invasive breast cancer. Breast Cancer Research, 2010, 12, R1.   | 5.0  | 285       |
| 60 | High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. Genome Biology, 2007, 8, R215.   | 9.6  | 275       |
| 61 | Caring for patients with cancer in the COVID-19 era. Nature Medicine, 2020, 26, 665-671.  | 30.7 | 269       |
| 62 | A new genome-driven integrated classification of breast cancer and its implications. EMBO Journal, 2013, 32, 617-628.   | 7.8  | 267       |
| 63 | Maintaining Tumor Heterogeneity in Patient-Derived Tumor Xenografts. Cancer Research, 2015, 75, 2963-2968.  | 0.9  | 267       |
| 64 | Phenotypic and functional characterisation of the luminal cell hierarchy of the mammary gland. Breast Cancer Research, 2012, 14, R134.  | 5.0  | 260       |
| 65 | Allele-Specific Up-Regulation of FGFR2 Increases Susceptibility to Breast Cancer. PLoS Biology, 2008, 6, e108.  | 5.6  | 254       |
| 66 | Copynumber: Efficient algorithms for single- and multi-track copy number segmentation. BMC Genomics, 2012, 13, 591.   | 2.8  | 251       |
| 67 | DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. Genome Biology, 2012, 13, R124.   | 9.6  | 247       |
| 68 | Model of the early development of diffuse gastric cancer in E-cadherin mutation carriers and its implications for patient screening. Journal of Pathology, 2004, 203, 681-687.                                    | 4.5  | 242       |
| 69 | TP53 Mutation Spectrum in Breast Cancer Is Subtype Specific and Has Distinct Prognostic Relevance. Clinical Cancer Research, 2014, 20, 3569-3580.   | 7.0  | 240       |
| 70 | Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. Nature, 2019, 567, 399-404.  | 27.8 | 239       |
| 71 | Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. Genome Research, 2012, 22, 1995-2007. | 5.5  | 237       |
| 72 | Human and mouse oligonucleotide-based array CGH. Nucleic Acids Research, 2005, 33, e192-e192.   | 14.5 | 231       |

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|----|---|------|-----------|
| 73 | Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017, 543, 714-718.  | 27.8 | 229       |
| 74 | 6 versus 12 months of adjuvant trastuzumab for HER2-positive early breast cancer (PERSEPHONE): 4-year disease-free survival results of a randomised phase 3 non-inferiority trial. <i>Lancet, The</i> , 2019, 393, 2599-2612. | 13.7 | 225       |
| 75 | Cancer genetics of epigenetic genes. <i>Human Molecular Genetics</i> , 2007, 16, R28-R49.   | 2.9  | 223       |
| 76 | Differential expression of selected histone modifier genes in human solid cancers. <i>BMC Genomics</i> , 2006, 7, 90.   | 2.8  | 209       |
| 77 | Imaging mass cytometry and multiplatform genomics define the phenogenomic landscape of breast cancer. <i>Nature Cancer</i> , 2020, 1, 163-175.  | 13.2 | 209       |
| 78 | The Extracellular Matrix Protein TGFBI Induces Microtubule Stabilization and Sensitizes Ovarian Cancers to Paclitaxel. <i>Cancer Cell</i> , 2007, 12, 514-527.  | 16.8 | 202       |
| 79 | The clinical use of circulating tumor cells (CTCs) enumeration for staging of metastatic breast cancer (MBC): International expert consensus paper. <i>Critical Reviews in Oncology/Hematology</i> , 2019, 134, 39-45.        | 4.4  | 200       |
| 80 | Breast Cancer Molecular Stratification. <i>American Journal of Pathology</i> , 2017, 187, 2152-2162.  | 3.8  | 198       |
| 81 | Personalized circulating tumor DNA analysis to detect residual disease after neoadjuvant therapy in breast cancer. <i>Science Translational Medicine</i> , 2019, 11, .  | 12.4 | 197       |
| 82 | Sizing up miRNAs as cancer genes. <i>Nature Medicine</i> , 2005, 11, 712-714.   | 30.7 | 189       |
| 83 | Bcl-2 Is a Prognostic Marker in Breast Cancer Independently of the Nottingham Prognostic Index. <i>Clinical Cancer Research</i> , 2006, 12, 2468-2475.  | 7.0  | 188       |
| 84 | Alpha6 integrin is necessary for the tumorigenicity of a stem cell-like subpopulation within the MCF7 breast cancer cell line. <i>International Journal of Cancer</i> , 2008, 122, 298-304.                                   | 5.1  | 187       |
| 85 | Multi-omic machine learning predictor of breast cancer therapy response. <i>Nature</i> , 2022, 601, 623-629.  | 27.8 | 187       |
| 86 | A Recurrent Chromosome Breakpoint in Breast Cancer at the NRG1/Neuregulin 1/Heregulin Gene. <i>Cancer Research</i> , 2004, 64, 6840-6844.   | 0.9  | 185       |
| 87 | Germline CDH1 deletions in hereditary diffuse gastric cancer families. <i>Human Molecular Genetics</i> , 2009, 18, 1545-1555.   | 2.9  | 185       |
| 88 | Master regulators of FGFR2 signalling and breast cancer risk. <i>Nature Communications</i> , 2013, 4, 2464.   | 12.8 | 180       |
| 89 | Genome-driven integrated classification of breast cancer validated in over 7,500 samples. <i>Genome Biology</i> , 2014, 15, 431.  | 8.8  | 178       |
| 90 | A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus. <i>Nature Genetics</i> , 2013, 45, 1487-1493.   | 21.4 | 174       |

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|-----|---|------|-----------|
| 91  | JARID1B Is a Luminal Lineage-Driving Oncogene in Breast Cancer. <i>Cancer Cell</i> , 2014, 25, 762-777.   | 16.8 | 170       |
| 92  | A <sc>RAD</sc> 51 assay feasible in routine tumor samples calls <sc>PARP</sc> inhibitor response beyond <sc>BRCA</sc> mutation. <i>EMBO Molecular Medicine</i> , 2018, 10, .  | 6.9  | 169       |
| 93  | Identification of CDH1 germline missense mutations associated with functional inactivation of the E-cadherin protein in young gastric cancer probands. <i>Human Molecular Genetics</i> , 2003, 12, 575-582.         | 2.9  | 167       |
| 94  | Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22.  | 28.9 | 162       |
| 95  | Meta-analysis confirms BCL2 is an independent prognostic marker in breast cancer. <i>BMC Cancer</i> , 2008, 8, 153.   | 2.6  | 159       |
| 96  | Cancer-associated fibroblast compositions change with breast cancer progression linking the ratio of S100A4+ and PDPN+ CAFs to clinical outcome. <i>Nature Cancer</i> , 2020, 1, 692-708.                           | 13.2 | 159       |
| 97  | Screening E-cadherin in gastric cancer families reveals germline mutations only in hereditary diffuse gastric cancer kindred. <i>Human Mutation</i> , 2002, 19, 510-517.  | 2.5  | 153       |
| 98  | Molecular Classification of Breast Carcinomas Using Tissue Microarrays. <i>Diagnostic Molecular Pathology</i> , 2003, 12, 27-34.  | 2.1  | 153       |
| 99  | Molecular genetic profiles of colitis-associated neoplasms. <i>Gastroenterology</i> , 1994, 107, 420-428.   | 1.3  | 152       |
| 100 | Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 3289-3303. | 2.9  | 152       |
| 101 | Residual cancer burden after neoadjuvant chemotherapy and long-term survival outcomes in breast cancer: a multicentre pooled analysis of 5161 patients. <i>Lancet Oncology</i> , The, 2022, 23, 149-160.            | 10.7 | 148       |
| 102 | A 1â€‰Mb minimal amplicon at 8p11â€‰12 in breast cancer identifies new candidate oncogenes. <i>Oncogene</i> , 2005, 24, 5235-5245.  | 5.9  | 146       |
| 103 | Improved prognostic classification of breast cancer defined by antagonistic activation patterns of immune response pathway modules. <i>BMC Cancer</i> , 2010, 10, 604.  | 2.6  | 144       |
| 104 | Integration of genomic, transcriptomic and proteomic data identifies two biologically distinct subtypes of invasive lobular breast cancer. <i>Scientific Reports</i> , 2016, 6, 18517.                              | 3.3  | 143       |
| 105 | Common occurrence of APC and K-ras gene mutations in the spectrum of colitis-associated neoplasias. <i>Gastroenterology</i> , 1995, 108, 383-392.   | 1.3  | 139       |
| 106 | Genomic Architecture Characterizes Tumor Progression Paths and Fate in Breast Cancer Patients. <i>Science Translational Medicine</i> , 2010, 2, 38ra47.   | 12.4 | 138       |
| 107 | Imaging breast cancer using hyperpolarized carbon-13 MRI. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2092-2098.  | 7.1  | 138       |
| 108 | Identification and validation of prognostic markers in breast cancer with the complementary use of arrayâ€‰CGH and tissue microarrays. <i>Journal of Pathology</i> , 2005, 205, 388-396.                            | 4.5  | 137       |

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|-----|---|------|-----------|
| 109 | A 4-Gene Signature Predicts Survival of Patients With Resected Adenocarcinoma of the Esophagus, Junction, and Gastric Cardia. <i>Gastroenterology</i> , 2010, 139, 1995-2004.e15.   | 1.3  | 135       |
| 110 | BCL11A is a triple-negative breast cancer gene with critical functions in stem and progenitor cells. <i>Nature Communications</i> , 2015, 6, 5987.  | 12.8 | 135       |
| 111 | p300 regulates p53-dependent apoptosis after DNA damage in colorectal cancer cells by modulation of PUMA/p21 levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7386-7391.                                       | 7.1  | 133       |
| 112 | Genome-wide association studies in oesophageal adenocarcinoma and Barrett's oesophagus: a large-scale meta-analysis. <i>Lancet Oncology</i> , The, 2016, 17, 1363-1373.   | 10.7 | 133       |
| 113 | Dysregulated expression of Fau and MELK is associated with poor prognosis in breast cancer. <i>Breast Cancer Research</i> , 2009, 11, R60.  | 5.0  | 129       |
| 114 | K-ras mutation and pancreatic adenocarcinoma. <i>International Journal of Gastrointestinal Cancer</i> , 1995, 18, 1-6.  | 0.4  | 127       |
| 115 | Determinants of anti-PD-1 response and resistance in clear cell renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 1497-1518.e11.   | 16.8 | 126       |
| 116 | Predictive markers of anthracycline benefit: a prospectively planned analysis of the UK National Epirubicin Adjuvant Trial (NEAT/BR9601). <i>Lancet Oncology</i> , The, 2010, 11, 266-274.  | 10.7 | 122       |
| 117 | Landscape of G-quadruplex DNA structural regions in breast cancer. <i>Nature Genetics</i> , 2020, 52, 878-883.  | 21.4 | 122       |
| 118 | G-Quadruplex DNA as a Molecular Target for Induced Synthetic Lethality in Cancer Cells. <i>Journal of the American Chemical Society</i> , 2013, 135, 9640-9643.   | 13.7 | 121       |
| 119 | Saliva samples are a viable alternative to blood samples as a source of DNA for high throughput genotyping. <i>BMC Medical Genomics</i> , 2012, 5, 19.  | 1.5  | 120       |
| 120 | Circulating Tumor DNA to Monitor Metastatic Breast Cancer. <i>New England Journal of Medicine</i> , 2013, 369, 93-94.   | 27.0 | 120       |
| 121 | <i>ZNF703</i> is a common Luminal B breast cancer oncogene that differentially regulates luminal and basal progenitors in human mammary epithelium. <i>EMBO Molecular Medicine</i> , 2011, 3, 167-180.  | 6.9  | 119       |
| 122 | Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.  | 12.8 | 119       |
| 123 | Characterisation of microRNA expression in post-natal mouse mammary gland development. <i>BMC Genomics</i> , 2009, 10, 548.   | 2.8  | 117       |
| 124 | ctDNA monitoring using patient-specific sequencing and integration of variant reads. <i>Science Translational Medicine</i> , 2020, 12, .  | 12.4 | 116       |
| 125 | Efficacy of neoadjuvant bevacizumab added to docetaxel followed by fluorouracil, epirubicin, and cyclophosphamide, for women with HER2-negative early breast cancer (ARTemis): an open-label, randomised, phase 3 trial. <i>Lancet Oncology</i> , The, 2015, 16, 656-666. | 10.7 | 114       |
| 126 | A comprehensive analysis of prognostic signatures reveals the high predictive capacity of the Proliferation, Immune response and RNA splicing modules in breast cancer. <i>Breast Cancer Research</i> , 2008, 10, R93.  | 5.0  | 113       |



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|-----|--|------|-----------|
| 127 | Genomic and protein expression analysis reveals flap endonuclease 1 (FEN1) as a key biomarker in breast and ovarian cancer. <i>Molecular Oncology</i> , 2014, 8, 1326-1338.  | 4.6  | 109       |
| 128 | Elucidating the Altered Transcriptional Programs in Breast Cancer using Independent Component Analysis. <i>PLoS Computational Biology</i> , 2007, 3, e161.   | 3.2  | 108       |
| 129 | Systematic Analysis of Challenge-Driven Improvements in Molecular Prognostic Models for Breast Cancer. <i>Science Translational Medicine</i> , 2013, 5, 181re1.  | 12.4 | 108       |
| 130 | ARID1A influences HDAC1/BRD4 activity, intrinsic proliferative capacity and breast cancer treatment response. <i>Nature Genetics</i> , 2020, 52, 187-197.  | 21.4 | 108       |
| 131 | Effects of the addition of gemcitabine, and paclitaxel-first sequencing, in neoadjuvant sequential epirubicin, cyclophosphamide, and paclitaxel for women with high-risk early breast cancer (Neo-tAnGo): an open-label, 2A–2 factorial randomised phase 3 trial. <i>Lancet Oncology</i> , The, 2014, 15, 201-212. | 10.7 | 106       |
| 132 | Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.  | 12.8 | 105       |
| 133 | APOBEC3B-Mediated Cytidine Deamination Is Required for Estrogen Receptor Action in Breast Cancer. <i>Cell Reports</i> , 2015, 13, 108-121.   | 6.4  | 105       |
| 134 | SPAG5 as a prognostic biomarker and chemotherapy sensitivity predictor in breast cancer: a retrospective, integrated genomic, transcriptomic, and protein analysis. <i>Lancet Oncology</i> , The, 2016, 17, 1004-1018.   | 10.7 | 105       |
| 135 | MAP3K1 and MAP2K4 mutations are associated with sensitivity to MEK inhibitors in multiple cancer models. <i>Cell Research</i> , 2018, 28, 719-729.   | 12.0 | 105       |
| 136 | Common Germline Genetic Variation in Antioxidant Defense Genes and Survival After Diagnosis of Breast Cancer. <i>Journal of Clinical Oncology</i> , 2007, 25, 3015-3023.   | 1.6  | 102       |
| 137 | Cell-free circulating tumour DNA as a liquid biopsy in breast cancer. <i>Molecular Oncology</i> , 2016, 10, 464-474.   | 4.6  | 101       |
| 138 | Deep Sequencing of B Cell Receptor Repertoires From COVID-19 Patients Reveals Strong Convergent Immune Signatures. <i>Frontiers in Immunology</i> , 2020, 11, 605170.  | 4.8  | 101       |
| 139 | MLL2, the second human homolog of the <i>Drosophila</i> trithorax gene, maps to 19q13.1 and is amplified in solid tumor cell lines. <i>Oncogene</i> , 1999, 18, 7975-7984.   | 5.9  | 100       |
| 140 | Regulation of p53 tetramerization and nuclear export by ARC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20826-20831.  | 7.1  | 100       |
| 141 | A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76.  | 12.4 | 100       |
| 142 | Pharmacogenomic Identification of Novel Determinants of Response to Chemotherapy in Colon Cancer. <i>Cancer Research</i> , 2006, 66, 2765-2777.  | 0.9  | 99        |
| 143 | Degenerate Oligonucleotide Primed-Polymerase Chain Reaction-Based Array Comparative Genomic Hybridization for Extensive Amplicon Profiling of Breast Cancers. <i>American Journal of Pathology</i> , 2001, 158, 1623-1631.   | 3.8  | 98        |
| 144 | MicroRNAs and breast cancer. <i>Molecular Oncology</i> , 2010, 4, 230-241.   | 4.6  | 96        |

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|-----|---|------|-----------|
| 145 | TGF $\beta$ 2 induces the formation of tumour-initiating cells in claudinlow breast cancer. Nature Communications, 2012, 3, 1055.   | 12.8 | 95        |
| 146 | The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. Cell Reports, 2019, 27, 2690-2708.e10.  | 6.4  | 95        |
| 147 | PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. Cancer Research, 2017, 77, e62-e66.   | 0.9  | 92        |
| 148 | Evidence for a role of FGF-2 and FGF receptors in the proliferation of non-small cell lung cancer cells. , 1999, 83, 415-423.   |      | 91        |
| 149 | The molecular outlook. Nature, 2002, 415, 484-485.  | 27.8 | 91        |
| 150 | Replication of Genetic Polymorphisms Reported to Be Associated with Taxane-Related Sensory Neuropathy in Patients with Early Breast Cancer Treated with Paclitaxel. Clinical Cancer Research, 2014, 20, 2466-2475.                                | 7.0  | 91        |
| 151 | MYC functions are specific in biological subtypes of breast cancer and confers resistance to endocrine therapy in luminal tumours. British Journal of Cancer, 2016, 114, 917-928.   | 6.4  | 91        |
| 152 | Breast tumor microenvironment structures are associated with genomic features and clinical outcome. Nature Genetics, 2022, 54, 660-669.   | 21.4 | 88        |
| 153 | A robust classifier of high predictive value to identify good prognosis patients in ER-negative breast cancer. Breast Cancer Research, 2008, 10, R73.   | 5.0  | 87        |
| 154 | Cancer stem cell markers in breast cancer: pathological, clinical and prognostic significance. Breast Cancer Research, 2011, 13, R118.  | 5.0  | 87        |
| 155 | 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        |
| 156 | Integrative clustering reveals a novel split in the luminal A subtype of breast cancer with impact on outcome. Breast Cancer Research, 2017, 19, 44.  | 5.0  | 85        |
| 157 | Comparative study of endoscopic surveillance in hereditary diffuse gastric cancer according to CDH1 mutation status. Gastrointestinal Endoscopy, 2018, 87, 408-418.   | 1.0  | 85        |
| 158 | The circular RNome of primary breast cancer. Genome Research, 2019, 29, 356-366.  | 5.5  | 85        |
| 159 | Next Generation-Targeted Amplicon Sequencing (NG-TAS): an optimised protocol and computational pipeline for cost-effective profiling of circulating tumour DNA. Genome Medicine, 2019, 11, 1.   | 8.2  | 84        |
| 160 | Facilitating a culture of responsible and effective sharing of cancer genome data. Nature Medicine, 2016, 22, 464-471.  | 30.7 | 83        |
| 161 | A consensus prognostic gene expression classifier for ER positive breast cancer. Genome Biology, 2006, 7, R101.   | 9.6  | 82        |
| 162 | <i>BEX2</i> Is Overexpressed in a Subset of Primary Breast Cancers and Mediates Nerve Growth Factor/Nuclear Factor- $\kappa$ B Inhibition of Apoptosis in Breast Cancer Cell Lines. Cancer Research, 2007, 67, 6725-6736.                         | 0.9  | 81        |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 163 | Prognostic significance of androgen receptor expression in invasive breast cancer: transcriptomic and protein expression analysis. <i>Breast Cancer Research and Treatment</i> , 2016, 159, 215-227.                     | 2.5  | 81        |
| 164 | Effects of Collection and Processing Procedures on Plasma Circulating Cell-Free DNA from Cancer Patients. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 883-892.   | 2.8  | 81        |
| 165 | The pitfalls of platform comparison: DNA copy number array technologies assessed. <i>BMC Genomics</i> , 2009, 10, 588.   | 2.8  | 80        |
| 166 | Genomic gain of 5p15 leads to over-expression of Misu (NSUN2) in breast cancer. <i>Cancer Letters</i> , 2010, 289, 71-80.  | 7.2  | 80        |
| 167 | Therapeutic Rationale to Target Highly Expressed CDK7 Conferring Poor Outcomes in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2017, 77, 3834-3845.   | 0.9  | 79        |
| 168 | Aberrant splicing of the TSG101 and FHIT genes occurs frequently in multiple malignancies and in normal tissues and mimics alterations previously described in tumours. <i>Oncogene</i> , 1997, 15, 2119-2126.           | 5.9  | 78        |
| 169 | Expression of androgen receptor splice variants in clinical breast cancers. <i>Oncotarget</i> , 2015, 6, 44728-44744.  | 1.8  | 77        |
| 170 | CYP2D6 gene variants: association with breast cancer specific survival in a cohort of breast cancer patients from the United Kingdom treated with adjuvant tamoxifen. <i>Breast Cancer Research</i> , 2010, 12, R64.     | 5.0  | 76        |
| 171 | Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. <i>PLoS Computational Biology</i> , 2013, 9, e1003047.  | 3.2  | 76        |
| 172 | Prospective cohort study assessing outcomes of patients from families fulfilling criteria for hereditary diffuse gastric cancer undergoing endoscopic surveillance. <i>Gastrointestinal Endoscopy</i> , 2014, 80, 78-87. | 1.0  | 75        |
| 173 | A variational Bayesian mixture modelling framework for cluster analysis of gene-expression data. <i>Bioinformatics</i> , 2005, 21, 3025-3033.  | 4.1  | 73        |
| 174 | Targeting BRCA1- $\beta$ -BER deficient breast cancer by ATM or DNA-PKcs blockade either alone or in combination with cisplatin for personalized therapy. <i>Molecular Oncology</i> , 2015, 9, 204-217.                  | 4.6  | 72        |
| 175 | Intestinal microbiota influences clinical outcome and side effects of early breast cancer treatment. <i>Cell Death and Differentiation</i> , 2021, 28, 2778-2796.  | 11.2 | 72        |
| 176 | Exon scrambling of MLL transcripts occur commonly and mimic partial genomic duplication of the gene. <i>Gene</i> , 1998, 208, 167-176.   | 2.2  | 71        |
| 177 | Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021, 595, 585-590.  | 27.8 | 71        |
| 178 | A Ki67/BCL2 index based on immunohistochemistry is highly prognostic in ER $\alpha$ -positive breast cancer. <i>Journal of Pathology</i> , 2012, 226, 97-107.  | 4.5  | 70        |
| 179 | Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. <i>Genome Research</i> , 2015, 25, 814-824.  | 5.5  | 69        |
| 180 | DNA repair polymorphisms and the risk of stomach adenocarcinoma and severe chronic gastritis in the EPIC-EURGAST study. <i>International Journal of Epidemiology</i> , 2008, 37, 1316-1325.                              | 1.9  | 68        |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 181 | Fine scale mapping of the breast cancer 16q12 locus. Human Molecular Genetics, 2010, 19, 2507-2515.  | 2.9  | 68        |
| 182 | Biological and prognostic associations of <i>miR-205</i> and <i>let-7b</i> in breast cancer revealed by <i>in situ</i> hybridization analysis of microRNA expression in arrays of archival tumour tissue. Journal of Pathology, 2012, 227, 306-314.  | 4.5  | 68        |
| 183 | Therapeutic relevance of the PP2A-B55 inhibitory kinase MASTL/Greatwall in breast cancer. Cell Death and Differentiation, 2018, 25, 828-840.   | 11.2 | 67        |
| 184 | Determining Risk of Barrett's Esophagus and Esophageal Adenocarcinoma Based on Epidemiologic Factors and Genetic Variants. Gastroenterology, 2018, 154, 1273-1281.e3.  | 1.3  | 67        |
| 185 | Computational pathology of pre-treatment biopsies identifies lymphocyte density as a predictor of response to neoadjuvant chemotherapy in breast cancer. Breast Cancer Research, 2016, 18, 21.   | 5.0  | 66        |
| 186 | ESR1 gene amplification in breast cancer: a common phenomenon?. Nature Genetics, 2008, 40, 806-807.  | 21.4 | 62        |
| 187 | Intra-Tumour Signalling Entropy Determines Clinical Outcome in Breast and Lung Cancer. PLoS Computational Biology, 2015, 11, e1004115.   | 3.2  | 62        |
| 188 | A Prognostic Gene Signature for Metastasis-Free Survival of Triple Negative Breast Cancer Patients. PLoS ONE, 2013, 8, e82125.   | 2.5  | 62        |
| 189 | PACK: Profile Analysis using Clustering and Kurtosis to find molecular classifiers in cancer. Bioinformatics, 2006, 22, 2269-2275.   | 4.1  | 61        |
| 190 | Small molecule inhibition of group I p21-activated kinases in breast cancer induces apoptosis and potentiates the activity of microtubule stabilizing agents. Breast Cancer Research, 2015, 17, 59.  | 5.0  | 61        |
| 191 | Dynamics of multiple resistance mechanisms in plasma DNA during EGFR-targeted therapies in non-small cell lung cancer. EMBO Molecular Medicine, 2018, 10, .  | 6.9  | 61        |
| 192 | Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.  | 12.8 | 60        |
| 193 | PERSEPHONE: 6 versus 12 months (m) of adjuvant trastuzumab in patients (pts) with HER2 positive (+) early breast cancer (EBC): Randomised phase 3 non-inferiority trial with definitive 4-year (yr) disease-free survival (DFS) results.. Journal of Clinical Oncology, 2018, 36, 506-506. | 1.6  | 59        |
| 194 | The BRCA1ness signature is associated significantly with response to PARP inhibitor treatment versus control in the I-SPY 2 randomized neoadjuvant setting. Breast Cancer Research, 2017, 19, 99.  | 5.0  | 58        |
| 195 | Microarray segmentation methods significantly influence data precision. Nucleic Acids Research, 2004, 32, e50-e50.   | 14.5 | 57        |
| 196 | Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.  | 6.1  | 56        |
| 197 | Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .  | 6.3  | 56        |
| 198 | Support systems to guide clinical decision-making in precision oncology: The Cancer Core Europe Molecular Tumor Board Portal. Nature Medicine, 2020, 26, 992-994.  | 30.7 | 56        |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 199 | The Breast Cancer Oncogene EMSY Represses Transcription of Antimetastatic microRNA miR-31. <i>Molecular Cell</i> , 2014, 53, 806-818.   | 9.7  | 55        |
| 200 | Predicting Anthracycline Benefit: <i>TOP2A</i> and CEP170 Not Only but Also. <i>Journal of Clinical Oncology</i> , 2015, 33, 1680-1687.   | 1.6  | 55        |
| 201 | Computational approach to discriminate human and mouse sequences in patient-derived tumour xenografts. <i>BMC Genomics</i> , 2018, 19, 19.  | 2.8  | 55        |
| 202 | BRCA1-like signature in triple negative breast cancer: Molecular and clinical characterization reveals subgroups with therapeutic potential. <i>Molecular Oncology</i> , 2015, 9, 1528-1538.        | 4.6  | 54        |
| 203 | High USP6NL Levels in Breast Cancer Sustain Chronic AKT Phosphorylation and GLUT1 Stability Fueling Aerobic Glycolysis. <i>Cancer Research</i> , 2018, 78, 3432-3444.                               | 0.9  | 54        |
| 204 | Genetic predisposition to gastro-oesophageal cancer. <i>Current Opinion in Genetics and Development</i> , 2010, 20, 210-217.  | 3.3  | 53        |
| 205 | Synaptojanin 2 is a druggable mediator of metastasis and the gene is overexpressed and amplified in breast cancer. <i>Science Signaling</i> , 2015, 8, ra7.   | 3.6  | 53        |
| 206 | Lymphocyte Invasion in IC10/Basal-Like Breast Tumors Is Associated with Wild-Type <i>TP53</i> . <i>Molecular Cancer Research</i> , 2015, 13, 493-501.   | 3.4  | 53        |
| 207 | Subtype-specific microRNA expression signatures in breast cancer progression. <i>International Journal of Cancer</i> , 2016, 139, 1117-1128.  | 5.1  | 53        |
| 208 | Tumor diversity and the trade-off between universal cancer tasks. <i>Nature Communications</i> , 2019, 10, 5423.  | 12.8 | 53        |
| 209 | Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.   | 6.4  | 52        |
| 210 | Combined quantitative measures of ER, PR, HER2, and Ki67 provide more prognostic information than categorical combinations in luminal breast cancer. <i>Modern Pathology</i> , 2019, 32, 1244-1256. | 5.5  | 51        |
| 211 | Representative Sequencing: Unbiased Sampling of Solid Tumor Tissue. <i>Cell Reports</i> , 2020, 31, 107550.   | 6.4  | 51        |
| 212 | CDH1 c-160a promotor polymorphism is not associated with risk of stomach cancer. <i>International Journal of Cancer</i> , 2002, 101, 196-197.   | 5.1  | 50        |
| 213 | High-Resolution Magic Angle Spinning <sup>1</sup> H NMR Spectroscopy and Reverse Transcription-PCR Analysis of Apoptosis in a Rat Glioma. <i>Analytical Chemistry</i> , 2006, 78, 1546-1552.        | 6.5  | 50        |
| 214 | Androgen and Estrogen Receptors in Breast Cancer Coregulate Human UDP-Glucuronosyltransferases 2B15 and 2B17. <i>Cancer Research</i> , 2016, 76, 5881-5893.   | 0.9  | 50        |
| 215 | Intersect-then-combine approach: improving the performance of somatic variant calling in whole exome sequencing data using multiple aligners and callers. <i>Genome Medicine</i> , 2017, 9, 35.     | 8.2  | 48        |
| 216 | Genetic heterogeneity in breast cancer: the road to personalized medicine?. <i>BMC Medicine</i> , 2013, 11, 151.  | 5.5  | 47        |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 217 | <i>EN1 Is a Transcriptional Dependency in Triple-Negative Breast Cancer Associated with Brain Metastasis. Cancer Research, 2019, 79, 4173-4183.</i>                           | 0.9  | 47        |
| 218 | Genetic screening for hereditary diffuse gastric cancer. Expert Review of Molecular Diagnostics, 2003, 3, 201-215.  | 3.1  | 46        |
| 219 | Dihydrofolate reductase amplification and sensitization to methotrexate of methotrexate-resistant colon cancer cells. Molecular Cancer Therapeutics, 2009, 8, 424-432.        | 4.1  | 46        |
| 220 | Expression microarray reproducibility is improved by optimising purification steps in RNA amplification and labelling. BMC Genomics, 2004, 5, 9.                              | 2.8  | 45        |
| 221 | Genomic imbalances and patterns of karyotypic variability in mantle-cell lymphoma cell lines. Leukemia Research, 2006, 30, 923-934.   | 0.8  | 45        |
| 222 | Pathology findings and validation of gastric and esophageal cancer cases in a European cohort (EPIC/EUR-GAST). Scandinavian Journal of Gastroenterology, 2007, 42, 618-627.   | 1.5  | 45        |
| 223 | Array Comparative Genomic Hybridization Copy Number Profiling: A New Tool for Translational Research in Solid Malignancies. Seminars in Radiation Oncology, 2008, 18, 98-104. | 2.2  | 45        |
| 224 | Stratification and therapeutic potential of PML in metastatic breast cancer. Nature Communications, 2016, 7, 12595.   | 12.8 | 45        |
| 225 | Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.                                   | 1.9  | 45        |
| 226 | The Impact of Prophylactic Total Gastrectomy on Health-Related Quality of Life. Annals of Surgery, 2014, 260, 87-93.  | 4.2  | 44        |
| 227 | Ki67 expression in invasive breast cancer: the use of tissue microarrays compared with whole tissue sections. Breast Cancer Research and Treatment, 2017, 164, 341-348.       | 2.5  | 44        |
| 228 | The Molecular Tumor Board Portal supports clinical decisions and automated reporting for precision oncology. Nature Cancer, 2022, 3, 251-261.                                 | 13.2 | 44        |
| 229 | Context-Specific Effects of TGF- $\beta$ 2/SMAD3 in Cancer Are Modulated by the Epigenome. Cell Reports, 2015, 13, 2480-2490.   | 6.4  | 43        |
| 230 | Clonal replacement and heterogeneity in breast tumors treated with neoadjuvant HER2-targeted therapy. Nature Communications, 2019, 10, 657.                                   | 12.8 | 43        |
| 231 | Inclusion of Ki67 significantly improves performance of the PREDICT prognostication and prediction model for early breast cancer. BMC Cancer, 2014, 14, 908.                  | 2.6  | 42        |
| 232 | High-resolution array CGH clarifies events occurring on 8p in carcinogenesis. BMC Cancer, 2008, 8, 288.   | 2.6  | 41        |
| 233 | Imprinted Chromatin around DIRAS3 Regulates Alternative Splicing of GNG12-AS1, a Long Noncoding RNA. American Journal of Human Genetics, 2013, 93, 224-235.                   | 6.2  | 41        |
| 234 | SILAC identifies LAD1 as a filamin-binding regulator of actin dynamics in response to EGF and a marker of aggressive breast tumors. Science Signaling, 2018, 11, .            | 3.6  | 41        |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 235 | Hyperpolarized <sup>13</sup> C MRI of Tumor Metabolism Demonstrates Early Metabolic Response to Neoadjuvant Chemotherapy in Breast Cancer. <i>Radiology Imaging Cancer</i> , 2020, 2, e200017.   | 1.6  | 40        |
| 236 | Preclinical <i>In Vivo</i> Validation of the RAD51 Test for Identification of Homologous Recombination-Deficient Tumors and Patient Stratification. <i>Cancer Research</i> , 2022, 82, 1646-1657.  | 0.9  | 40        |
| 237 | Evidence that both genetic instability and selection contribute to the accumulation of chromosome alterations in cancer. <i>Carcinogenesis</i> , 2005, 26, 923-930.  | 2.8  | 39        |
| 238 | Cancer sequencing unravels clonal evolution. <i>Nature Biotechnology</i> , 2012, 30, 408-410.  | 17.5 | 38        |
| 239 | Amplification of TRIM44: Pairing a Prognostic Target With Potential Therapeutic Strategy. <i>Journal of the National Cancer Institute</i> , 2014, 106, .   | 6.3  | 38        |
| 240 | Pathway-based personalized analysis of breast cancer expression data. <i>Molecular Oncology</i> , 2015, 9, 1471-1483.  | 4.6  | 38        |
| 241 | A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015, 9, 115-127.   | 4.6  | 38        |
| 242 | Germline variation in inflammation-related pathways and risk of Barrett's oesophagus and oesophageal adenocarcinoma. <i>Gut</i> , 2017, 66, 1739-1747.   | 12.1 | 38        |
| 243 | Cancer Core Europe: A translational research infrastructure for a European mission on cancer. <i>Molecular Oncology</i> , 2019, 13, 521-527.   | 4.6  | 38        |
| 244 | Metabolic Imaging Detects Resistance to PI3K± Inhibition Mediated by Persistent FOXM1 Expression in ER+ Breast Cancer. <i>Cancer Cell</i> , 2020, 38, 516-533.e9.  | 16.8 | 38        |
| 245 | Case Report: Transverse Myelitis Associated With Epstein-Barr Virus Infection. <i>American Journal of the Medical Sciences</i> , 1994, 307, 45-48.   | 1.1  | 37        |
| 246 | High-Resolution Array-Based Comparative Genomic Hybridization of Bladder Cancers Identifies <i>Mouse Double Minute 4</i> ( <i>MDM4</i> ) as an Amplification Target Exclusive of <i>MDM2</i> and <i>TP53</i> . <i>Clinical Cancer Research</i> , 2008, 14, 2527-2534.  | 7.0  | 37        |
| 247 | SOX4 can redirect TGF-β-mediated SMAD3-transcriptional output in a context-dependent manner to promote tumorigenesis. <i>Nucleic Acids Research</i> , 2018, 46, 9578-9590.   | 14.5 | 37        |
| 248 | Landscapes of cellular phenotypic diversity in breast cancer xenografts and their impact on drug response. <i>Nature Communications</i> , 2021, 12, 1998.  | 12.8 | 37        |
| 249 | The molecular landscape of Asian breast cancers reveals clinically relevant population-specific differences. <i>Nature Communications</i> , 2020, 11, 6433.  | 12.8 | 37        |
| 250 | Familial gastric cancer “aetiology and pathogenesis. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2006, 20, 721-734.   | 2.4  | 36        |
| 251 | Re: CYP2D6 Genotype and Tamoxifen Response in Postmenopausal Women With Endocrine-Responsive Breast Cancer: The Breast International Group 1-98 Trial and Re: CYP2D6 and UGT2B7 Genotype and Risk of Recurrence in Tamoxifen-Treated Breast Cancer Patients. <i>Journal of the National Cancer Institute</i> , 2012, 104, 1263-1264. | 6.3  | 36        |
| 252 | Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 32-39.  | 9.6  | 35        |



| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 253 | Common germline polymorphisms in <i>COMT</i> , <i>CYP19A1</i> , <i>ESR1</i> , <i>PGR</i> , <i>SULT1E1</i> and <i>STS</i> and survival after a diagnosis of breast cancer. <i>International Journal of Cancer</i> , 2009, 125, 2687-2696. | 5.1  | 34        |
| 254 | Navigators, a modulator of cell migration, may act as a suppressor of breast cancer progression. <i>EMBO Molecular Medicine</i> , 2015, 7, 299-314.  | 6.9  | 34        |
| 255 | $\beta$ -catenin is a candidate tumor suppressor for the development of E-cadherin-expressing lobular-type breast cancer. <i>Journal of Pathology</i> , 2018, 245, 456-467.  | 4.5  | 34        |
| 256 | Time-resolved single-cell analysis of Brca1 associated mammary tumorigenesis reveals aberrant differentiation of luminal progenitors. <i>Nature Communications</i> , 2021, 12, 1502.   | 12.8 | 34        |
| 257 | Effects of common germline genetic variation in cell cycle control genes on breast cancer survival: results from a population-based cohort. <i>Breast Cancer Research</i> , 2008, 10, R47.   | 5.0  | 33        |
| 258 | Extent of differential allelic expression of candidate breast cancer genes is similar in blood and breast. <i>Breast Cancer Research</i> , 2009, 11, R88.  | 5.0  | 33        |
| 259 | DNA polymerase $\delta$ deficiency is linked to aggressive breast cancer: A comprehensive analysis of gene copy number, mRNA and protein expression in multiple cohorts. <i>Molecular Oncology</i> , 2014, 8, 520-532.                   | 4.6  | 33        |
| 260 | EZH2 Is Overexpressed in <i>BRCA1</i> -like Breast Tumors and Predictive for Sensitivity to High-Dose Platinum-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2019, 25, 4351-4362.  | 7.0  | 33        |
| 261 | Towards a cancer mission in Horizon Europe: recommendations. <i>Molecular Oncology</i> , 2020, 14, 1589-1615.  | 4.6  | 33        |
| 262 | Molecular profiling of breast cancer: portraits but not physiognomy. <i>Breast Cancer Research</i> , 2001, 3, 77.  | 5.0  | 32        |
| 263 | Chromosome abnormalities in 10 lung cancer cell lines of the NCI-H series analyzed with spectral karyotyping. <i>Cancer Genetics and Cytogenetics</i> , 2005, 162, 1-9.  | 1.0  | 32        |
| 264 | ZNF198, a zinc finger protein rearranged in myeloproliferative disease, localizes to the PML nuclear bodies and interacts with SUMO-1 and PML. <i>Experimental Cell Research</i> , 2006, 312, 3739-3751.                                 | 2.6  | 32        |
| 265 | Structural analysis of the genome of breast cancer cell line ZR-75-30 identifies twelve expressed fusion genes. <i>BMC Genomics</i> , 2012, 13, 719.   | 2.8  | 32        |
| 266 | Global transcriptional analysis identifies a novel role for SOX4 in tumor-induced angiogenesis. <i>ELife</i> , 2018, 7, .  | 6.0  | 32        |
| 267 | Isolation and characterization of a Pufferfish MLL (Mixed lineage leukemia)-like gene (fMLL) reveals evolutionary conservation in vertebrate genes related to <i>Drosophila trithorax</i> . <i>Oncogene</i> , 1998, 16, 3233-3241.       | 5.9  | 31        |
| 268 | Prognostic Value of MammaPrint <sup>®</sup> in Invasive Lobular Breast Cancer. <i>Biomarker Insights</i> , 2016, 11, BMI.S38435.   | 2.5  | 31        |
| 269 | Double-stranded microRNA mimics can induce length- and passenger strand-dependent effects in a cell type-specific manner. <i>Rna</i> , 2016, 22, 193-203.  | 3.5  | 31        |
| 270 | Data-driven analysis of immune infiltrate in a large cohort of breast cancer and its association with disease progression, ER activity, and genomic complexity. <i>Oncotarget</i> , 2017, 8, 57121-57133.                                | 1.8  | 31        |



| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 271 | Genomic analysis of the 8p11-12 amplicon in familial breast cancer. International Journal of Cancer, 2007, 120, 714-717.   | 5.1  | 30        |
| 272 | A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.  | 12.8 | 30        |
| 273 | Synchronous mature teratomas of the ovary and liver: A case presenting 11 years following chemotherapy for immature teratoma. Gynecologic Oncology, 1992, 47, 385-390.   | 1.4  | 29        |
| 274 | Robust BRCA1-like classification of copy number profiles of samples repeated across different datasets and platforms. Molecular Oncology, 2015, 9, 1274-1286.  | 4.6  | 29        |
| 275 | The Psychosocial Impact of Undergoing Prophylactic Total Gastrectomy (PTG) to Manage the Risk of Hereditary Diffuse Gastric Cancer (HDGC). Journal of Genetic Counseling, 2017, 26, 752-762.                             | 1.6  | 29        |
| 276 | DNA methylation landscapes of 1538 breast cancers reveal a replication-linked clock, epigenomic instability and cis-regulation. Nature Communications, 2021, 12, 5406.   | 12.8 | 29        |
| 277 | TOMM34 expression in early invasive breast cancer: a biomarker associated with poor outcome. Breast Cancer Research and Treatment, 2012, 136, 419-427.   | 2.5  | 28        |
| 278 | An investigation of the factors effecting high-risk individuals' decision-making about prophylactic total gastrectomy and surveillance for hereditary diffuse gastric cancer (HDGC). Familial Cancer, 2016, 15, 665-676. | 1.9  | 28        |
| 279 | Differential gene expression in the murine gastric fundus lacking interstitial cells of Cajal. BMC Gastroenterology, 2003, 3, 14.  | 2.0  | 27        |
| 280 | Metabolic Consequences of p300 Gene Deletion in Human Colon Cancer Cells. Cancer Research, 2006, 66, 7606-7614.  | 0.9  | 27        |
| 281 | Co-amplification of 8p12 and 11q13 in breast cancers is not the result of a single genomic event. Genes Chromosomes and Cancer, 2007, 46, 427-439.   | 2.8  | 27        |
| 282 | The breast cancer somatic 'muta-ome': tackling the complexity. Breast Cancer Research, 2009, 11, 301.  | 5.0  | 27        |
| 283 | Calpastatin is associated with lymphovascular invasion in breast cancer. Breast, 2011, 20, 413-418.  | 2.2  | 27        |
| 284 | A Sparse Regulatory Network of Copy-Number Driven Gene Expression Reveals Putative Breast Cancer Oncogenes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 947-954.                         | 3.0  | 27        |
| 285 | miR-342-5p as a Potential Regulator of HER2 Breast Cancer Cell Growth. MicroRNA (Shariqah, United) Tj ETQq1 1 0,784314 rgBT /Overl   | 1.2  | 27        |
| 286 | A metadata approach for clinical data management in translational genomics studies in breast cancer. BMC Medical Genomics, 2009, 2, 66.  | 1.5  | 26        |
| 287 | A nested cohort study of 6,248 early breast cancer patients treated in neoadjuvant and adjuvant chemotherapy trials investigating the prognostic value of chemotherapy-related toxicities. BMC Medicine, 2015, 13, 306.  | 5.5  | 26        |
| 288 | Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.   | 5.0  | 26        |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 289 | Chlorambucil targets <scp>BRCA</scp> 1/2-deficient tumours and counteracts <scp>PARP</scp> inhibitor resistance. EMBO Molecular Medicine, 2019, 11, e9982.   | 6.9  | 26        |
| 290 | Cell memory and cancer--the story of the trithorax and Polycomb group genes. , 1999, 18, 313-329.  |      | 25        |
| 291 | Up-regulation of the interferon-related genes in BRCA2 knockout epithelial cells. Journal of Pathology, 2014, 234, 386-397.  | 4.5  | 25        |
| 292 | Cancer Core Europe: A consortium to address the cancer care " Cancer research continuum challenge. European Journal of Cancer, 2014, 50, 2745-2746.  | 2.8  | 25        |
| 293 | Shallow whole genome sequencing for robust copy number profiling of formalin-fixed paraffin-embedded breast cancers. Experimental and Molecular Pathology, 2018, 104, 161-169.   | 2.1  | 25        |
| 294 | A key genomic subtype associated with lymphovascular invasion in invasive breast cancer. British Journal of Cancer, 2019, 120, 1129-1136.  | 6.4  | 25        |
| 295 | Hyperpolarized Carbon-13 MRI for Early Response Assessment of Neoadjuvant Chemotherapy in Breast Cancer Patients. Cancer Research, 2021, 81, 6004-6017.  | 0.9  | 25        |
| 296 | Telomerase- and Alternative Telomere Lengthening-independent Telomere Stabilization in a Metastasis-Derived Human Non-Small Cell Lung Cancer Cell Line: Effect of Ectopic hTERT. Cancer Research, 2006, 66, 3584-3592. | 0.9  | 24        |
| 297 | Oncogenic <i>KRAS</i> is not necessary for Wnt signalling activation in APC-associated FAP adenomas. Journal of Pathology, 2010, 221, 57-67.   | 4.5  | 24        |
| 298 | A co-culture genome-wide RNAi screen with mammary epithelial cells reveals transmembrane signals required for growth and differentiation. Breast Cancer Research, 2015, 17, 4.   | 5.0  | 24        |
| 299 | Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. Journal of Pathology: Clinical Research, 2015, 1, 18-32.             | 3.0  | 24        |
| 300 | Cancer Treatment in the Genomic Era. Annual Review of Biochemistry, 2019, 88, 247-280.   | 11.1 | 24        |
| 301 | Expression profiling of nuclear receptors in breast cancer identifies TLX as a mediator of growth and invasion in triple-negative breast cancer. Oncotarget, 2015, 6, 21685-21703.                                     | 1.8  | 24        |
| 302 | TOX3 Mutations in Breast Cancer. PLoS ONE, 2013, 8, e74102.  | 2.5  | 23        |
| 303 | Expression and protein-binding studies of the EEN gene family, new interacting partners for dynamin, synaptojanin and huntingtin proteins. Biochemical Journal, 2000, 348, 447-458.                                    | 3.7  | 22        |
| 304 | PMC42, a breast progenitor cancer cell line, has normal-like mRNA and microRNA transcriptomes. Breast Cancer Research, 2008, 10, R54.  | 5.0  | 22        |
| 305 | Effects of BRCA2 cis-regulation in normal breast and cancer risk amongst BRCA2 mutation carriers. Breast Cancer Research, 2012, 14, R63.   | 5.0  | 22        |
| 306 | Trial watch : the gut microbiota as a tool to boost the clinical efficacy of anticancer immunotherapy. OncoImmunology, 2020, 9, 1774298.   | 4.6  | 22        |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 307 | Serial Analysis of Circulating Tumor Cells in Metastatic Breast Cancer Receiving First-Line Chemotherapy. <i>Journal of the National Cancer Institute</i> , 2021, 113, 443-452.   | 6.3  | 22        |
| 308 | FGFR1 amplification or overexpression and hormonal resistance in luminal breast cancer: rationale for a triple blockade of ER, CDK4/6, and FGFR1. <i>Breast Cancer Research</i> , 2021, 23, 21.   | 5.0  | 22        |
| 309 | Deciphering the signaling network of breast cancer improves drug sensitivity prediction. <i>Cell Systems</i> , 2021, 12, 401-418.e12.   | 6.2  | 22        |
| 310 | Analytical demands to use whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 16-22.   | 9.6  | 22        |
| 311 | Genetic Alterations in the PI3K/AKT Pathway and Baseline AKT Activity Define AKT Inhibitor Sensitivity in Breast Cancer Patient-derived Xenografts. <i>Clinical Cancer Research</i> , 2020, 26, 3720-3731.  | 7.0  | 21        |
| 312 | Pharmacogenetics of cancer chemotherapy. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2006, 1766, 168-183.   | 7.4  | 19        |
| 313 | Nucleosome mapping in plasma DNA predicts cancer gene expression. <i>Nature Genetics</i> , 2016, 48, 1105-1106.   | 21.4 | 19        |
| 314 | Familial gastric cancer – clinical management. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2006, 20, 735-743.  | 2.4  | 18        |
| 315 | Addition of gemcitabine to paclitaxel, epirubicin, and cyclophosphamide adjuvant chemotherapy for women with early-stage breast cancer (tAnGo): final 10-year follow-up of an open-label, randomised, phase 3 trial. <i>Lancet Oncology</i> , The, 2017, 18, 755-769.                               | 10.7 | 18        |
| 316 | BET Inhibition as a Rational Therapeutic Strategy for Invasive Lobular Breast Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 7139-7150.  | 7.0  | 18        |
| 317 | NRG1 fusions in breast cancer. <i>Breast Cancer Research</i> , 2021, 23, 3.   | 5.0  | 18        |
| 318 | Predictive cancer genomics – what do we need?. <i>Lancet</i> , The, 2003, 362, 340-341.   | 13.7 | 17        |
| 319 | p120-catenin prevents multinucleation through control of MKLP1-dependent RhoA activity during cytokinesis. <i>Nature Communications</i> , 2016, 7, 13874.   | 12.8 | 17        |
| 320 | Predicting treatment resistance and relapse through circulating DNA. <i>Breast</i> , 2017, 34, S31-S35.   | 2.2  | 17        |
| 321 | POSEIDON Trial Phase 1b Results: Safety, Efficacy and Circulating Tumor DNA Response of the Beta Isoform-Sparing PI3K Inhibitor Taselisib (GDC-0032) Combined with Tamoxifen in Hormone Receptor Positive Metastatic Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2019, 25, 6598-6605. | 7.0  | 17        |
| 322 | Chromosome 12p Amplification in Triple-Negative/BRCA1-Mutated Breast Cancer Associates with Emergence of Docetaxel Resistance and Carboplatin Sensitivity. <i>Cancer Research</i> , 2019, 79, 4258-4270.  | 0.9  | 17        |
| 323 | Does massively parallel transcriptome analysis signify the end of cancer histopathology as we know it?. <i>Genome Biology</i> , 2000, 1, reviews1021.1.   | 9.6  | 16        |
| 324 | From genomic landscapes to personalized cancer management – is there a roadmap?. <i>Annals of the New York Academy of Sciences</i> , 2010, 1210, 34-44.   | 3.8  | 16        |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 325 | Breast cancer susceptibility risk associations and heterogeneity by E-cadherin tumor tissue expression. <i>Breast Cancer Research and Treatment</i> , 2014, 143, 181-187.  | 2.5  | 16        |
| 326 | Rho-GTPase activating-protein 18: a biomarker associated with good prognosis in invasive breast cancer. <i>British Journal of Cancer</i> , 2017, 117, 1176-1184.   | 6.4  | 16        |
| 327 | Interactions Between Genetic Variants and Environmental Factors Affect Risk of Esophageal Adenocarcinoma and Barrett's Esophagus. <i>Clinical Gastroenterology and Hepatology</i> , 2018, 16, 1598-1606.e4.                                  | 4.4  | 16        |
| 328 | No Association Between Vitamin D Status and Risk of Barrett's Esophagus or Esophageal Adenocarcinoma: A Mendelian Randomization Study. <i>Clinical Gastroenterology and Hepatology</i> , 2019, 17, 2227-2235.e1.                             | 4.4  | 16        |
| 329 | Sex-Specific Genetic Associations for Barrett's Esophagus and Esophageal Adenocarcinoma. <i>Gastroenterology</i> , 2020, 159, 2065-2076.e1.  | 1.3  | 16        |
| 330 | Allele-specific expression analysis methods for high-density SNP microarray data. <i>Bioinformatics</i> , 2012, 28, 1102-1108.   | 4.1  | 15        |
| 331 | Prognosis of early breast cancer by immunohistochemistry defined intrinsic sub-types in patients treated with adjuvant chemotherapy in the NEAT/BR9601 trial. <i>International Journal of Cancer</i> , 2013, 133, 1470-1478.                 | 5.1  | 15        |
| 332 | Central pathology review with two-stage quality assurance for pathological response after neoadjuvant chemotherapy in the ARTemis Trial. <i>Modern Pathology</i> , 2017, 30, 1069-1077.  | 5.5  | 15        |
| 333 | Cancer Core Europe: A European cancer research alliance realizing a research infrastructure with critical mass and programmatic approach to cure cancer in the 21st century. <i>European Journal of Cancer</i> , 2018, 103, 155-159.         | 2.8  | 15        |
| 334 | Germline <i>APOBEC3B</i> deletion increases somatic hypermutation in Asian breast cancer that is associated with Her2 subtype, <i>PIK3CA</i> mutations and immune activation. <i>International Journal of Cancer</i> , 2021, 148, 2489-2501. | 5.1  | 15        |
| 335 | The Relationship between Common Genetic Markers of Breast Cancer Risk and Chemotherapy-Induced Toxicity: A Case-Control Study. <i>PLoS ONE</i> , 2016, 11, e0158984.   | 2.5  | 15        |
| 336 | Analysis of the region of the 5' end of the MLL gene involved in genomic duplication events. <i>British Journal of Haematology</i> , 1999, 105, 256-264.   | 2.5  | 14        |
| 337 | The importance of platform annotation in interpreting microarray data. <i>Lancet Oncology</i> , 2010, 11, 717.   | 10.7 | 14        |
| 338 | PDLIM2 Is a Marker of Adhesion and $\beta$ -Catenin Activity in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2019, 79, 2619-2633.   | 0.9  | 14        |
| 339 | Positive correlation between transcriptomic stemness and PI3K/AKT/mTOR signaling scores in breast cancer, and a counterintuitive relationship with PIK3CA genotype. <i>PLoS Genetics</i> , 2021, 17, e1009876.                               | 3.5  | 14        |
| 340 | <i>Saccharomyces cerevisiae</i> -like 1 (SEC14L1) is a prognostic factor in breast cancer associated with lymphovascular invasion. <i>Modern Pathology</i> , 2018, 31, 1675-1682.  | 5.5  | 13        |
| 341 | Differential gene expression profile in the small intestines of mice lacking pacemaker interstitial cells of Cajal. <i>BMC Gastroenterology</i> , 2003, 3, 17.   | 2.0  | 12        |
| 342 | Further evidence to support bimodality of oestrogen receptor expression in breast cancer. <i>Histopathology</i> , 2017, 70, 456-465.   | 2.9  | 12        |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 343 | Association Between Levels of Sex Hormones and Risk of Esophageal Adenocarcinoma and Barrett's Esophagus. <i>Clinical Gastroenterology and Hepatology</i> , 2020, 18, 2701-2709.e3.   | 4.4  | 12        |
| 344 | The GATA3 X308_Splice breast cancer mutation is a hormone context-dependent oncogenic driver. <i>Oncogene</i> , 2020, 39, 5455-5467.  | 5.9  | 12        |
| 345 | PI3K activation promotes resistance to eribulin in HER2-negative breast cancer. <i>British Journal of Cancer</i> , 2021, 124, 1581-1591.  | 6.4  | 12        |
| 346 | Nucleoporin-93 reveals a common feature of aggressive breast cancers: robust nucleocytoplasmic transport of transcription factors. <i>Cell Reports</i> , 2022, 38, 110418.  | 6.4  | 12        |
| 347 | CYP2D6 Gene Variants and Their Association with Breast Cancer Susceptibility. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1255-1258.   | 2.5  | 11        |
| 348 | Genome co-amplification upregulates a mitotic gene network activity that predicts outcome and response to mitotic protein inhibitors in breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 70.  | 5.0  | 11        |
| 349 | Reliable gene expression profiling of formalin-fixed paraffin-embedded breast cancer tissue (FFPE) using cDNA-mediated annealing, extension, selection, and ligation whole-genome (DASL WG) assay. <i>BMC Medical Genomics</i> , 2016, 9, 54. | 1.5  | 11        |
| 350 | Integrative analysis of copy number and gene expression in breast cancer using formalin-fixed paraffin-embedded core biopsy tissue: a feasibility study. <i>BMC Genomics</i> , 2017, 18, 526.   | 2.8  | 11        |
| 351 | Age-correlated protein and transcript expression in breast cancer and normal breast tissues is dominated by host endocrine effects. <i>Nature Cancer</i> , 2020, 1, 518-532.  | 13.2 | 11        |
| 352 | Six versus 12 months' adjuvant trastuzumab in patients with HER2-positive early breast cancer: the PERSEPHONE non-inferiority RCT. <i>Health Technology Assessment</i> , 2020, 24, 1-190.   | 2.8  | 11        |
| 353 | Decline in Antigenicity of Tumor Markers by Storage Time Using Pathology Sections Cut From Tissue Microarrays. <i>Applied Immunohistochemistry and Molecular Morphology</i> , 2016, 24, 221-226.  | 1.2  | 10        |
| 354 | Fbxl17 is rearranged in breast cancer and loss of its activity leads to increased global O-GlcNAcylation. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 2605-2620.  | 5.4  | 10        |
| 355 | Clinical interpretation of whole-genome and whole-transcriptome sequencing for precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 23-31.   | 9.6  | 10        |
| 356 | Molecular staging of cancer: is it time?. <i>Lancet, The</i> , 1997, 350, 231.  | 13.7 | 9         |
| 357 | The breast cancer genome - a key for better oncology. <i>BMC Cancer</i> , 2011, 11, 501.  | 2.6  | 9         |
| 358 | Polymorphisms in Genes of Relevance for Oestrogen and Oxytocin Pathways and Risk of Barrett's Esophagus and Esophageal Adenocarcinoma: A Pooled Analysis from the BEACON Consortium. <i>PLoS ONE</i> , 2015, 10, e0138738.                    | 2.5  | 9         |
| 359 | 3D deformable registration of longitudinal abdominopelvic CT images using unsupervised deep learning. <i>Computer Methods and Programs in Biomedicine</i> , 2021, 208, 106261.  | 4.7  | 9         |
| 360 | DNA copy number motifs are strong and independent predictors of survival in breast cancer. <i>Communications Biology</i> , 2020, 3, 153.  | 4.4  | 9         |

| #   | ARTICLE   | IF   | CITATIONS |
|-----|---|------|-----------|
| 361 | Expression and protein-binding studies of the EEN gene family, new interacting partners for dynamin, synaptojanin and huntingtin proteins. Biochemical Journal, 2000, 348, 447.   | 3.7  | 8         |
| 362 | Novel human, mouse and xenopus genes encoding a member of the RAS superfamily of low-molecular-weight GTP-binding proteins and its downregulation in W/WV mouse jejunum. Journal of Gastroenterology and Hepatology (Australia), 2004, 19, 211-217. | 2.8  | 8         |
| 363 | How to validate a breast cancer prognostic signature. Nature Reviews Clinical Oncology, 2010, 7, 615-616.   | 27.6 | 8         |
| 364 | Transcriptional profiling reveals a subset of human breast tumors that retain wt <i>TP53</i> but display mutant p53-associated features. Molecular Oncology, 2020, 14, 1640-1652.   | 4.6  | 8         |
| 365 | Assessing excellence in translational cancer research: a consensus based framework. Journal of Translational Medicine, 2013, 11, 274.   | 4.4  | 7         |
| 366 | <i>scp</i> eEF <sup>2K</sup> a new target in breast cancers with combined inactivation of p53 and PTEN. EMBO Molecular Medicine, 2014, 6, 1512-1514.  | 6.9  | 7         |
| 367 | Modeling Breast Cancer Intertumor and Intratumor Heterogeneity Using Xenografts. Cold Spring Harbor Symposia on Quantitative Biology, 2016, 81, 227-230.  | 1.1  | 7         |
| 368 | High-risk individuals'™ perceptions of reproductive genetic testing for CDH1 mutations. Familial Cancer, 2017, 16, 531-535.   | 1.9  | 7         |
| 369 | TSHZ2 is an EGF-regulated tumor suppressor that binds to the cytokinesis regulator PRC1 and inhibits metastasis. Science Signaling, 2021, 14, .   | 3.6  | 7         |
| 370 | Calling Sample Mix-Ups in Cancer Population Studies. PLoS ONE, 2012, 7, e41815.   | 2.5  | 6         |
| 371 | Characterisation of PALB2 tumours through whole-exome and whole-transcriptomic analyses. Npj Breast Cancer, 2021, 7, 46.  | 5.2  | 6         |
| 372 | Clonal populations of a human TNBC model display significant functional heterogeneity and divergent growth dynamics in distinct contexts. Oncogene, 2022, 41, 112-124.  | 5.9  | 6         |
| 373 | High-throughput surface marker screen on primary human breast tissues reveals further cellular heterogeneity. Breast Cancer Research, 2021, 23, 66.   | 5.0  | 5         |
| 374 | Functional genomics approaches to improve pre-clinical drug screening and biomarker discovery. EMBO Molecular Medicine, 2021, 13, e13189.   | 6.9  | 5         |
| 375 | ARTEMIS: A randomised trial of bevacizumab with neoadjuvant chemotherapy (NACT) for patients with HER2-negative early breast cancerâ€™Primary endpoint, pathological complete response (pCR).. Journal of Clinical Oncology, 2014, 32, 1014-1014.   | 1.6  | 5         |
| 376 | Modeling the Prognostic Impact of Circulating Tumor Cells Enumeration in Metastatic Breast Cancer for Clinical Trial Design Simulation. Oncologist, 2022, 27, e561-e570.  | 3.7  | 5         |
| 377 | MTAP homozygous deletion: An achilles heel of human cancers ready for clinical use?. Cancer Biology and Therapy, 2005, 4, 347-347.  | 3.4  | 4         |
| 378 | Optimal Amounts of Fluorescent Dye Improve Expression Microarray Results in Tumor Specimens. Molecular Biotechnology, 2005, 30, 151-154.  | 2.4  | 4         |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
| 379 | WSRF-Based Modeling of Clinical Trial Information for Collaborative Cancer Research. , 2008, , .   |      | 4         |
| 380 | Circulating tumor DNA is readily detectable among Ghanaian breast cancer patients supporting non-invasive cancer genomic studies in Africa. Npj Precision Oncology, 2021, 5, 83.   | 5.4  | 4         |
| 381 | Molecular genetics and the assessment of human cancers. Expert Reviews in Molecular Medicine, 1999, 1, 1-19.   | 3.9  | 3         |
| 382 | A quantum leap in our knowledge of breast cancer mutations. Breast Cancer Research, 2006, 8, 304.  | 5.0  | 3         |
| 383 | Tamoxifen“when more might be better. Nature Reviews Clinical Oncology, 2013, 10, 125-126.  | 27.6 | 3         |
| 384 | Disease-free (DFS) and overall survival (OS) at 3.4 years (yrs) for neoadjuvant bevacizumab (Bev) added to docetaxel followed by fluorouracil, epirubicin and cyclophosphamide (D-FEC), for women with HER2 negative early breast cancer: The ARTEMIS trial.. Journal of Clinical Oncology, 2016, 34, 1014-1014. | 1.6  | 3         |
| 385 | A sparse regulatory network of copy-number driven expression reveals putative breast cancer oncogenes. , 2010, , .   |      | 2         |
| 386 | PathTracer: High-sensitivity detection of differential pathway activity in tumours. Scientific Reports, 2019, 9, 16332.  | 3.3  | 2         |
| 387 | Association of Sperm-Associated Antigen 5 and Treatment Response in Patients With Estrogen Receptor“Positive Breast Cancer. JAMA Network Open, 2020, 3, e209486.   | 5.9  | 2         |
| 388 | Abstract GS4-08: Clinical utility of repeated circulating tumor cell (CTC) enumeration as early treatment monitoring tool in metastatic breast cancer (MBC) - a global pooled analysis with individual patient data. , 2021, , .   |      | 2         |
| 389 | The temporal mutational and immune tumour microenvironment remodelling of HER2-negative primary breast cancers. Npj Breast Cancer, 2021, 7, 73.  | 5.2  | 2         |
| 390 | Metabolic imaging with hyperpolarized [1-13C] pyruvate in patient-derived preclinical mouse models of breast cancer. STAR Protocols, 2021, 2, 100608.  | 1.2  | 2         |
| 391 | Analysis of the region of the 5' end of the MLL gene involved in genomic duplication events. British Journal of Haematology, 1999, 105, 256-264.   | 2.5  | 2         |
| 392 | ARTEMIS: Randomized trial with neoadjuvant chemotherapy for patients with early breast cancer.. Journal of Clinical Oncology, 2012, 30, TPS1144-TPS1144.   | 1.6  | 2         |
| 393 | Gastric Cancer “ Keeping It in the Family. Cancer Reviews: Asia-Pacific, 2004, 02, 69-79.  | 0.1  | 1         |
| 394 | Translational genomics in breast cancer. European Journal of Cancer, 2011, 47, S381-S382.  | 2.8  | 1         |
| 395 | A metadata-aware application for remote scoring and exchange of tissue microarray images. BMC Bioinformatics, 2013, 14, 147.   | 2.6  | 1         |
| 396 | Corrigendum to “Basic cancer research is essential for the success of personalised medicine“ [European Journal of Cancer 49(12) pp. 2619“2620 (2013)]. European Journal of Cancer, 2013, 49, 3577.   | 2.8  | 1         |



| #   | ARTICLE   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 397 | Replication of Genetic Polymorphisms Reported to Be Associated with Taxane-Related Sensory Neuropathy in Patients with Early Breast Cancer Treated with Paclitaxel. Clinical Cancer Research, 2015, 21, 3094-3094.                  | 7.0 | 1         |
| 398 | Abstract A8: The EurOPDX consortium: Sharing patient tumor-derived xenografts for collaborative multicentric preclinical trials.. , 2013, , .   |     | 1         |
| 399 | Abstract 3596: Biomarkers of response to CDK4/6 inhibitor (CDK4/6i) in hormone receptor (HR) positive and HER2-positive breast cancer (BC) patient-derived xenografts (PDX).. , 2018, , .   |     | 1         |
| 400 | Allelic expression imbalance of PIK3CA mutations is frequent in breast cancer and prognostically significant. Npj Breast Cancer, 2022, 8, .   | 5.2 | 1         |
| 401 | eQTL set-based association analysis identifies novel susceptibility loci for Barrett's esophagus and esophageal adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 0, , .   | 2.5 | 1         |
| 402 | P38: DNA copy number changes predicting resistance to therapy in ovarian cancer patients. European Journal of Medical Genetics, 2005, 48, 503-504.  | 1.3 | 0         |
| 403 | Metamodel-Based Generation of WSRF-Compliant SOA for Collaborative Cancer Research.. , 2008, , .  |     | 0         |
| 404 | Prognostic gene network modules in breast cancer hold promise. Breast Cancer Research, 2010, 12, 317.   | 5.0 | 0         |
| 405 | Finding Common Regions of Alteration in Copy Number Data. Methods in Molecular Biology, 2013, 973, 339-353.   | 0.9 | 0         |
| 406 | Elucidating the Altered Transcriptional Programs in Breast Cancer using Independent Component Analysis. PLoS Computational Biology, 2005, preprint, e161.   | 3.2 | 0         |
| 407 | A retrospective study of SPAG5 expression and its clinical implications in >8,000 patients of ER positive (ER+) breast cancer (BC): Genomic, transcriptomic and protein analysis.. Journal of Clinical Oncology, 2016, 34, 575-575. | 1.6 | 0         |
| 408 | Bcl11a Marks Mammary Progenitor Cells and Promotes Early Cellular Changes Associated with TNBC by Recruiting Chd8. SSRN Electronic Journal, 0, , .  | 0.4 | 0         |
| 409 | Interview with Carlos Caldas. European Medical Journal Oncology, 0, , .   | 0.0 | 0         |
| 410 | Germline allelic expression of genes at 17q22 locus associates with risk of breast cancer. European Journal of Cancer, 2022, 172, 146-157.  | 2.8 | 0         |