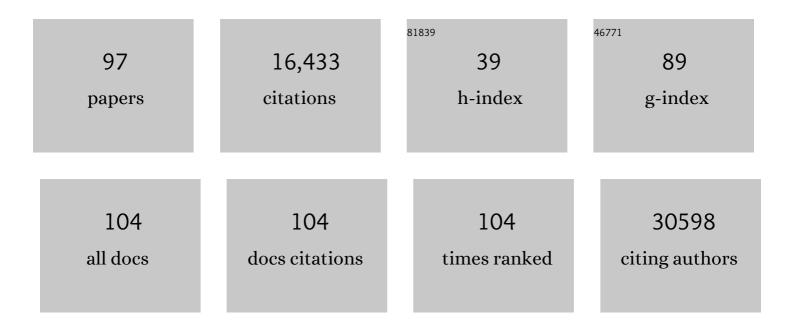
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	An mRNA expression-based signature for oncogene-induced replication-stress. Oncogene, 2022, 41, 1216-1224.	2.6	17
2	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. Nature Medicine, 2022, 28, 535-544.	15.2	158
3	Intraoperative MET-receptor targeted fluorescent imaging and spectroscopy for lymph node detection in papillary thyroid cancer: novel diagnostic tools for more selective central lymph node compartment dissection. European Journal of Nuclear Medicine and Molecular Imaging, 2022, 49, 3557-3570.	3.3	7
4	Immunogenicity after second and third mRNA-1273 vaccination doses in patients receiving chemotherapy, immunotherapy, or both for solid tumours. Lancet Oncology, The, 2022, 23, 833-835.	5.1	18
5	The gut wall's potential as a partner for precision oncology in immune checkpoint treatment. Cancer Treatment Reviews, 2022, 107, 102406.	3.4	2
6	Validation of Novel Molecular Imaging Targets Identified by Functional Genomic mRNA Profiling to Detect Dysplasia in Barrett's Esophagus. Cancers, 2022, 14, 2462.	1.7	4
7	Liver glycogen phosphorylase is upregulated in glioblastoma and provides a metabolic vulnerability to high dose radiation. Cell Death and Disease, 2022, 13, .	2.7	6
8	Genome-wide association study of cardiovascular disease in testicular cancer patients treated with platinum-based chemotherapy. Pharmacogenomics Journal, 2021, 21, 152-164.	0.9	4
9	COVID-19 vaccination: the VOICE for patients with cancer. Nature Medicine, 2021, 27, 568-569.	15.2	53
10	Improving gene function predictions using independent transcriptional components. Nature Communications, 2021, 12, 1464.	5.8	20
11	Perioperative Systemic Therapy vs Cytoreductive Surgery and Hyperthermic Intraperitoneal Chemotherapy Alone for Resectable Colorectal Peritoneal Metastases. JAMA Surgery, 2021, 156, 710-720.	2.2	34
12	Identification and Validation of Esophageal Squamous Cell Carcinoma Targets for Fluorescence Molecular Endoscopy. International Journal of Molecular Sciences, 2021, 22, 9270.	1.8	3
13	Robust metabolic transcriptional components in 34,494 patient-derived cancer-related samples and cell lines. Cancer & Metabolism, 2021, 9, 35.	2.4	4
14	Gallbladder Cancer: Current Insights in Genetic Alterations and Their Possible Therapeutic Implications. Cancers, 2021, 13, 5257.	1.7	22
15	mRNA-1273 COVID-19 vaccination in patients receiving chemotherapy, immunotherapy, or chemoimmunotherapy for solid tumours: a prospective, multicentre, non-inferiority trial. Lancet Oncology, The, 2021, 22, 1681-1691.	5.1	118
16	Serotonin and Dopamine Receptor Expression in Solid Tumours Including Rare Cancers. Pathology and Oncology Research, 2020, 26, 1539-1547.	0.9	35
17	Molecular imaging biomarkers for immune checkpoint inhibitor therapy. Theranostics, 2020, 10, 1708-1718.	4.6	68
18	Overexpression of Cyclin E1 or Cdc25A leads to replication stress, mitotic aberrancies, and increased sensitivity to replication checkpoint inhibitors. Oncogenesis, 2020, 9, 88.	2.1	37

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19	Cyclin E expression is associated with high levels of replication stress in triple-negative breast cancer, 2020, 6, 40.	2.3	27
20	Clinical utility of circulating tumor DNA as a response and follow-up marker in cancer therapy. Cancer and Metastasis Reviews, 2020, 39, 999-1013.	2.7	38
21	Transcriptional Activity and Stability of CD39+CD103+CD8+ T Cells in Human High-Grade Endometrial Cancer. International Journal of Molecular Sciences, 2020, 21, 3770.	1.8	13
22	Immune microenvironment composition in nonâ€small cell lung cancer and its association with survival. Clinical and Translational Immunology, 2020, 9, e1142.	1.7	119
23	Comparison of Carboplatin With 5-Fluorouracil vs. Cisplatin as Concomitant Chemoradiotherapy for Locally Advanced Head and Neck Squamous Cell Carcinoma. Frontiers in Oncology, 2020, 10, 761.	1.3	14
24	Transcriptional effects of copy number alterations in a large set of human cancers. Nature Communications, 2020, 11, 715.	5.8	53
25	Data-driven prioritization and preclinical evaluation of therapeutic targets in glioblastoma. Neuro-Oncology Advances, 2020, 2, vdaa151.	0.4	1
26	BRCA2 deficiency instigates cGAS-mediated inflammatory signaling and confers sensitivity to tumor necrosis factor-alpha-mediated cytotoxicity. Nature Communications, 2019, 10, 100.	5.8	91
27	CD47 Expression Defines Efficacy of Rituximab with CHOP in Non–Germinal Center B-cell (Non-GCB) Diffuse Large B-cell Lymphoma Patients (DLBCL), but Not in GCB DLBCL. Cancer Immunology Research, 2019, 7, 1663-1671.	1.6	28
28	Cancer cell-expressed SLAMF7 is not required for CD47-mediated phagocytosis. Nature Communications, 2019, 10, 533.	5.8	26
29	Consideration of breast cancer subtype in targeting the androgen receptor. , 2019, 200, 135-147.		65
30	Transcriptional regulators CITED2 and PU.1 cooperate in maintaining hematopoietic stem cells. Experimental Hematology, 2019, 73, 38-49.e7.	0.2	4
31	Perioperative systemic therapy and cytoreductive surgery with HIPEC versus upfront cytoreductive surgery with HIPEC alone for isolated resectable colorectal peritoneal metastases: protocol of a multicentre, open-label, parallel-group, phase II-III, randomised, superiority study (CAIRO6). BMC Cancer, 2019, 19, 390.	1.1	83
32	A large pooled analysis refines gene expression-based molecular subclasses in cutaneous melanoma. OncoImmunology, 2019, 8, 1558664.	2.1	0
33	MAPK pathway activity plays a key role in PD‣1 expression of lung adenocarcinoma cells. Journal of Pathology, 2019, 249, 52-64.	2.1	117
34	89Zr-labeled Bispecific T-cell Engager AMG 211 PET Shows AMG 211 Accumulation in CD3-rich Tissues and Clear, Heterogeneous Tumor Uptake. Clinical Cancer Research, 2019, 25, 3517-3527.	3.2	34
35	Driving innovation for rare skin cancers: utilizing common tumours and machine learning to predict immune checkpoint inhibitor response. Immuno-Oncology Technology, 2019, 4, 1-7.	0.2	2
36	TPX2/Aurora kinase A signaling as a potential therapeutic target in genomically unstable cancer cells. Oncogene, 2019, 38, 852-867.	2.6	43

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37	Quantitative proteomics analysis identifies MUC1 as an effect sensor of EGFR inhibition. Oncogene, 2019, 38, 1477-1488.	2.6	11
38	Integrative Kinome Profiling Identifies mTORC1/2 Inhibition as Treatment Strategy in Ovarian Clear Cell Carcinoma. Clinical Cancer Research, 2018, 24, 3928-3940.	3.2	35
39	Data-Driven prioritisation of antibody-drug conjugate targets in head and neck squamous cell carcinoma. Oral Oncology, 2018, 80, 33-39.	0.8	5
40	P04.22 Data-driven prioritization and evaluation of novel therapeutic targets in glioblastoma. Neuro-Oncology, 2018, 20, iii283-iii283.	0.6	0
41	Clypican 3 Overexpression across a Broad Spectrum of Tumor Types Discovered with Functional Genomic mRNA Profiling of a Large CancerÂDatabase. American Journal of Pathology, 2018, 188, 1973-1981.	1.9	30
42	Considering the biology of late recurrences in selecting patients for extended endocrine therapy in breast cancer. Cancer Treatment Reviews, 2018, 70, 118-126.	3.4	13
43	Identification of relevant drugable targets in diffuse large B-cell lymphoma using a genome-wide unbiased CD20 guilt-by association approach. PLoS ONE, 2018, 13, e0193098.	1.1	20
44	CD47 Expression Defines the Efficacy of Rituximab in Non-Germinal Center B-Cell (non-GCB) Diffuse Large B-Cell Lymphoma (DLBCL). Blood, 2018, 132, 2852-2852.	0.6	0
45	Data-Driven Prioritization and Review of Targets for Molecular-Based Theranostic Approaches in Pancreatic Cancer. Journal of Nuclear Medicine, 2017, 58, 1899-1903.	2.8	9
46	The antibody–drug conjugate target landscape across a broad range of tumour types. Annals of Oncology, 2017, 28, 3083-3091.	0.6	40
47	Theranostics Using Antibodies and Antibody-Related Therapeutics. Journal of Nuclear Medicine, 2017, 58, 83S-90S.	2.8	85
48	Relevance of Tumor-Infiltrating Immune Cell Composition and Functionality for Disease Outcome in Breast Cancer. Journal of the National Cancer Institute, 2017, 109, djw192.	3.0	296
49	Identification of novel therapeutic targets in anaplastic thyroid carcinoma using functional genomic mRNA-profiling: Paving the way for new avenues?. Surgery, 2017, 161, 202-211.	1.0	16
50	Indispensable benefit of independent investigator-driven research in a changing clinical trial landscape. ESMO Open, 2017, 2, e000272.	2.0	2
51	Functional Genomic mRNA Profiling of Colorectal Adenomas: Identification and <i>in vivo</i> Validation of CD44 and Splice Variant CD44v6 as Molecular Imaging Targets. Theranostics, 2017, 7, 482-492.	4.6	10
52	Abstract 1406: Towards an RNA expression-based signature for oncogene-induced replication stress. , 2017, , .		0
53	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	1.4	27
54	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	4.1	134

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#	Article	IF	CITATIONS
55	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25 000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	4.1	59
56	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
57	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
58	A large lung gene expression study identifying fibulin-5 as a novel player in tissue repair in COPD. Thorax, 2015, 70, 21-32.	2.7	89
59	Gene expression analysis identifies global gene dosage sensitivity in cancer. Nature Genetics, 2015, 47, 115-125.	9.4	313
60	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
61	Regulators of homologous recombination repair as novel targets for cancer treatment. Frontiers in Genetics, 2015, 6, 96.	1.1	58
62	ATR inhibition preferentially targets homologous recombination-deficient tumor cells. Oncogene, 2015, 34, 3474-3481.	2.6	80
63	Growth Differentiation Factor 15 (GDF-15) Plasma Levels Increase during Bleomycin- and Cisplatin-Based Treatment of Testicular Cancer Patients and Relate to Endothelial Damage. PLoS ONE, 2015, 10, e0115372.	1.1	37
64	Functional Genomic mRNA Profiling of a large cancer data base demonstrates mesothelin overexpression in a broad range of tumor types. Oncotarget, 2015, 6, 28164-28172.	0.8	22
65	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	3.3	244
66	Polygenic scores associated with educational attainment in adults predict educational achievement and ADHD symptoms in children. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 510-520.	1.1	40
67	Extraintestinal Manifestations and Complications in Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2014, 20, 1.	0.9	31
68	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
69	Abstract 1315: CtIP is regulated by the APC/C-Cdh1 to mediate cell cycle-dependent control of DNA repair. , 2014, , .		0
70	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	9.4	96
71	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
72	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. PLoS Genetics, 2013, 9, e1003201.	1.5	247

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73	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. PLoS Genetics, 2012, 8, e1002431.	1.5	194
74	Defining the risk of toxicity in phase I oncology trials of novel molecularly targeted agents: a single centre experience. Annals of Oncology, 2012, 23, 1968-1973.	0.6	26
75	Treatment with high-dose simvastatin inhibits geranylgeranylation in AML blast cells in a subset of AML patients. Experimental Hematology, 2012, 40, 177-186.e6.	0.2	15
76	Macrophage inhibitory cytokine 1 plasma levels in testicular cancer patients during cisplatin combination treatment and their relation to endothelial damage Journal of Clinical Oncology, 2012, 30, e15035-e15035.	0.8	0
77	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	9.4	1,201
78	A bioinformatical and functional approach to identify novel strategies for chemoprevention of colorectal cancer. Oncogene, 2011, 30, 2026-2036.	2.6	22
79	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for <i>IL2, REL</i> , and <i>CARD9</i> . Hepatology, 2011, 53, 1977-1985.	3.6	110
80	Meta-analysis of genome-wide association studies in celiac disease and rheumatoid arthritis identifies fourteen non-HLA shared loci. Annals of the Rheumatic Diseases, 2011, 70, A21-A21.	0.5	0
81	MixupMapper: correcting sample mix-ups in genome-wide datasets increases power to detect small genetic effects. Bioinformatics, 2011, 27, 2104-2111.	1.8	81
82	Involvement of the TGF-β and β-Catenin Pathways in Pelvic Lymph Node Metastasis in Early-Stage Cervical Cancer. Clinical Cancer Research, 2011, 17, 1317-1330.	3.2	113
83	Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. PLoS Genetics, 2011, 7, e1002004.	1.5	307
84	Trans-eQTLs Reveal That Independent Genetic Variants Associated with a Complex Phenotype Converge on Intermediate Genes, with a Major Role for the HLA. PLoS Genetics, 2011, 7, e1002197.	1.5	324
85	Abstract 2960: A combined bioinformatics and proteomics approach identifies DNA repair factors regulated by the APC/C. , 2011, , .		0
86	A retrospective analysis of clinical outcome of patients with chemo-refractory metastatic breast cancer treated in a single institution phase I unit. British Journal of Cancer, 2010, 103, 607-612.	2.9	11
87	Identification of genes and pathways associated with cytotoxic T lymphocyte infiltration of serous ovarian cancer. British Journal of Cancer, 2010, 103, 685-692.	2.9	43
88	Multiple common variants for celiac disease influencing immune gene expression. Nature Genetics, 2010, 42, 295-302.	9.4	871
89	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308
90	Abstract 161: Discovery of novel methylation-based biomarkers for epithelial ovarian cancer using oligonucleotide microarrays. , 2010, , .		0

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#	Article	IF	CITATIONS
91	In Vivo Treatment of AML Patients with High-Dose Simvastatin Inhibits Geranylgeranylation In AML Cells. Blood, 2010, 116, 3280-3280.	0.6	0
92	Current smokingâ€specific gene expression signature in normal bronchial epithelium is enhanced in squamous cell lung cancer. Journal of Pathology, 2009, 218, 182-191.	2.1	63
93	Survival-Related Profile, Pathways, and Transcription Factors in Ovarian Cancer. PLoS Medicine, 2009, 6, e1000024.	3.9	156
94	A New Perspective on Transcriptional System Regulation (TSR): Towards TSR Profiling. PLoS ONE, 2008, 3, e1656.	1.1	11
95	Profiling Studies in Ovarian Cancer: A Review. Oncologist, 2007, 12, 960-966.	1.9	63
96	Evidence Based Selection of Housekeeping Genes. PLoS ONE, 2007, 2, e898.	1.1	617
97	Application of a comprehensive subtelomere array in clinical diagnosis of mental retardation. European Journal of Medical Genetics, 2005, 48, 250-262.	0.7	29