## Diether Lambrechts

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4037662/publications.pdf

Version: 2024-02-01

548 papers 49,230 citations

100 h-index 198 g-index

596 all docs

596 docs citations

596 times ranked

65102 citing authors

#	Article	IF	CITATIONS
1	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	13.7	1,937
2	Effects of KRAS, BRAF, NRAS, and PIK3CA mutations on the efficacy of cetuximab plus chemotherapy in chemotherapy-refractory metastatic colorectal cancer: a retrospective consortium analysis. Lancet Oncology, The, 2010, 11, 753-762.	10.7	1,915
3	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	21.4	1,685
4	Phenotype molding of stromal cells in the lung tumor microenvironment. Nature Medicine, 2018, 24, 1277-1289.	30.7	1,126
5	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
6	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
7	Addition of cetuximab to oxaliplatin-based first-line combination chemotherapy for treatment of advanced colorectal cancer: results of the randomised phase 3 MRC COIN trial. Lancet, The, 2011, 377, 2103-2114.	13.7	876
8	VEGF is a modifier of amyotrophic lateral sclerosis in mice and humans and protects motoneurons against ischemic death. Nature Genetics, 2003, 34, 383-394.	21.4	794
9	Gene prioritization through genomic data fusion. Nature Biotechnology, 2006, 24, 537-544.	17.5	787
10	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
11	Role of PIGF in the intra- and intermolecular cross talk between the VEGF receptors Flt1 and Flk1. Nature Medicine, 2003, 9, 936-943.	30.7	699
12	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. Journal of the National Cancer Institute, 2011, 103, 250-263.	6.3	596
13	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
14	Association Between <emph type="ital">BRCA1</emph> and <emph type="ital"&gt;BRCA2 Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. JAMA - Journal of the American Medical Association, 2012, 307, 382.</emph 	7.4	546
15	Tumour hypoxia causes DNA hypermethylation by reducing TET activity. Nature, 2016, 537, 63-68.	27.8	521
16	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
17	Thrombomodulin Mutations in Atypical Hemolytic–Uremic Syndrome. New England Journal of Medicine, 2009, 361, 345-357.	27.0	495
18	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493

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19	VEGF: once regarded as a specific angiogenic factor, now implicated in neuroprotection. BioEssays, 2004, 26, 943-954.	2.5	476
20	Treatment of motoneuron degeneration by intracerebroventricular delivery of VEGF in a rat model of ALS. Nature Neuroscience, 2005, 8, 85-92.	14.8	464
21	Inhibition of the Glycolytic Activator PFKFB3 in Endothelium Induces Tumor Vessel Normalization, Impairs Metastasis, and Improves Chemotherapy. Cancer Cell, 2016, 30, 968-985.	16.8	464
22	Gain of function of mutant p53 by coaggregation with multiple tumor suppressors. Nature Chemical Biology, 2011, 7, 285-295.	8.0	450
23	Deficiency or inhibition of oxygen sensor Phd1 induces hypoxia tolerance by reprogramming basal metabolism. Nature Genetics, 2008, 40, 170-180.	21.4	433
24	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, $2015,107,$	6.3	428
25	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
26	Genome dynamics of the human embryonic kidney 293 lineage in response to cell biology manipulations. Nature Communications, 2014, 5, 4767.	12.8	421
27	A pan-cancer blueprint of the heterogeneous tumor microenvironment revealed by single-cell profiling. Cell Research, 2020, 30, 745-762.	12.0	391
28	Role and Therapeutic Potential of VEGF in the Nervous System. Physiological Reviews, 2009, 89, 607-648.	28.8	385
29	Lineage-dependent gene expression programs influence the immune landscape of colorectal cancer. Nature Genetics, 2020, 52, 594-603.	21.4	380
30	Vitamin D deficiency is highly prevalent in COPD and correlates with variants in the vitamin D-binding gene. Thorax, 2010, 65, 215-220.	5.6	379
31	Progranulin functions as a neurotrophic factor to regulate neurite outgrowth and enhance neuronal survival. Journal of Cell Biology, 2008, 181, 37-41.	5.2	376
32	Genome-wide association studies identify four ER negative–specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
33	p53 induces formation of NEAT1 IncRNA-containing paraspeckles that modulate replication stress response and chemosensitivity. Nature Medicine, 2016, 22, 861-868.	30.7	372
34	Self-Maintaining Gut Macrophages Are Essential for Intestinal Homeostasis. Cell, 2018, 175, 400-415.e13.	28.9	371
35	Underestimated and under-recognized: the late consequences of acute coronary syndrome (GRACE) Tj ETQq1 1	. 0.784314 2.2	rgBT/Overlo
36	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357

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37	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer.  Nature Genetics, 2017, 49, 680-691.	21.4	356
38	A single-cell map of intratumoral changes during anti-PD1 treatment of patients with breast cancer. Nature Medicine, 2021, 27, 820-832.	30.7	330
39	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
40	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
41	Neurovascular signalling defects in neurodegeneration. Nature Reviews Neuroscience, 2008, 9, 169-181.	10.2	316
42	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor–negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	21.4	309
43	Markers of Response for the Antiangiogenic Agent Bevacizumab. Journal of Clinical Oncology, 2013, 31, 1219-1230.	1.6	309
44	PIK3CA Mutations Are Not a Major Determinant of Resistance to the Epidermal Growth Factor Receptor Inhibitor Cetuximab in Metastatic Colorectal Cancer. Clinical Cancer Research, 2009, 15, 3184-3188.	7.0	296
45	Centrosome Amplification Is Sufficient to Promote Spontaneous Tumorigenesis in Mammals. Developmental Cell, 2017, 40, 313-322.e5.	7.0	291
46	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
47	VEGF: A modifier of the del22q11 (DiGeorge) syndrome?. Nature Medicine, 2003, 9, 173-182.	30.7	288
48	Single-cell profiling of myeloid cells in glioblastoma across species and disease stage reveals macrophage competition and specialization. Nature Neuroscience, 2021, 24, 595-610.	14.8	288
49	Patient-derived organoids from endometrial disease capture clinical heterogeneity and are amenable to drug screening. Nature Cell Biology, 2019, 21, 1041-1051.	10.3	281
50	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor–negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
51	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
52	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
53	An Integrated Gene Expression Landscape Profiling Approach to Identify Lung Tumor Endothelial Cell Heterogeneity and Angiogenic Candidates. Cancer Cell, 2020, 37, 21-36.e13.	16.8	253
54	Genomic Characterization of Primary Invasive Lobular Breast Cancer. Journal of Clinical Oncology, 2016, 34, 1872-1881.	1.6	249

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55	The role of fatty acid $\hat{I}^2$ -oxidation in lymphangiogenesis. Nature, 2017, 542, 49-54.	27.8	240
56	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
57	Prognostic Significance of POLE Proofreading Mutations in Endometrial Cancer. Journal of the National Cancer Institute, 2015, 107, 402.	6.3	229
58	Discriminating mild from critical COVID-19 by innate and adaptive immune single-cell profiling of bronchoalveolar lavages. Cell Research, 2021, 31, 272-290.	12.0	229
59	CPS1 maintains pyrimidine pools and DNA synthesis in KRAS/LKB1-mutant lung cancer cells. Nature, 2017, 546, 168-172.	27.8	222
60	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
61	A genetic Xenopus laevis tadpole model to study lymphangiogenesis. Nature Medicine, 2005, 11, 998-1004.	30.7	212
62	Optimized filtering reduces the error rate in detecting genomic variants by short-read sequencing. Nature Biotechnology, 2012, 30, 61-68.	17.5	211
63	The BRCA1-Δ11q Alternative Splice Isoform Bypasses Germline Mutations and Promotes Therapeutic Resistance to PARP Inhibition and Cisplatin. Cancer Research, 2016, 76, 2778-2790.	0.9	208
64	Plasma circulating tumor DNA as an alternative to metastatic biopsies for mutational analysis in breast cancer. Annals of Oncology, 2014, 25, 1959-1965.	1.2	206
65	Large-Scale Gene-Centric Analysis Identifies Novel Variants for Coronary Artery Disease. PLoS Genetics, 2011, 7, e1002260.	3.5	203
66	25(OH)D2 Half-Life Is Shorter Than 25(OH)D3 Half-Life and Is Influenced by DBP Concentration and Genotype. Journal of Clinical Endocrinology and Metabolism, 2014, 99, 3373-3381.	3.6	203
67	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	6.2	201
68	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
69	Genomic landscape of carcinogen-induced and genetically induced mouse skin squamous cell carcinoma. Nature Medicine, 2015, 21, 946-954.	30.7	179
70	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
71	VEGF pathway genetic variants as biomarkers of treatment outcome with bevacizumab: an analysis of data from the AViTA and AVOREN randomised trials. Lancet Oncology, The, 2012, 13, 724-733.	10.7	174
72	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174

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73	Quiescent Endothelial Cells Upregulate Fatty Acid $\hat{I}^2$ -Oxidation for Vasculoprotection via Redox Homeostasis. Cell Metabolism, 2018, 28, 881-894.e13.	16.2	174
74	Monocyte-driven atypical cytokine storm and aberrant neutrophil activation as key mediators of COVID-19 disease severity. Nature Communications, 2021, 12, 4117.	12.8	170
75	<i>CHEK2</i> *1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancer–Specific Death, and Increased Risk of a Second Breast Cancer. Journal of Clinical Oncology, 2012, 30, 4308-4316.	1.6	162
76	Genome-wide CRISPR screening identifies TMEM106B as a proviral host factor for SARS-CoV-2. Nature Genetics, 2021, 53, 435-444.	21.4	162
77	Relief of hypoxia by angiogenesis promotes neural stem cell differentiation by targeting glycolysis. EMBO Journal, 2016, 35, 924-941.	7.8	161
78	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
79	Sequencing an Ashkenazi reference panel supports population-targeted personal genomics and illuminates Jewish and European origins. Nature Communications, 2014, 5, 4835.	12.8	156
80	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2011, 20, 3289-3303.	2.9	152
81	CYP2D6 Genotype and Adjuvant Tamoxifen: Meta-Analysis of Heterogeneous Study Populations. Clinical Pharmacology and Therapeutics, 2014, 95, 216-227.	4.7	150
82	Lessons From the Adjuvant Bevacizumab Trial on Colon Cancer: What Next?. Journal of Clinical Oncology, 2011, 29, 1-4.	1.6	148
83	Semiautomated isolation and molecular characterisation of single or highly purified tumour cells from CellSearch enriched blood samples using dielectrophoretic cell sorting. British Journal of Cancer, 2013, 108, 1358-1367.	6.4	148
84	Transient PLK4 overexpression accelerates tumorigenesis in p53-deficient epidermis. Nature Cell Biology, 2016, 18, 100-110.	10.3	145
85	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
86	HIF-1α Promotes Glutamine-Mediated Redox Homeostasis and Glycogen-Dependent Bioenergetics to Support Postimplantation Bone Cell Survival. Cell Metabolism, 2016, 23, 265-279.	16.2	142
87	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	21.4	141
88	Lipid availability determines fate of skeletal progenitor cells via SOX9. Nature, 2020, 579, 111-117.	27.8	140
89	Inhibition of Tumor Angiogenesis and Growth by a Small-Molecule Multi-FGF Receptor Blocker with Allosteric Properties. Cancer Cell, 2013, 23, 477-488.	16.8	138
90	Somatic Mutation Profiling and Associations With Prognosis and Trastuzumab Benefit in Early Breast Cancer. Journal of the National Cancer Institute, 2013, 105, 960-967.	6.3	138

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91	Germline Mutation in <i>BRCA1</i> or <i>BRCA2</i> and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. Clinical Cancer Research, 2015, 21, 652-657.	7.0	138
92	Evidence of Gene–Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
93	Phylogenetic analysis of metastatic progression in breast cancer using somatic mutations and copy number aberrations. Nature Communications, 2017, 8, 14944.	12.8	126
94	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
95	Expression profiling of budding cells in colorectal cancer reveals an EMT-like phenotype and molecular subtype switching. British Journal of Cancer, 2017, 116, 58-65.	6.4	124
96	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
97	Novel Role for Vascular Endothelial Growth Factor (VEGF) Receptor-1 and Its Ligand VEGF-B in Motor Neuron Degeneration. Journal of Neuroscience, 2008, 28, 10451-10459.	3.6	119
98	Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts. Nature Genetics, 2021, 53, 86-99.	21.4	118
99	Genetic predisposition for beta cell fragility underlies type 1 and type 2 diabetes. Nature Genetics, 2016, 48, 519-527.	21.4	117
100	The P450 oxidoreductase <i>*28</i> SNP is associated with low initial tacrolimus exposure and increased dose requirements in CYP3A5-expressing renal recipients. Pharmacogenomics, 2011, 12, 1281-1291.	1.3	116
101	Obesity and survival among women with ovarian cancer: results from the Ovarian Cancer Association Consortium. British Journal of Cancer, 2015, 113, 817-826.	6.4	111
102	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	1.9	111
103	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.9	109
104	ABCA Transporter Gene Expression and Poor Outcome in Epithelial Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	6.3	107
105	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
106	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
107	Developing Organoids from Ovarian Cancer as Experimental and Preclinical Models. Stem Cell Reports, 2020, 14, 717-729.	4.8	105
108	19p13.1 Is a Triple-Negative–Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100

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109	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
110	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98
111	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
112	Lineage-specific functions of TET1 in the postimplantation mouse embryo. Nature Genetics, 2017, 49, 1061-1072.	21.4	96
113	Vitamin D status at breast cancer diagnosis: correlation with tumor characteristics, disease outcome, and genetic determinants of vitamin D insufficiency. Carcinogenesis, 2012, 33, 1319-1326.	2.8	95
114	Somatic Profiling of the Epidermal Growth Factor Receptor Pathway in Tumors from Patients with Advanced Colorectal Cancer Treated with Chemotherapy $\hat{A}\pm$ Cetuximab. Clinical Cancer Research, 2013, 19, 4104-4113.	7.0	95
115	No evidence that protein truncating variants in <i>BRIP1</i> ii>are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
116	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
117	The 15q24/25 Susceptibility Variant for Lung Cancer and Chronic Obstructive Pulmonary Disease Is Associated with Emphysema. American Journal of Respiratory and Critical Care Medicine, 2010, 181, 486-493.	5.6	92
118	VEGF at the neurovascular interface: Therapeutic implications for motor neuron disease. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2006, 1762, 1109-1121.	3.8	91
119	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
120	Single-nucleotide polymorphisms associated with outcome in metastatic renal cell carcinoma treated with sunitinib. British Journal of Cancer, 2013, 108, 887-900.	6.4	88
121	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2018, 47, 526-536.	1.9	88
122	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
123	Role of Gas6 in erythropoiesis and anemia in mice. Journal of Clinical Investigation, 2008, 118, 583-96.	8.2	84
124	Evolutionary predictability of genetic versus nongenetic resistance to anticancer drugs in melanoma. Cancer Cell, 2021, 39, 1135-1149.e8.	16.8	83
125	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. Breast Cancer Research, 2010, 12, R110.	5.0	82
126	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81

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127	Clinical practice guidelines for BRCA1 and BRCA2 genetic testing. European Journal of Cancer, 2021, 146, 30-47.	2.8	81
128	Endovascular Treatment of the Descending Thoracic Aorta. European Journal of Vascular and Endovascular Surgery, 2003, 26, 437-444.	1.5	80
129	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	80
130	Chromosomal Instability in Cell-Free DNA as a Highly Specific Biomarker for Detection of Ovarian Cancer in Women with Adnexal Masses. Clinical Cancer Research, 2017, 23, 2223-2231.	7.0	80
131	Genome-wide significant risk associations for mucinous ovarian carcinoma. Nature Genetics, 2015, 47, 888-897.	21.4	78
132	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast–ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
133	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
134	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
135	PHGDH heterogeneity potentiates cancerÂcell dissemination and metastasis. Nature, 2022, 605, 747-753.	27.8	77
136	The Association of the 4q25 Susceptibility Variant for Atrial Fibrillation With Stroke Is Limited to Stroke of Cardioembolic Etiology. Stroke, 2010, 41, 1850-1857.	2.0	76
137	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	6.2	76
138	Matrix-Binding Vascular Endothelial Growth Factor (VEGF) Isoforms Guide Granule Cell Migration in the Cerebellum via VEGF Receptor Flk1. Journal of Neuroscience, 2010, 30, 15052-15066.	3.6	75
139	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	<b>7</b> 5
140	Uncovering the genomic heterogeneity of multifocal breast cancer. Journal of Pathology, 2015, 236, 457-466.	4.5	72
141	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	2.9	71
142	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	1.9	71
143	Somatic <i>POLE</i> exonuclease domain mutations are early events in sporadic endometrial and colorectal carcinogenesis, determining driver mutational landscape, clonal neoantigen burden and immune response. Journal of Pathology, 2018, 245, 283-296.	4.5	71
144	Mismatch repair deficiency endows tumors with a unique mutation signature and sensitivity to DNA double-strand breaks. ELife, 2014, 3, e02725.	6.0	71

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145	Meta-analysis of vascular endothelial growth factor variations in amyotrophic lateral sclerosis: increased susceptibility in male carriers of the -2578AA genotype. Journal of Medical Genetics, 2009, 46, 840-846.	3.2	70
146	High-grade serous tubo-ovarian cancer refined with single-cell RNA sequencing: specific cell subtypes influence survival and determine molecular subtype classification. Genome Medicine, 2021, 13, 111.	8.2	70
147	High-throughput interrogation of PIK3CA, PTEN, KRAS, FBXW7 and TP53 mutations in primary endometrial carcinoma. Gynecologic Oncology, 2013, 128, 327-334.	1.4	68
148	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
149	European experts consensus: BRCA/homologous recombination deficiency testing in first-line ovarian cancer. Annals of Oncology, 2022, 33, 276-287.	1.2	68
150	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
151	The Cancer Cell Oxygen Sensor PHD2 Promotes Metastasis via Activation of Cancer-Associated Fibroblasts. Cell Reports, 2015, 12, 992-1005.	6.4	66
152	Do COPD subtypes really exist? COPD heterogeneity and clustering in 10 independent cohorts. Thorax, 2017, 72, 998-1006.	<b>5.</b> 6	65
153	Microglial Upregulation of Progranulin as a Marker of Motor Neuron Degeneration. Journal of Neuropathology and Experimental Neurology, 2010, 69, 1191-1200.	1.7	64
154	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1503-1510.	<b>2.</b> 5	64
155	Neurogenic Radial Glia-like Cells in Meninges Migrate and Differentiate into Functionally Integrated Neurons in the Neonatal Cortex. Cell Stem Cell, 2017, 20, 360-373.e7.	11.1	64
156	DNA methylation-driven EMT is a common mechanism of resistance to various therapeutic agents in cancer. Clinical Epigenetics, 2020, 12, 27.	4.1	64
157	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
158	Implementing liquid biopsies into clinical decision making for cancer immunotherapy. Oncotarget, 2017, 8, 48507-48520.	1.8	63
159	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62
160	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
161	Clinical and genetic risk factors for epirubicin-induced cardiac toxicity in early breast cancer patients. Breast Cancer Research and Treatment, 2015, 152, 67-76.	2.5	61
162	Low expression VEGF haplotype increases the risk for tetralogy of Fallot: a family based association study. Journal of Medical Genetics, 2005, 42, 519-522.	3.2	59

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163	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	6.2	59
164	Integrated genome analysis of uterine leiomyosarcoma to identify novel driver genes and targetable pathways. International Journal of Cancer, 2018, 142, 1230-1243.	5.1	59
165	Increased ILâ€10â€producing regulatory T cells are characteristic of severe cases of COVIDâ€19. Clinical and Translational Immunology, 2020, 9, e1204.	3.8	59
166	Biology of breast cancer during pregnancy using genomic profiling. Endocrine-Related Cancer, 2014, 21, 545-554.	3.1	58
167	Platinum Sensitivity–Related Germline Polymorphism Discovered via a Cell-Based Approach and Analysis of Its Association with Outcome in Ovarian Cancer Patients. Clinical Cancer Research, 2011, 17, 5490-5500.	<b>7.</b> O	57
168	Genetic variability in the multidrug resistance associated protein-1 (ABCC1/MRP1) predicts hematological toxicity in breast cancer patients receiving (neo-)adjuvant chemotherapy with 5-fluorouracil, epirubicin and cyclophosphamide (FEC). Annals of Oncology, 2013, 24, 1513-1525.	1.2	57
169	Differences in MWCNT- and SWCNT-induced DNA methylation alterations in association with the nuclear deposition. Particle and Fibre Toxicology, 2018, 15, 11.	6.2	57
170	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
171	Copy number load predicts outcome of metastatic colorectal cancer patients receiving bevacizumab combination therapy. Nature Communications, 2018, 9, 4112.	12.8	55
172	Vascular endothelial growth factor counteracts the loss of phosphoâ€Akt preceding motor neurone degeneration in amyotrophic lateral sclerosis. Neuropathology and Applied Neurobiology, 2007, 33, 499-509.	3.2	53
173	The molecular genetic basis of ovarian cancer and its roadmap towards a better treatment. Gynecologic Oncology, 2010, 117, 358-365.	1.4	53
174	Systemic anti-vascular endothelial growth factor therapies induce a painful sensory neuropathy. Brain, 2012, 135, 2629-2641.	7.6	53
175	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
176	Characterization of patient-derived tumor xenograft models of endometrial cancer for preclinical evaluation of targeted therapies. Gynecologic Oncology, 2015, 139, 118-126.	1.4	52
177	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
178	Genetics, epigenetics and pharmacoâ€(epi)genomics in angiogenesis. Journal of Cellular and Molecular Medicine, 2008, 12, 2533-2551.	3.6	51
179	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
180	Tamoxifen Metabolism and Efficacy in Breast Cancer: A Prospective Multicenter Trial. Clinical Cancer Research, 2018, 24, 2312-2318.	7.0	51

#	Article	IF	CITATIONS
181	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	2.5	51
182	A variant at chromosome 9p21 is associated with recurrent myocardial infarction and cardiac death after acute coronary syndrome: The GRACE Genetics Study. European Heart Journal, 2010, 31, 1132-1141.	2.2	50
183	Genetic evidence for a role of IL33 in nasal polyposis. Allergy: European Journal of Allergy and Clinical Immunology, 2010, 65, 616-622.	5.7	50
184	Therapeutic potential of VEGF and VEGF-derived peptide in peripheral neuropathies. Neuroscience, 2013, 244, 77-89.	2.3	50
185	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
186	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
187	Genetic variants in <i>CDC42</i> and <i>NXPH1</i> as susceptibility factors for constipation and diarrhoea predominant irritable bowel syndrome. Gut, 2014, 63, 1103-1111.	12.1	49
188	Genomic signatures as predictive biomarkers of homologous recombination deficiency in ovarian cancer. European Journal of Cancer, 2017, 86, 5-14.	2.8	49
189	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. Cancer Research, 2019, 79, 505-517.	0.9	49
190	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. PLoS ONE, 2011, 6, e24987.	2.5	48
191	Risk of Ovarian Cancer and the NF-κB Pathway: Genetic Association with <i>IL1A</i> and <i>TNFSF10</i> Cancer Research, 2014, 74, 852-861.	0.9	48
192	DNA methylation in imprinted genes <scp><i>IGF2</i></scp> and <scp><i>GNASXL</i></scp> is associated with prenatal maternal stress. Genes, Brain and Behavior, 2015, 14, 573-582.	2.2	48
193	The diagnostic value of next generation sequencing in familial nonsyndromic congenital heart defects. American Journal of Medical Genetics, Part A, 2015, 167, 1822-1829.	1.2	48
194	Allele-specific DNA methylation reinforces PEAR1 enhancer activity. Blood, 2016, 128, 1003-1012.	1.4	48
195	$\rm IL1\hat{I}^2$ Promotes Immune Suppression in the Tumor Microenvironment Independent of the Inflammasome and Gasdermin D. Cancer Immunology Research, 2021, 9, 309-323.	3.4	48
196	Role of VEGF-D and VEGFR-3 in developmental lymphangiogenesis, a chemicogenetic study in Xenopus tadpoles. Blood, 2008, 112, 1740-1749.	1.4	47
197	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. Clinical Cancer Research, 2011, 17, 3742-3750.	7.0	47
198	Epigenetic effects of carbon nanotubes in human monocytic cells. Mutagenesis, 2017, 32, 181-191.	2.6	46

#	Article	IF	Citations
199	Mixed adenoneuroendocrine carcinoma of the colon: molecular pathogenesis and treatment. Anticancer Research, 2014, 34, 5517-21.	1.1	46
200	VEGF: necessary to prevent motoneuron degeneration, sufficient to treat ALS?. Trends in Molecular Medicine, 2004, 10, 275-282.	6.7	45
201	Prediction of lymph node involvement in breast cancer from primary tumor tissue using gene expression profiling and miRNAs. Breast Cancer Research and Treatment, 2011, 129, 767-776.	2.5	45
202	Neuronal FLT1 receptor and its selective ligand VEGFâ€B protect against retrograde degeneration of sensory neurons. FASEB Journal, 2011, 25, 1461-1473.	0.5	45
203	Olmsted syndrome: exploration of the immunological phenotype. Orphanet Journal of Rare Diseases, 2013, 8, 79.	2.7	45
204	VEGFR1 single nucleotide polymorphisms associated with outcome in patients with metastatic renal cell carcinoma treated with sunitinib $\hat{a} \in \hat{a}$ a multicentric retrospective analysis. Acta Oncol $\hat{A}^3$ gica, 2014, 53, 103-112.	1.8	45
205	Genetic heterogeneity after first-line chemotherapy in high-grade serous ovarian cancer. European Journal of Cancer, 2016, 53, 51-64.	2.8	45
206	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
207	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	6.3	45
208	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
209	The genetic landscape of 87 ovarian germ cell tumors. Gynecologic Oncology, 2018, 151, 61-68.	1.4	44
210	Opportunities and Challenges in the Genetics of COPD 2010: An International COPD Genetics Conference Report. COPD: Journal of Chronic Obstructive Pulmonary Disease, 2011, 8, 121-135.	1.6	43
211	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
212	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
213	Single-cell transcriptome analysis of the Akimba mouse retina reveals cell-type-specific insights into the pathobiology of diabetic retinopathy. Diabetologia, 2020, 63, 2235-2248.	6.3	43
214	Fat Induces Glucose Metabolism in Nontransformed Liver Cells and Promotes Liver Tumorigenesis. Cancer Research, 2021, 81, 1988-2001.	0.9	43
215	A new protocol for single-cell RNA-seq reveals stochastic gene expression during lag phase in budding yeast. ELife, 2020, 9, .	6.0	43
216	Clinical practices underlie COVID-19 patient respiratory microbiome composition and its interactions with the host. Nature Communications, 2021, 12, 6243.	12.8	42

#	Article	IF	Citations
217	Comprehensive fine mapping of chr12q12-14 and follow-up replication identify activin receptor 1B (ACVR1B) as a muscle strength gene. European Journal of Human Genetics, 2011, 19, 208-215.	2.8	40
218	Influence of rs5065 Atrial Natriuretic Peptide Gene Variant on Coronary Artery Disease. Journal of the American College of Cardiology, 2012, 59, 1763-1770.	2.8	40
219	Genetic variability of VEGF pathway genes in six randomized phase III trials assessing the addition of bevacizumab to standard therapy. Angiogenesis, 2014, 17, 909-920.	7.2	40
220	Phospholipase C gamma 1 (PLCG1) R707Q mutation is counterselected under targeted therapy in a patient with hepatic angiosarcoma. Oncotarget, 2015, 6, 36418-36425.	1.8	40
221	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
222	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
223	Genomic, Transcriptomic, Epigenetic, and Immune Profiling of Mucinous Breast Cancer. Journal of the National Cancer Institute, 2019, 111, 742-746.	6.3	40
224	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
225	Chronic Fatigue Syndrome and DNA Hypomethylation of the Glucocorticoid Receptor Gene Promoter 1F Region. Psychosomatic Medicine, 2015, 77, 853-862.	2.0	39
226	DNA methylation repels binding of hypoxia-inducible transcription factors to maintain tumor immunotolerance. Genome Biology, 2020, 21, 182.	8.8	39
227	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
228	Downregulation of genes with a function in axon outgrowth and synapse formation in motor neurones of the VEGFÎ'/Î' mouse model of amyotrophic lateral sclerosis. BMC Genomics, 2010, 11, 203.	2.8	38
229	Somatic copy number alterations predict response to platinum therapy in epithelial ovarian cancer. Gynecologic Oncology, 2014, 135, 415-422.	1.4	38
230	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	2.9	38
231	Regeneration Defects in Yap and Taz Mutant Mouse Livers Are Caused by Bile Duct Disruption and Cholestasis. Gastroenterology, 2021, 160, 847-862.	1.3	38
232	Impaired Autonomic Regulation of Resistance Arteries in Mice With Low Vascular Endothelial Growth Factor or Upon Vascular Endothelial Growth Factor Trap Delivery. Circulation, 2010, 122, 273-281.	1.6	37
233	Genomic Copy Number Determines Functional Expression of $\hat{l}^2$ -Defensin 2 in Airway Epithelial Cells and Associates with Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2010, 182, 163-169.	5.6	37
234	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	6.2	37

#	Article	IF	CITATIONS
235	DNA methylation profiling of non-small cell lung cancer reveals a COPD-driven immune-related signature. Thorax, 2015, 70, 1113-1122.	5.6	37
236	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	1.0	37
237	Acriflavine Inhibits Acquired Drug Resistance by Blocking the Epithelial-to-Mesenchymal Transition and the Unfolded Protein Response. Translational Oncology, 2017, 10, 59-69.	3.7	37
238	Amplification of $1q32.1$ Refines the Molecular Classification of Endometrial Carcinoma. Clinical Cancer Research, 2017, 23, 7232-7241.	7.0	37
239	Vascular endothelial growth factor pathway in endometriosis: genetic variants and plasma biomarkers. Fertility and Sterility, 2016, 105, 988-996.	1.0	36
240	Randomized phase II CLIO study on olaparib monotherapy versus chemotherapy in platinum-resistant ovarian cancer Journal of Clinical Oncology, 2019, 37, 5507-5507.	1.6	36
241	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35
242	Influence of 23 coronary artery disease variants on recurrent myocardial infarction or cardiac death: the GRACE Genetics Study. European Heart Journal, 2013, 34, 993-1001.	2.2	35
243	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. Scientific Reports, 2015, 5, 17369.	3.3	35
244	Improved metabolite identification with MIDAS and MAGMa through MS/MS spectral dataset-driven parameter optimization. Metabolomics, 2016, 12, 1.	3.0	35
245	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	5.1	35
246	Genetics in Zebrafish, Mice, and Humans to Dissect Congenital Heart Disease: Insights in the Role of VEGF. Current Topics in Developmental Biology, 2004, 62, 189-224.	2.2	34
247	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	5.1	34
248	Mutation profile and clinical outcome of mixed endometrioid-serous endometrial carcinomas are different from that of pure endometrioid or serous carcinomas. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2015, 466, 415-422.	2.8	34
249	Candidate locus analysis of the TERT–CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	3.8	34
250	Evaluation of efficacy and safety markers in a phase II study of metastatic colorectal cancer treated with aflibercept in the first-line setting. British Journal of Cancer, 2015, 113, 1027-1034.	6.4	34
251	Newborn genome-wide DNA methylation in association with pregnancy anxiety reveals a potential role for GABBR1. Clinical Epigenetics, 2017, 9, 107.	4.1	34
252	Gemcitabine Recruits M2-Type Tumor-Associated Macrophages into the Stroma of Pancreatic Cancer. Translational Oncology, 2020, 13, 100743.	3.7	34

#	Article	IF	Citations
253	Whole-genome sequencing reveals a coding non-pathogenic variant tagging a non-coding pathogenic hexanucleotide repeat expansion in C9orf72 as cause of amyotrophic lateral sclerosis. Human Molecular Genetics, 2012, 21, 2412-2419.	2.9	33
254	Exome sequencing reveals HINT1 mutations as a cause of distal hereditary motor neuropathy. European Journal of Human Genetics, 2014, 22, 847-850.	2.8	33
255	DNA methylation analysis of Homeobox genes implicates <i>HOXB7</i> hypomethylation as risk factor for neural tube defects. Epigenetics, 2015, 10, 92-101.	2.7	33
256	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. Clinical Cancer Research, 2015, 21, 5264-5276.	7.0	33
257	Genetic variability in drug transport, metabolism or DNA repair affecting toxicity of chemotherapy in ovarian cancer. BMC Pharmacology & Doxicology, 2015, 16, 2.	2.4	33
258	Genomic and epigenomic analysis of high-risk prostate cancer reveals changes in hydroxymethylation and TET1. Oncotarget, 2016, 7, 24326-24338.	1.8	33
259	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	2.9	33
260	Genome-Wide Association Study Identifies a Possible Susceptibility Locus for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 980-987.	2.5	32
261	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	2.9	32
262	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
263	Assessment of Hepatocyte Growth Factor in Ovarian Cancer Mortality. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1638-1648.	2.5	31
264	Genetic variants in <scp>VEGF</scp> pathway genes in neoadjuvant breast cancer patients receiving bevacizumab: Results from the randomized phase III <scp>G</scp> epar <scp>Q</scp> uinto study. International Journal of Cancer, 2015, 137, 2981-2988.	5.1	31
265	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	1.8	31
266	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the $12p11$ locus. Breast Cancer Research, 2016, 18, 64.	5.0	31
267	A Complex Network of Tumor Microenvironment in Human High-Grade Serous Ovarian Cancer. Clinical Cancer Research, 2017, 23, 7621-7632.	7.0	31
268	Vitamin D supplementation in cutaneous malignant melanoma outcome (ViDMe): a randomized controlled trial. BMC Cancer, 2017, 17, 562.	2.6	31
269	Another angiogenic gene linked to amyotrophic lateral sclerosis. Trends in Molecular Medicine, 2006, 12, 345-347.	6.7	30
270	Efflux pump ABCB1 single nucleotide polymorphisms and dose reductions in patients with metastatic renal cell carcinoma treated with sunitinib. Acta Oncol $\tilde{A}^3$ gica, 2014, 53, 1413-1422.	1.8	30

#	Article	IF	CITATIONS
271	Epithelial Ovarian Cancer: Rationale for Changing the One-Fits-All Standard Treatment Regimen to Subtype-Specific Treatment. International Journal of Gynecological Cancer, 2014, 24, 468-477.	2.5	30
272	Induction and recovery of CpG site specific methylation changes in human bronchial cells after long-term exposure to carbon nanotubes and asbestos. Environment International, 2020, 137, 105530.	10.0	30
273	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
274	Precision Therapy in RAS Mutant Colorectal Cancer. Gastroenterology, 2020, 158, 806-811.	1.3	29
275	Germline polymorphisms in an enhancer of <i>PSIP1</i> are associated with progression-free survival in epithelial ovarian cancer. Oncotarget, 2016, 7, 6353-6368.	1.8	29
276	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28
277	Network-Based Integration of GWAS and Gene Expression Identifies a <i>HOX</i> -Centric Network Associated with Serous Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1574-1584.	2.5	28
278	Impact of Selection Bias on Estimation of Subsequent Event Risk. Circulation: Cardiovascular Genetics, $2017,10,10$	5.1	28
279	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
280	The genomic landscape of nonsmall cell lung carcinoma in never smokers. International Journal of Cancer, 2020, 146, 3207-3218.	5.1	28
281	The role of KRAS, BRAF, NRAS, and PIK3CA mutations as markers of resistance to cetuximab in chemorefractory metastatic colorectal cancer. Journal of Clinical Oncology, 2009, 27, 4020-4020.	1.6	28
282	Sculpting Heart Valves with NFATc and VEGF. Cell, 2004, 118, 532-534.	28.9	27
283	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptor–Positive, Lower Grade Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2222-2231.	2.5	27
284	Interleukin-17 receptor polymorphism predisposes to primary graft dysfunction after lung transplantation. Journal of Heart and Lung Transplantation, 2015, 34, 941-949.	0.6	27
285	Ischemia-Induced DNA Hypermethylation during Kidney Transplant Predicts Chronic Allograft Injury. Journal of the American Society of Nephrology: JASN, 2018, 29, 1566-1576.	6.1	27
286	Dual blockade of PI3K/AKT/mTOR (NVP-BEZ235) and Ras/Raf/MEK (AZD6244) pathways synergistically inhibit growth of primary endometrioid endometrial carcinoma cultures, whereas NVP-BEZ235 reduces tumor growth in the corresponding xenograft models. Gynecologic Oncology, 2015, 138, 165-173.	1.4	26
287	Loss of Chromosome 18q11.2-q12.1 Is Predictive for Survival in Patients With Metastatic Colorectal Cancer Treated With Bevacizumab. Journal of Clinical Oncology, 2018, 36, 2052-2060.	1.6	26
288	Comparative oncogenomics identifies tyrosine kinase FES as a tumor suppressor in melanoma. Journal of Clinical Investigation, 2017, 127, 2310-2325.	8.2	26

#	Article	IF	CITATIONS
289	Pharmaco-epigenomics: discovering therapeutic approaches and biomarkers for cancer therapy. Heredity, 2010, 105, 152-160.	2.6	25
290	The TERT-CLPTM1L locus for lung cancer predisposes to bronchial obstruction and emphysema. European Respiratory Journal, 2011, 38, 924-931.	6.7	25
291	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	3.1	25
292	Interleukin-6 is an activator of pituitary stem cells upon local damage, a competence quenched in the aging gland. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	25
293	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
294	No Association between <i>FTO</i> or <i>HHEX</i> and Endometrial Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2106-2109.	2.5	24
295	A new approach to imprinting mutation detection in GNAS by Sequenom EpiTYPER system. Clinica Chimica Acta, 2010, 411, 2033-2039.	1.1	24
296	Genetic Predisposition Scores Associate with Muscular Strength, Size, and Trainability. Medicine and Science in Sports and Exercise, 2013, 45, 1451-1459.	0.4	24
297	Genetic markers of bevacizumab-induced hypertension. Angiogenesis, 2014, 17, 685-94.	7.2	24
298	Common variants at the <i>CHEK2 </i> gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
299	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	2.5	24
300	Loss of 1p36.33 Frequent in Low-Grade Serous Ovarian Cancer. Neoplasia, 2019, 21, 582-590.	5.3	24
301	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
302	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	3.8	23
303	Impact of genetic variability and treatment-related factors on outcome in early breast cancer patients receiving (neo-) adjuvant chemotherapy with 5-fluorouracil, epirubicin and cyclophosphamide, and docetaxel. Breast Cancer Research and Treatment, 2014, 147, 557-570.	2.5	23
304	Epidermal Growth Factor Receptor (EGFR) Pathway Biomarkers in the Randomized Phase III Trial of Erlotinib Versus Observation in Ovarian Cancer Patients with No Evidence of Disease Progression after First-Line Platinum-Based Chemotherapy. Targeted Oncology, 2015, 10, 583-596.	3.6	23
305	Validation of <scp>VEGFR</scp> 1 rs9582036 as predictive biomarker in metastatic clearâ€eell renal cell carcinoma patients treated with sunitinib. BJU International, 2016, 118, 890-901.	2.5	23
306	Genetic variant in the osteoprotegerin gene is associated with aromatase inhibitor-related musculoskeletal toxicity in breast cancer patients. European Journal of Cancer, 2016, 56, 31-36.	2.8	23

#	Article	IF	CITATIONS
307	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	6.4	23
308	Establishment and Characterization of Histologically and Molecularly Stable Soft-tissue Sarcoma Xenograft Models for Biological Studies and Preclinical Drug Testing. Molecular Cancer Therapeutics, 2019, 18, 1168-1178.	4.1	23
309	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	2.8	23
310	Progesterone receptor gene variants and risk of endometrial cancer. Carcinogenesis, 2011, 32, 331-335.	2.8	22
311	Polymorphisms in Inflammation Pathway Genes and Endometrial Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 216-223.	2.5	22
312	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
313	Molecular characterization of 7 new established cell lines from high grade serous ovarian cancer. Cancer Letters, 2015, 362, 218-228.	7.2	22
314	The Emerging Role of DNA Methylation in Kidney Transplantation: A Perspective. American Journal of Transplantation, 2016, 16, 1070-1078.	4.7	22
315	The footprint of the ageing stroma in older patients with breast cancer. Breast Cancer Research, 2017, 19, 78.	5.0	22
316	Glucocorticoid receptor DNA methylation and childhood trauma in chronic fatigue syndrome patients. Journal of Psychosomatic Research, 2018, 104, 55-60.	2.6	22
317	Association of Chromosome 9p21 With Subsequent Coronary Heart Disease Events. Circulation Genomic and Precision Medicine, 2019, 12, e002471.	3.6	22
318	Phylogenetic reconstruction of breast cancer reveals two routes of metastatic dissemination associated with distinct clinical outcome. EBioMedicine, 2020, 56, 102793.	6.1	22
319	Characterization of Stromal Tumor-infiltrating Lymphocytes and Genomic Alterations in Metastatic Lobular Breast Cancer. Clinical Cancer Research, 2020, 26, 6254-6265.	7.0	22
320	Methylation Defect in Imprinted Genes Detected in Patients with an Albright's Hereditary Osteodystrophy Like Phenotype and Platelet Gs Hypofunction. PLoS ONE, 2012, 7, e38579.	2.5	21
321	Genetic variation in the <i>lymphotoxin-<math>\hat{l}</math> + &lt; i&gt;(<i>LTA&lt; i&gt;) <i>tumour necrosis factor-<math>\hat{l}</math> + &lt; i&gt;(<i>TNF<math>\hat{l}</math> + &lt; i&gt;) locus as a risk factor for idiopathic achalasia. Gut, 2014, 63, 1401-1409.</i></i></i></i>	12.1	21
322	Large-Scale Evaluation of Common Variation in Regulatory T Cell–Related Genes and Ovarian Cancer Outcome. Cancer Immunology Research, 2014, 2, 332-340.	3.4	21
323	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. British Journal of Cancer, 2014, 110, 1088-1100.	6.4	21
324	Current Methodological Challenges of Single-Cell and Single-Nucleus RNA-Sequencing in Glomerular Diseases. Journal of the American Society of Nephrology: JASN, 2021, 32, 1838-1852.	6.1	21

#	Article	IF	CITATIONS
325	Huvariome: a web server resource of whole genome next-generation sequencing allelic frequencies to aid in pathological candidate gene selection. Journal of Clinical Bioinformatics, 2012, 2, 19.	1.2	20
326	VEGF Receptor-2 (Flk-1) Overexpression in Mice Counteracts Focal Epileptic Seizures. PLoS ONE, 2012, 7, e40535.	2.5	20
327	Comprehensive Mutation Analysis in Colorectal Flat Adenomas. PLoS ONE, 2012, 7, e41963.	2.5	20
328	Analysis of Over 10,000 Cases Finds No Association between Previously Reported Candidate Polymorphisms and Ovarian Cancer Outcome. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 987-992.	2.5	20
329	Multivariable regression analysis of febrile neutropenia occurrence in early breast cancer patients receiving chemotherapy assessing patient-related, chemotherapy-related and genetic risk factors. BMC Cancer, 2014, 14, 201.	2.6	20
330	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. Breast Cancer Research, 2015, 17, 18.	5.0	20
331	Predictors of pretreatment CA125 at ovarian cancer diagnosis: a pooled analysis in the Ovarian Cancer Association Consortium. Cancer Causes and Control, 2017, 28, 459-468.	1.8	20
332	Geneâ€"environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	5.1	20
333	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
334	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	3.3	19
335	The <i>BRCA2</i> c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	2.5	19
336	GLI2 promoter hypermethylation in saliva of children with a respiratory allergy. Clinical Epigenetics, 2018, 10, 50.	4.1	19
337	Cigarette Smoke–Induced Emphysema Exhausts Early Cytotoxic CD8+ T Cell Responses against Nascent Lung Cancer Cells. Journal of Immunology, 2018, 201, 1558-1569.	0.8	19
338	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	12.8	19
339	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	2.5	19
340	Genetic variation in interleukin-17 receptor A is functionally associated with chronic rejection after lung transplantation. Journal of Heart and Lung Transplantation, 2013, 32, 1233-1240.	0.6	18
341	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
342	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	3.8	18

#	Article	lF	CITATIONS
343	Heterogeneity in motoneuron disease. Trends in Neurosciences, 2007, 30, 536-544.	8.6	17
344	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1783-1791.	2.5	17
345	Age-related changes in DNA methylation affect renal histology and post-transplant fibrosis. Kidney International, 2019, 96, 1195-1204.	5.2	17
346	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002470.	3.6	17
347	Experimental and computational modeling for signature and biomarker discovery of renal cell carcinoma progression. Molecular Cancer, 2021, 20, 136.	19.2	17
348	Genetic changes in nonepithelial ovarian cancer. Expert Review of Anticancer Therapy, 2013, 13, 871-882.	2.4	16
349	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	12.8	16
350	Consortium analysis of gene and gene–folate interactions in purine and pyrimidine metabolism pathways with ovarian carcinoma risk. Molecular Nutrition and Food Research, 2014, 58, 2023-2035.	3.3	16
351	Effect of ABCB1 diplotype on tacrolimus disposition in renal recipients depends on CYP3A5 and CYP3A4 genotype. Pharmacogenomics Journal, 2017, 17, 556-562.	2.0	16
352	Establishment and characterization of uterine sarcoma and carcinosarcoma patient-derived xenograft models. Gynecologic Oncology, 2017, 146, 538-545.	1.4	16
353	Geneâ€based interaction analysis shows <scp>GABA</scp> ergic genes interacting with parenting in adolescent depressive symptoms. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2017, 58, 1301-1309.	5.2	16
354	CRAF mutations in lung cancer can be oncogenic and predict sensitivity to combined type II RAF and MEK inhibition. Oncogene, 2019, 38, 5933-5941.	5.9	16
355	Patient-derived cell line models revealed therapeutic targets and molecular mechanisms underlying disease progression of high grade serous ovarian cancer. Cancer Letters, 2019, 459, 1-12.	7.2	16
356	Expression of immuneâ€related genes in rectum and colon <i>descendens</i> of Irritable Bowel Syndrome patients is unrelated to clinical symptoms. Neurogastroenterology and Motility, 2019, 31, e13579.	3.0	16
357	BCL9 regulates CD226 and CD96 checkpoints in CD8+ T cells to improve PD-1 response in cancer. Signal Transduction and Targeted Therapy, 2021, 6, 313.	17.1	16
358	Analysis of <i>FGGY </i> as a risk factor for sporadic amyotrophic lateral sclerosis. Amyotrophic Lateral Sclerosis and Other Motor Neuron Disorders, 2009, 10, 441-447.	2.1	15
359	Association of <i>CDH11</i> with nonâ€syndromic ASD. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 391-398.	1.7	15
360	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	1.4	15

#	Article	IF	CITATIONS
361	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. British Journal of Cancer, 2018, 118, 1123-1129.	6.4	15
362	Assessment of moderate coffee consumption and risk of epithelial ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2018, 47, 450-459.	1.9	15
363	The genetic landscape of 5T models for multiple myeloma. Scientific Reports, 2018, 8, 15030.	3.3	15
364	Menopausal hormone therapy prior to the diagnosis of ovarian cancer is associated with improved survival. Gynecologic Oncology, 2020, 158, 702-709.	1.4	15
365	BCL(X)L and BCL2 increase the metabolic fitness of breast cancer cells: a single-cell imaging study. Cell Death and Differentiation, 2021, 28, 1512-1531.	11.2	15
366	Prdm16 Supports Arterial Flow Recovery by Maintaining Endothelial Function. Circulation Research, 2021, 129, 63-77.	4.5	15
367	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	1.8	15
368	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
369	Prevalent breast cancer patients with a homozygous mutant status for CYP2D6*4: response and biomarkers in tamoxifen users. Breast Cancer Research and Treatment, 2009, 118, 531-538.	2.5	14
370	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
371	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	2.8	14
372	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	2.5	14
373	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. Oncotarget, 2017, 8, 18381-18398.	1.8	14
374	Randomized CLIO/BGOG-ov10 trial of olaparib monotherapy versus physician's choice chemotherapy in relapsed ovarian cancer. Gynecologic Oncology, 2022, 165, 14-22.	1.4	14
375	Variation in NF-κB Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1421-1427.	2.5	13
376	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	1.8	13
377	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
378	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 217-228.	2.5	12

#	Article	IF	Citations
379	Molecular underpinnings of glandular tropism in metastatic clear cell renal cell carcinoma: therapeutic implications. Acta Oncol $\tilde{A}^3$ gica, 2021, 60, 1499-1506.	1.8	12
380	Comprehensive Molecular Analysis of Inflammatory Myofibroblastic Tumors Reveals Diverse Genomic Landscape and Potential Predictive Markers for Response to Crizotinib. Clinical Cancer Research, 2021, 27, 6737-6748.	7.0	12
381	Detection of microsatellite instability (MSI) in colorectal cancer samples with a novel set of highly sensitive markers by means of the Idylla MSI Test prototype Journal of Clinical Oncology, 2018, 36, e15639-e15639.	1.6	12
382	Assessment of concordance between fresh-frozen and formalin-fixed paraffin embedded tumor DNA methylation using a targeted sequencing approach. Oncotarget, 2017, 8, 48126-48137.	1.8	12
383	Organoids from human tooth showing epithelial stemness phenotype and differentiation potential. Cellular and Molecular Life Sciences, 2022, 79, 153.	5.4	12
384	Breast Cancer Risk and 6q22.33: Combined Results from Breast Cancer Association Consortium and Consortium of Investigators on Modifiers of BRCA1/2. PLoS ONE, 2012, 7, e35706.	2.5	11
385	The rs1800716 variant in CYP2D6 is associated with an increased double endometrial thickness in postmenopausal women on tamoxifen. Annals of Oncology, 2014, 25, 90-95.	1.2	11
386	Polymorphisms in the Von Hippel–Lindau Gene Are Associated With Overall Survival in Metastatic Clear-Cell Renal-Cell Carcinoma Patients Treated With VEGFR Tyrosine Kinase Inhibitors. Clinical Genitourinary Cancer, 2018, 16, 266-273.	1.9	11
387	Establishing a Unified COVID-19 "Immunome― Integrating Coronavirus Pathogenesis and Host Immunopathology. Frontiers in Immunology, 2020, 11, 1642.	4.8	11
388	Multi-tissue transcriptome-wide association study identifies eight candidate genes and tissue-specific gene expression underlying endometrial cancer susceptibility. Communications Biology, 2021, 4, 1211.	4.4	11
389	16LBA VEGFR-1 polymorphisms as potential predictors of clinical outcome in bevacizumab-treated patients with metastatic pancreatic cancer. European Journal of Cancer, Supplement, 2009, 7, 10.	2.2	10
390	Successful application of endoscopic ultrasound-guided fine needle biopsy to establish pancreatic patient-derived tumor xenografts: a pilot study. Endoscopy, 2016, 48, 1016-1022.	1.8	10
391	Outcome of Colorectal Cancer Patients Treated with Combination Bevacizumab Therapy: A Pooled Retrospective Analysis of Three European Cohorts from the Angiopredict Initiative. Digestion, 2016, 94, 129-137.	2.3	10
392	Limited potential of genetic predisposition scores to predict muscle mass and strength performance in Flemish Caucasians between 19 and 73 years of age. Physiological Genomics, 2017, 49, 160-166.	2.3	10
393	Global and gene-specific DNA methylation effects of different asbestos fibres on human bronchial epithelial cells. Environment International, 2018, 115, 301-311.	10.0	10
394	Genetic biomarkers in the VEGF pathway predicting response to anti-VEGF therapy in age-related macular degeneration. BMJ Open Ophthalmology, 2019, 4, e000273.	1.6	10
395	Exposure–response analysis of endoxifen serum concentrations in early-breast cancer. Cancer Chemotherapy and Pharmacology, 2020, 85, 1141-1152.	2.3	10
396	Associations between Genetically Predicted Circulating Protein Concentrations and Endometrial Cancer Risk. Cancers, 2021, 13, 2088.	3.7	10

#	Article	IF	CITATIONS
397	Decoding the activated stem cell phenotype of the neonatally maturing pituitary. ELife, 0, $11$ , .	6.0	10
398	Genetic spotlight on a blood defect. Nature, 2004, 427, 592-593.	27.8	9
399	1414 POSTER Single Nucleotide Polymorphism Analysis and Outcome in Advanced-stage Cancer Patients Treated With Bevacizumab. European Journal of Cancer, 2011, 47, S173.	2.8	9
400	Identification and prioritization of NUAK1 and PPP1CC as positional candidate loci for skeletal muscle strength phenotypes. Physiological Genomics, 2011, 43, 981-992.	2.3	9
401	International Experts Panel Meeting of the Italian Association of Thoracic Oncology on Antiangiogenetic Drugs for Non–Small Cell Lung Cancer: Realities and Hopes. Journal of Thoracic Oncology, 2016, 11, 1153-1169.	1.1	9
402	TET enzymes as oxygen-dependent tumor suppressors: exciting new avenues for cancer management. Epigenomics, 2016, 8, 1445-1448.	2.1	9
403	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	2.5	9
404	MicroRNAs Possibly Involved in the Development of Bone Metastasis in Clear-Cell Renal Cell Carcinoma. Cancers, 2021, 13, 1554.	3.7	9
405	Molecular Subtypes and Gene Expression Signatures as Prognostic Features in Fully Resected Clear Cell Renal Cell Carcinoma: A Tailored Approach to Adjuvant Trials. Clinical Genitourinary Cancer, 2021, 19, e382-e394.	1.9	9
406	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
407	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
408	Histopathological and Molecular Profiling of Clear Cell Sarcoma and Correlation with Response to Crizotinib: An Exploratory Study Related to EORTC 90101 "CREATE―Trial. Cancers, 2021, 13, 6057.	3.7	9
409	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. Twin Research and Human Genetics, 2012, 15, 615-623.	0.6	8
410	Tumors smother their epigenome. Molecular and Cellular Oncology, 2016, 3, e1240549.	0.7	8
411	RNA-sequencing in non-small cell lung cancer shows gene downregulation of therapeutic targets in tumor tissue compared to non-malignant lung tissue. Radiation Oncology, 2018, 13, 131.	2.7	8
412	Single-cell Transcriptomics Uncover a Novel Role of Myeloid Cells and T-lymphocytes in the Fibrotic Microenvironment in Peyronie's Disease. European Urology Focus, 2022, 8, 814-828.	3.1	8
413	MCM3 is a novel proliferation marker associated with longer survival for patients with tubo-ovarian high-grade serous carcinoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2022, 480, 855-871.	2.8	8
414	Interrogating breast cancer heterogeneity using single and pooled circulating tumor cell analysis. Npj Breast Cancer, 2022, 8, .	5.2	8

#	Article	IF	CITATIONS
415	7000 Kidney ccRCC immune classification (KIC) enhances the predictive value of T effector (Teff) and angiogenesis (Angio) signatures in response to nivolumab (N). Annals of Oncology, 2020, 31, S553.	1.2	7
416	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	5.0	7
417	Breast cancer diagnosed in the post-weaning period is indicative for a poor outcome. European Journal of Cancer, 2021, 155, 13-24.	2.8	7
418	Analyses of germline variants associated with ovarian cancer survival identify functional candidates at the 1q22 and 19p12 outcome loci. Oncotarget, 2017, 8, 64670-64684.	1.8	7
419	POLRMT as a Novel Susceptibility Gene for Cardiotoxicity in Epirubicin Treatment of Breast Cancer Patients. Pharmaceutics, 2021, 13, 1942.	4.5	7
420	Genetic Variation in Caveolin-1 Affects Survival After Lung Transplantation. Transplantation, 2014, 98, 354-359.	1.0	6
421	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. BMC Cancer, 2015, 15, 978.	2.6	6
422	A Genetic Predisposition Score Associates with Reduced Aerobic Capacity in Response to Acute Normobaric Hypoxia in Lowlanders. High Altitude Medicine and Biology, 2015, 16, 34-42.	0.9	6
423	Microsatellite Instable and Microsatellite Stable Primary Endometrial Carcinoma Cells and Their Subcutaneous and Orthotopic Xenografts Recapitulate the Characteristics of the Corresponding Primary Tumor. International Journal of Gynecological Cancer, 2015, 25, 363-371.	2.5	6
424	It's T Time for Normal Blood Vessels. Developmental Cell, 2017, 41, 125-126.	7.0	6
425	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. Cancer Medicine, 2019, 8, 2503-2513.	2.8	6
426	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6
427	Genomic Characterisation and Response to Trastuzumab and Paclitaxel in Advanced or Recurrent HER2-positive Endometrial Carcinoma. Anticancer Research, 2016, 36, 5381-5384.	1.1	6
428	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
429	Role for Granulocyte <scp>Colonyâ€Stimulating</scp> Factor in Neutrophilic Extramedullary Myelopoiesis in a Murine Model of Systemic Juvenile Idiopathic Arthritis. Arthritis and Rheumatology, 2022, 74, 1257-1270.	5.6	6
430	Pan-Cancer Detection and Typing by Mining Patterns in Large Genome-Wide Cell-Free DNA Sequencing Datasets. Clinical Chemistry, 2022, 68, 1164-1176.	3.2	6
431	Breast cancer susceptibility polymorphisms and endometrial cancer risk: a Collaborative Endometrial Cancer Study. Carcinogenesis, 2011, 32, 1862-1866.	2.8	5
432	Why Should Results From Metastatic Trials No Longer Matter for Early-Stage Disease?. Journal of Clinical Oncology, 2013, 31, 2753-2753.	1.6	5

#	Article	IF	CITATIONS
433	Variants in the 15q24/25 Locus Associate with Lung Function Decline in Active Smokers. PLoS ONE, 2013, 8, e53219.	2.5	5
434	The antitumor effect of metformin with and without carboplatin on primary endometrioid endometrial carcinoma in vivo. Gynecologic Oncology, 2015, 138, 378-382.	1.4	5
435	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
436	Combination of variations in inflammation- and endoplasmic reticulum-associated genes as putative biomarker for bevacizumab response in KRAS wild-type colorectal cancer. Scientific Reports, 2020, 10, 9778.	3.3	5
437	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	6.4	5
438	Molecular Biomarkers of Response to Eribulin in Patients with Leiomyosarcoma. Clinical Cancer Research, 2021, 27, 3106-3115.	7.0	5
439	Identification of a Locus Near <i>ULK1</i> Associated With Progression-Free Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1669-1680.	2.5	5
440	Molecular Subtyping Combined with Biological Pathway Analyses to Study Regorafenib Response in Clinically Relevant Mouse Models of Colorectal Cancer. Clinical Cancer Research, 2021, 27, 5979-5992.	7.0	5
441	Abstract 986: Unraveling breast cancer progression through geographical and temporal sequencing. , 2014, , .		5
442	Polymorphisms in Stromal Genes and Susceptibility to Serous Epithelial Ovarian Cancer: A Report from the Ovarian Cancer Association Consortium. PLoS ONE, 2011, 6, e19642.	2.5	5
443	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	1.8	5
444	Genetic Variation in Immunoglobulin G Receptor Affects Survival After Lung Transplantation. American Journal of Transplantation, 2014, 14, 1672-1677.	4.7	4
445	Chromosome 18q11.2 loss as a predictive marker for response to bevacizumab in metastatic colorectal cancer. European Journal of Cancer, 2016, 69, S29.	2.8	4
446	ABCG2 Polymorphism rs2231142 and hypothyroidism in metastatic renal cell carcinoma patients treated with sunitinib. Acta Clinica Belgica, 2019, 74, 180-188.	1.2	4
447	Fibroblast Growth Factor Receptor-2 Polymorphism rs2981582 is Correlated With Progression-free Survival and Overall Survival in Patients With Metastatic Clear-cell Renal Cell Carcinoma Treated With Sunitinib. Clinical Genitourinary Cancer, 2019, 17, e235-e246.	1.9	4
448	A variant in <i>FTO</i> gene shows association with histological ulceration in cutaneous melanoma. Journal of Cutaneous Pathology, 2020, 47, 98-101.	1.3	4
449	Targeting the RhoGEF Î <sup>2</sup> PIX/COOL-1 in Glioblastoma: Proof of Concept Studies. Cancers, 2020, 12, 3531.	3.7	4
450	LBA78 A microsimulation model to assess the impact of SARS-CoV-2 on cancer outcomes, healthcare organization and economic burden. Annals of Oncology, 2020, 31, S1207.	1.2	4

#	Article	IF	CITATIONS
451	Resistance to Immune Checkpoint Blockade in Uterine Leiomyosarcoma: What Can We Learn from Other Cancer Types?. Cancers, 2021, 13, 2040.	3.7	4
452	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	3.7	4
453	Prospective study evaluating the effect of impaired tamoxifen metabolisation on efficacy in breast cancer patients receiving tamoxifen in the neo-adjuvant or metastatic setting Journal of Clinical Oncology, 2016, 34, 523-523.	1.6	4
454	Nucleosome footprinting in plasma cell-free DNA for the pre-surgical diagnosis of ovarian cancer. Npj Genomic Medicine, 2022, 7, 30.	3.8	4
455	FISH analysis of PTEN in endometrial carcinoma. comparison with SNP arrays and MLPA. Histopathology, 2014, 65, 371-388.	2.9	3
456	Expression profiling of tumour budding cells in colorectal cancer suggests an EMT-like phenotype and molecular subtype switching. European Journal of Cancer, 2016, 61, S88.	2.8	3
457	No Evidence That Genetic Variation in the Myeloid-Derived Suppressor Cell Pathway Influences Ovarian Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 420-424.	2.5	3
458	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	4.1	3
459	Identification, clinical-pathological characteristics and treatment outcomes of patients with metastatic breast cancer and somatic human epidermal growth factor receptor 2 (ERBB2) mutations. Breast Cancer Research and Treatment, 2019, 174, 55-63.	2.5	3
460	Randomized phase II CLIO study on olaparib monotherapy versus chemotherapy in platinum-sensitive recurrent ovarian cancer. Gynecologic Oncology, 2020, 159, 17-18.	1.4	3
461	Antizyme Inhibitor 1 Regulates Matrikine Expression and Enhances the Metastatic Potential of Aggressive Primary Prostate Cancer. Molecular Cancer Research, 2022, 20, 527-541.	3.4	3
462	c-MET/VEGFR-2 co-localisation impacts on survival following bevacizumab therapy in epithelial ovarian cancer: an exploratory biomarker study of the phase 3 ICON7 trial. BMC Medicine, 2022, 20, 59.	5.5	3
463	CA-125 Levels Are Predictive of Survival in Low-Grade Serous Ovarian Cancer—A Multicenter Analysis. Cancers, 2022, 14, 1954.	3.7	3
464	Identification of Two Genetic Loci Associated with Leukopenia after Chemotherapy in Patients with Breast Cancer. Clinical Cancer Research, 2022, 28, 3342-3355.	7.0	3
465	Melanoma susceptibility variant rs869330 in the MTAP gene is associated with melanoma outcome. Melanoma Research, 2019, 29, 590-595.	1.2	2
466	Data describing the poor outcome associated with a breast cancer diagnosis in the post-weaning period. Data in Brief, 2021, 38, 107354.	1.0	2
467	Identification of a novel predictive genomic biomarker for response to combination bevacizumab in metastatic colorectal cancer (mCRC) Journal of Clinical Oncology, 2017, 35, 3580-3580.	1.6	2
468	Association of a novel set of 7 homopolymer indels for detection of MSI with tumor mutation burden and total indel load in endometrial and colorectal cancers Journal of Clinical Oncology, 2018, 36, e15654-e15654.	1.6	2

#	Article	IF	CITATIONS
469	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	3.3	2
470	Abstract P3-07-46: CYPTAM-BRUT 3: Endometrial thickness cannot be used as a marker for tamoxifen metabolization in postmenopausal breast cancer patients. Cancer Research, 2016, 76, P3-07-46-P3-07-46.	0.9	2
471	Determinants of 25-hydroxyvitamin D Status in a Cutaneous Melanoma Population. Acta Dermato-Venereologica, 0, 102, adv00692.	1.3	2
472	Molecular Heterogeneity Between Paired Primary and Metastatic Lesions from Clear Cell Renal Cell Carcinoma. European Urology Open Science, 2022, 40, 54-57.	0.4	2
473	Correlation of Immunological and Molecular Profiles with Response to Crizotinib in Alveolar Soft Part Sarcoma: An Exploratory Study Related to the EORTC 90101 "CREATE―Trial. International Journal of Molecular Sciences, 2022, 23, 5689.	4.1	2
474	7115 POSTER DISCUSSION ABCB-1 and VEGFR-3 Single Nucleotide Polymorphisms (SNPs) and Outcome on Sunitinib (SUN) Treatment in Metastatic Clear Cell Renal Cell Carcinoma (RCC). European Journal of Cancer, 2011, 47, S509.	2.8	1
475	1412 POSTER Genetic Markers in Relation to Bevacizumab-induced Hypertension. European Journal of Cancer, 2011, 47, S172-S173.	2.8	1
476	796 Establishment of Primary Endometrial Carcinoma Cell Cultures as a Preclinical Tool for Drug Screening – Methods and Characterization. European Journal of Cancer, 2012, 48, S189-S190.	2.8	1
477	Postmortem Examination of an Aggressive Case of Medullary Thyroid Carcinoma Characterized by Catastrophic Genomic Abnormalities. JCO Precision Oncology, 2017, 1, 1-7.	3.0	1
478	Immune cell dynamics induced by a single dose of pembrolizumab as revealed by single-cell RNA profiling. Annals of Oncology, 2019, 30, iii45.	1.2	1
479	817P Response to olaparib monotherapy in relapsed ovarian cancer by HRR gene mutational status and HRD scarring analysis: Results from the randomized phase II CLIO trial. Annals of Oncology, 2020, 31, S617-S618.	1.2	1
480	689P Human leukocyte antigen (HLA) class I/II expression as a predictive biomarker for response to immune oncology (IO) therapy in metastatic clear-cell renal cell carcinoma (m-ccRCC). Annals of Oncology, 2021, 32, S706.	1.2	1
481	Abstract LB-447: Functional validation of a genetic locus in the VEGFR-1 tyrosine kinase (TK) domain as a predictive marker for bevacizumab. , 2012, , .		1
482	Abstract S2-05: Characterization and clinical relevance of the genomic alterations defining lobular breast cancer., 2015,,.		1
483	A machine-learning approach for the identification of highly predictive germline SNPs as biomarkers for response to bevacizumab in metastatic colorectal cancer using Elastic Net and Lasso Journal of Clinical Oncology, 2018, 36, e15584-e15584.	1.6	1
484	Abstract P3-07-04: Molecular characterization of mucinous breast cancers., 2019,,.		1
485	Homologous recombination repair deficiency (HRD) testing in newly diagnosed advanced-stage epithelial ovarian cancer: A Belgian expert opinion. Facts, Views & Vision in ObGyn, 2022, 14, 111-120.	1.1	1
486	Rare but Relevant Kidney Disorders. Clinical Journal of the American Society of Nephrology: CJASN, 2009, 4, 1701-1704.	4.5	0

#	Article	IF	CITATIONS
487	0183 Progranulin (PC-derived growth factor) levels in serum do not predict response to neoadjuvant capecitabine (X), docetaxel (T) and trastuzumab (H) for patients (pts) with locally advanced breast cancer (LABC). Breast, 2009, 18, S64-S65.	2.2	0
488	Vitamin D Binding Protein Phenotypes Have An Impact On Vitamin D Substitution In COPD., 2011,,.		0
489	208 IL-23R Locus Polymorphism Is Associated with Higher Mortality, after Lung Transplantation. Journal of Heart and Lung Transplantation, 2012, 31, S78.	0.6	0
490	210 Toll-Like Receptor 4 Polymorphisms and the Risk of Primary Graft Dysfunction after Lung Transplantation. Journal of Heart and Lung Transplantation, 2012, 31, S78.	0.6	0
491	Accelerated Lung Function Decline in Smokers. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 579-581.	5.6	0
492	Functional Association between a Genetic Variant in the IL-17 Receptor Gene and Chronic Rejection after Lung Transplantation. Journal of Heart and Lung Transplantation, 2013, 32, S33.	0.6	0
493	Survival after Lung Transplantation Is Linked with a Genetic Polymorphism in Caveolin-1. Journal of Heart and Lung Transplantation, 2013, 32, S120-S121.	0.6	0
494	15 Genetic and molecular validation of uterine sarcoma patient-derived xenograft models. European Journal of Cancer, 2014, 50, 11.	2.8	0
495	Genetic Variation in Immunoglobulin G Receptor Affects Survival After Lung Transplantation. Journal of Heart and Lung Transplantation, 2014, 33, S30.	0.6	0
496	A Genetic Polymorphism in IL-23 Receptor Is Protective for Primary Graft Dysfunction. Journal of Heart and Lung Transplantation, 2014, 33, S138-S139.	0.6	0
497	(Epi)genetic variation in ageing of metabolic fitness. Archives of Public Health, 2015, 73, .	2.4	0
498	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
499	Genomic hallmarks of invasive lobular breast carcinoma and their clinical relevance. Annals of Oncology, 2015, 26, vi3.	1.2	0
500	OC-0047: PD-L1/PD-L2 gene expression differs in tumor vs. lung tissue in non-small cell lung cancer patients. Radiotherapy and Oncology, 2016, 119, S19-S20.	0.6	0
501	An oncogenomics-based in vivo screen identifies novel melanoma tumor-suppressors. European Journal of Cancer, 2016, 61, S30-S31.	2.8	0
502	New cell line models for the development of personalized therapy for high grade serous ovarian cancer. Annals of Oncology, 2017, 28, vii15-vii16.	1.2	0
503	Advanced clear-cell renal cell carcinoma (accRCC): Association of microRNAs (miRNAs) with molecular subtypes, mRNA targets and outcome. Annals of Oncology, 2019, 30, v394-v395.	1.2	0
504	Pentraxin-3 Polymorphisms are Associated with Invasive Pulmonary Aspergillosis after Lung Transplantation. Journal of Heart and Lung Transplantation, 2019, 38, S117-S118.	0.6	0

#	Article	IF	CITATIONS
505	Tumour mutational burden ring trial: Evaluation of targeted next-generation sequencing platforms for implementation in clinical practice. Annals of Oncology, 2019, 30, xi10.	1.2	O
506	LBA81 Keeping exhausted T-cells in check in COVID-19. Annals of Oncology, 2020, 31, S1208.	1.2	0
507	Validation of the Correlation Between Single Nucleotide Polymorphism rs307826 in VEGFR3 and Outcome in Metastatic Clear-Cell Renal Cell Carcinoma Patients Treated with Sunitinib. Kidney Cancer, 2020, 4, 139-149.	0.4	0
508	VEGF, an Angiogenic Factor with Neurotrophic Activity, Useful for Treatment of ALS?., 2006,, 239-252.		0
509	CYPTAM-BRUT 2: A prospective multicenter observational study in the neoadjuvant and metastatic setting investigating tamoxifen response between women with a favorable versus unfavorable endoxifen profile Journal of Clinical Oncology, 2011, 29, TPS140-TPS140.	1.6	0
510	P2-06-02: FOXO3a Genotype Predicts Age of Breast Cancer Onset and Correlates with Lymph Node Involvement, 2011, , .		0
511	P5-05-01: Vitamin D Status in Newly Diagnosed Breast Cancer Patients Inversely Correlates with Tumor Size and Moderately Correlates with Outcome, 2011,,.		0
512	P1-08-20: Parity Interferes with the Effect of Age at Diagnosis on the Frequency Breast Cancers Are Triple-Negative , 2011, , .		0
513	Abstract LB-331: Polymorphisms in inflammation pathway genes and endometrial cancer. , 2012, , .		0
514	Abstract OT2-2-02: Prospective multicentre study evaluating the effect of impaired tamoxifen metabolization on efficacy in breast cancer patients receiving tamoxifen in the neo-adjuvant or metastatic setting - The CYPTAM-BRUT 2 trial , $2012$ , , .		0
515	Abstract P3-05-03: Characterization of PIK3CA mutations in lobular breast cancer. , 2012, , .		O
516	Abstract P6-07-14: Mutational and transcriptomic characterization of breast cancer (BC) arising in young patients (pts) and during pregnancy and their associations with long-term outcome., 2012,,.		0
517	Abstract OT3-2-04: Prospective multicenter study evaluating the effect of impaired tamoxifen metabolization on efficacy in breast cancer patients receiving tamoxifen in the neo-adjuvant or metastatic setting - The CYPTAM-BRUT 2 trial. , 2013, , .		O
518	Abstract OT2-1-05: Prospective multicenter study evaluating the effect of impaired tamoxifen metabolization on efficacy in breast cancer patients receiving tamoxifen in the neo-adjuvant or metastatic setting - The CYPTAM-BRUT 2 trial. , 2015, , .		0
519	Abstract PD3-7: Plasma circulating tumor DNA as an alternative to metastatic biopsies for mutational analyses in breast cancer. , 2015, , .		0
520	Abstract P1-03-05: Genetic variant in the OPG gene is associated with aromatase inhibitor-related musculoskeletal toxicity in breast cancer patients. , 2015, , .		0
521	Abstract 2779: A genome-wide analysis of more than 160,000 individuals identifies four novel pleiotropic risk loci shared between breast and ovarian cancer. , 2015, , .		0
522	Abstract CT135: Uncovering the genomic heterogeneity of multifocal breast cancer., 2015,,.		0

#	Article	IF	Citations
523	Abstract AS13: Epidemiologic predictors of pre-treatment CA125 in women with ovarian cancer. , 2015, , .		О
524	Abstract P4-10-07: Genetic predictors of chemotherapy-related amenorrhea., 2016,,.		0
525	Abstract 5197: Patient-derived xenograft (PDX) models of soft tissue sarcoma (STS): a preclinical platform for early drug testing. , 2016, , .		O
526	Abstract 4529: Tailoring approaches for global epigenome analysis from archival formalin-fixed paraffin-embedded tissue samples. , 2016, , .		0
527	A child's spit epigenome can reveal its respiratory allergy risk. , 2016, , .		0
528	Abstract P2-03-05: Identification, clinical characteristics and treatment outcomes of somatic human epidermal growth factor receptor 2 (ERBB2) mutations in metastatic breast cancer patients. , 2017, , .		0
529	Abstract P1-01-10: Exome sequencing of circulating tumor cells in metastatic breast cancer., 2017,,.		0
530	Abstract P4-03-01: The footprint of the aging stroma in older breast cancer patients. , 2017, , .		0
531	Abstract 3397: Post-mortem examination of an aggressive case of medullary thyroid cancer characterised by catastrophic genomic abnormalities. , 2017, , .		O
532	Genetic variation in the STAT3 gene has an impact on survival after lung transplantation. , 2017, , .		0
533	Polymorphisms in immunosuppression transporters affect outcome after lung transplantation. , 2017, , .		O
534	Abstract 2579: Loss of chromosome $18q11.2-18q12.1$ is predictive for progression-free survival in metastatic colorectal cancer patients treated with bevacizumab., $2018,$		0
535	Abstract 230: Joint genome-wide association study of endometrial cancer and ovarian cancer identifies a novel genetic risk region at 14q23.3., 2018,,.		0
536	Solar Lentigines are Associated with Better Outcome in Cutaneous Melanoma. Acta Dermato-Venereologica, 2019, 99, 1154-1159.	1.3	0
537	Abstract GS1-06: Unraveling lobular breast cancer progression and endocrine resistance mechanisms through genomic and immune characterization of matched primary and metastatic samples. , 2019, , .		0
538	Abstract P4-06-14: Single-cell RNA sequencing to delineate changes in tumor microenvironment induced by immunotherapy. , $2019$ , , .		0
539	EP1126â€Single-cell RNA-sequencing of 7 HGSOC cases reveals multiple prognostic cell subtype., 2019,,.		0
540	TP53 mutations in cell-free DNA as early markers of therapeutic response in platinum-resistant relapsed ovarian cancer (PROC): a prospective translational analysis of the phase II GANNET53 clinical trial. , 2019, , .		0

#	Article	IF	CITATIONS
541	P115â€Quality-of-life analysis in the randomized phase II CLIO trial comparing olaparib with standard chemotherapy in platinum-resistant recurrent ovarian cancer. , 2019, , .		O
542	Abstract 1118: Absence of mouse-specific tumor evolution in patient-derived cancer xenografts. , 2020, , .		0
543	Abstract 3402: BCAT1 as a druggable target in immuno-oncology. , 2020, , .		O
544	Abstract 4280: Potential molecular biomarkers of response to eribulin in patients with leiomyosarcoma. , 2020, , .		0
545	Abstract 794: Molecular analysis of archival inflammatory myofibroblastic tumor tissue samples from EORTC 90101 "CREATE―and correlation with response to crizotinib. , 2020, , .		O
546	Abstract PD8-02: Phylogenetic reconstruction of advanced breast cancer reveals two different routes of metastatic dissemination associated with distinct clinical outcome., 2020,,.		0
547	Plasma markers showing differential baseline expression in relapsing versus non-relapsing patients with hormone sensitive breast tumors. European Journal of Cancer, 2020, 138, S73.	2.8	0
548	Abstract P2-08-23: Early intratumoral changes after a single dose of anti-PD-1 treatment in patients with early breast cancer (BC). Cancer Research, 2022, 82, P2-08-23-P2-08-23.	0.9	O