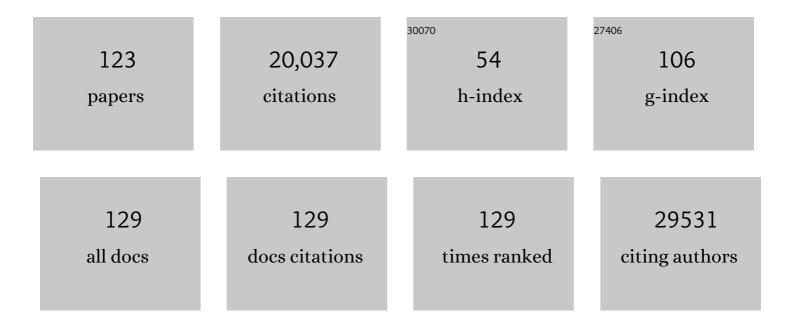
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The consensus molecular subtypes of colorectal cancer. Nature Medicine, 2015, 21, 1350-1356.	30.7	3,596
2	Estimating theÂpopulation abundance of tissue-infiltrating immune and stromal cell populations using gene expression. Genome Biology, 2016, 17, 218.	8.8	1,980
3	Gene Expression Classification of Colon Cancer into Molecular Subtypes: Characterization, Validation, and Prognostic Value. PLoS Medicine, 2013, 10, e1001453.	8.4	1,064
4	Transcriptome classification of HCC is related to gene alterations and to new therapeutic targets. Hepatology, 2007, 45, 42-52.	7.3	1,034
5	SDH Mutations Establish a Hypermethylator Phenotype in Paraganglioma. Cancer Cell, 2013, 23, 739-752.	16.8	606
6	Integrated genomic characterization of adrenocortical carcinoma. Nature Genetics, 2014, 46, 607-612.	21.4	560
7	The gene expression profile of nodal peripheral T-cell lymphoma demonstrates a molecular link between angioimmunoblastic T-cell lymphoma (AITL) and follicular helper T (TFH) cells. Blood, 2007, 109, 4952-4963.	1.4	533
8	Hepatic Stem-like Phenotype and Interplay of Wnt/β-Catenin and Myc Signaling in Aggressive Childhood Liver Cancer. Cancer Cell, 2008, 14, 471-484.	16.8	443
9	Immune and Stromal Classification of Colorectal Cancer Is Associated with Molecular Subtypes and Relevant for Precision Immunotherapy. Clinical Cancer Research, 2016, 22, 4057-4066.	7.0	433
10	Fusion Gene–Negative Alveolar Rhabdomyosarcoma Is Clinically and Molecularly Indistinguishable From Embryonal Rhabdomyosarcoma. Journal of Clinical Oncology, 2010, 28, 2151-2158.	1.6	426
11	Validated prediction of clinical outcome in sarcomas and multiple types of cancer on the basis of a gene expression signature related to genome complexity. Nature Medicine, 2010, 16, 781-787.	30.7	394
12	Ectopic Activation of Germline and Placental Genes Identifies Aggressive Metastasis-Prone Lung Cancers. Science Translational Medicine, 2013, 5, 186ra66.	12.4	392
13	Cancer stemness, intratumoral heterogeneity, and immune response across cancers. Proceedings of the United States of America, 2019, 116, 9020-9029.	7.1	372
14	Stratification of Pancreatic Ductal Adenocarcinomas Based on Tumor and Microenvironment Features. Gastroenterology, 2018, 155, 1999-2013.e3.	1.3	347
15	Gene Expression Profiling Reveals a New Classification of Adrenocortical Tumors and Identifies Molecular Predictors of Malignancy and Survival. Journal of Clinical Oncology, 2009, 27, 1108-1115.	1.6	341
16	EGFR as a potential therapeutic target for a subset of muscle-invasive bladder cancers presenting a basal-like phenotype. Science Translational Medicine, 2014, 6, 244ra91.	12.4	304
17	A Hepatocellular Carcinoma 5-Gene Score Associated With Survival of Patients After Liver Resection. Gastroenterology, 2013, 145, 176-187.	1.3	302
18	Gene expression profiling identifies emerging oncogenic pathways operating in extranodal NK/T-cell lymphoma, nasal type. Blood, 2010, 115, 1226-1237.	1.4	285

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19	Integrative genomic analysis reveals somatic mutations in pheochromocytoma and paraganglioma. Human Molecular Genetics, 2011, 20, 3974-3985.	2.9	266
20	Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors. Nature Communications, 2018, 9, 1048.	12.8	254
21	Molecular Subtypes of Clear Cell Renal Cell Carcinoma Are Associated with Sunitinib Response in the Metastatic Setting. Clinical Cancer Research, 2015, 21, 1329-1339.	7.0	250
22	The Warburg Effect Is Genetically Determined in Inherited Pheochromocytomas. PLoS ONE, 2009, 4, e7094.	2.5	203
23	Biological and clinical relevance of transcriptionally active human papillomavirus (HPV) infection in oropharynx squamous cell carcinoma. International Journal of Cancer, 2010, 126, 1882-1894.	5.1	194
24	Stem cell-like micro-RNA signature driven by Myc in aggressive liver cancer. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20471-20476.	7.1	187
25	Gene-expression profiling of systemic anaplastic large-cell lymphoma reveals differences based on ALK status and two distinct morphologic ALK+ subtypes. Blood, 2007, 109, 2156-2164.	1.4	182
26	Independent Component Analysis Uncovers the Landscape of the Bladder Tumor Transcriptome and Reveals Insights into Luminal and Basal Subtypes. Cell Reports, 2014, 9, 1235-1245.	6.4	181
27	Distinct epigenetic landscapes underlie the pathobiology of pancreatic cancer subtypes. Nature Communications, 2018, 9, 1978.	12.8	177
28	Activation of a promyelocytic leukemia–tumor protein 53 axis underlies acute promyelocytic leukemia cure. Nature Medicine, 2014, 20, 167-174.	30.7	166
29	Immune Contexture, Immunoscore, and Malignant Cell Molecular Subgroups for Prognostic and Theranostic Classifications of Cancers. Advances in Immunology, 2016, 130, 95-190.	2.2	160
30	Multi-omics analysis defines core genomic alterations in pheochromocytomas and paragangliomas. Nature Communications, 2015, 6, 6044.	12.8	153
31	Tumor Cells Hijack Macrophage-Produced Complement C1q to Promote Tumor Growth. Cancer Immunology Research, 2019, 7, 1091-1105.	3.4	153
32	Pancreatic Adenocarcinoma Therapeutic Targets Revealed by Tumor-Stroma Cross-Talk Analyses in Patient-Derived Xenografts. Cell Reports, 2017, 21, 2458-2470.	6.4	148
33	Tbx3 Is a Downstream Target of the Wnt/β-Catenin Pathway and a Critical Mediator of β-Catenin Survival Functions in Liver Cancer. Cancer Research, 2007, 67, 901-910.	0.9	147
34	Anaplastic oligodendrogliomas with 1p19q codeletion have a proneural gene expression profile. Molecular Cancer, 2008, 7, 41.	19.2	145
35	Exquisite Sensitivity of TP53 Mutant and Basal Breast Cancers to a Dose-Dense Epirubicinâ^'Cyclophosphamide Regimen. PLoS Medicine, 2007, 4, e90.	8.4	144
36	Transcriptome Analysis Reveals that p53 and β-Catenin Alterations Occur in a Group of Aggressive Adrenocortical Cancers. Cancer Research, 2010, 70, 8276-8281.	0.9	134

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#	Article	IF	CITATIONS
37	Stabilization of Î ² -catenin affects mouse embryonic liver growth and hepatoblast fate. Hepatology, 2008, 47, 247-258.	7.3	132
38	Dissecting heterogeneity in malignant pleural mesothelioma through histo-molecular gradients for clinical applications. Nature Communications, 2019, 10, 1333.	12.8	125
39	Diffuse large B-cell lymphomas with CDKN2A deletion have a distinct gene expression signature and a poor prognosis under R-CHOP treatment: a GELA study. Blood, 2010, 116, 1092-1104.	1.4	122
40	Molecular Classification of Malignant Pleural Mesothelioma: Identification of a Poor Prognosis Subgroup Linked to the Epithelial-to-Mesenchymal Transition. Clinical Cancer Research, 2014, 20, 1323-1334.	7.0	121
41	Should We Abandon the t-Test in the Analysis of Gene Expression Microarray Data: A Comparison of Variance Modeling Strategies. PLoS ONE, 2010, 5, e12336.	2.5	120
42	Sporadic Early-Onset Colorectal Cancer Is a Specific Sub-Type of Cancer: A Morphological, Molecular and Genetics Study. PLoS ONE, 2014, 9, e103159.	2.5	119
43	Methylation profiling identifies 2 groups of gliomas according to their tumorigenesis. Neuro-Oncology, 2011, 13, 84-98.	1.2	115
44	Identification of a CpG Island Methylator Phenotype in Adrenocortical Carcinomas. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E174-E184.	3.6	110
45	Molecular features of hepatosplenic T-cell lymphoma unravels potential novel therapeutic targets. Blood, 2012, 119, 5795-5806.	1.4	99
46	The Balance Between Cytotoxic T-cell Lymphocytes and Immune Checkpoint Expression in the Prognosis of Colon Tumors. Journal of the National Cancer Institute, 2018, 110, 68-77.	6.3	89
47	Transcriptomic analysis of the tumor microenvironment to guide prognosis and immunotherapies. Cancer Immunology, Immunotherapy, 2018, 67, 981-988.	4.2	89
48	CD8â€alpha Tâ€cell infiltration in human papillomavirusâ€related oropharyngeal carcinoma correlates with improved patient prognosis. International Journal of Cancer, 2013, 132, E26-36.	5.1	82
49	Telomerase Activation and ATRX Mutations Are Independent Risk Factors for Metastatic Pheochromocytoma and Paraganglioma. Clinical Cancer Research, 2019, 25, 760-770.	7.0	82
50	Integrated multi-omics analysis of oligodendroglial tumours identifies three subgroups of 1p/19q co-deleted gliomas. Nature Communications, 2016, 7, 11263.	12.8	73
51	Molecular Subtypes of Clear-cell Renal Cell Carcinoma are Prognostic for Outcome After Complete Metastasectomy. European Urology, 2018, 74, 474-480.	1.9	72
52	Co-occurring Mutations of Tumor Suppressor Genes, <i>LATS2</i> and <i>NF2</i> , in Malignant Pleural Mesothelioma. Clinical Cancer Research, 2017, 23, 3191-3202.	7.0	67
53	Integrated molecular characterization of chondrosarcoma reveals critical determinants of disease progression. Nature Communications, 2019, 10, 4622.	12.8	64
54	Gene Expression Profiling of Muscle Stem Cells Identifies Novel Regulators of Postnatal Myogenesis. Frontiers in Cell and Developmental Biology, 2016, 4, 58.	3.7	63

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55	Hepatocyte nuclear factor $1\hat{l}\pm$ suppresses steatosis-associated liver cancer by inhibiting PPAR \hat{l}^3 transcription. Journal of Clinical Investigation, 2017, 127, 1873-1888.	8.2	58
56	Transcriptional profiling of pure fibrolamellar hepatocellular carcinoma reveals an endocrine signature. Hepatology, 2014, 59, 2228-2237.	7.3	57
57	CD30-positive peripheral T-cell lymphomas share molecular and phenotypic features. Haematologica, 2013, 98, 1250-1258.	3.5	56
58	Molecular apocrine differentiation is a common feature of breast cancer in patients with germline PTEN mutations. Breast Cancer Research, 2010, 12, R63.	5.0	54
59	Prognostic and theranostic impact of molecular subtypes and immune classifications in renal cell cancer (RCC) and colorectal cancer (CRC). Oncolmmunology, 2015, 4, e1049804.	4.6	51
60	WNT/βâ€catenin pathway activation in Wilms tumors: A unifying mechanism with multiple entries?. Genes Chromosomes and Cancer, 2009, 48, 816-827.	2.8	50
61	Syntenic Relationships between Genomic Profiles of Fiber-Induced Murine and Human Malignant Mesothelioma. American Journal of Pathology, 2011, 178, 881-894.	3.8	48
62	Cyclooxygenase-2 Inhibitors Down-regulate Osteopontin and Nr4a2—New Therapeutic Targets for Colorectal Cancers. Gastroenterology, 2009, 137, 1358-1366.e3.	1.3	47
63	Quantitative Analyses of the Tumor Microenvironment Composition and Orientation in the Era of Precision Medicine. Frontiers in Oncology, 2018, 8, 390.	2.8	46
64	Comparison of the latest commercial short and long oligonucleotide microarray technologies. BMC Genomics, 2006, 7, 51.	2.8	45
65	Additional value of EGFR downstream signaling phosphoprotein expression to KRAS status for response to antiâ€EGFR antibodies in colorectal cancer. International Journal of Cancer, 2010, 127, 1321-1331.	5.1	45
66	A Poor Prognosis Subtype of HNSCC Is Consistently Observed across Methylome, Transcriptome, and miRNome Analysis. Clinical Cancer Research, 2013, 19, 4174-4184.	7.0	45
67	An essential role for decorin in bladder cancer invasiveness. EMBO Molecular Medicine, 2013, 5, 1835-1851.	6.9	45
68	Lung Squamous Cell Carcinomas with Basaloid Histology Represent a Specific Molecular Entity. Clinical Cancer Research, 2014, 20, 5777-5786.	7.0	44
69	Recurrent activating mutations of PPAR \hat{I}^3 associated with luminal bladder tumors. Nature Communications, 2019, 10, 253.	12.8	44
70	TCF12 is mutated in anaplastic oligodendroglioma. Nature Communications, 2015, 6, 7207.	12.8	42
71	Clinical and Pathophysiological Implications of Chromosomal Alterations in Adrenocortical Tumors: An Integrated Genomic Approach. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E301-E311.	3.6	41
72	Pro-angiogenic gene expression is associated with better outcome on sunitinib in metastatic clear-cell renal cell carcinoma. Acta Oncológica, 2018, 57, 498-508.	1.8	41

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73	IGF2 Promotes Growth of Adrenocortical Carcinoma Cells, but Its Overexpression Does Not Modify Phenotypic and Molecular Features of Adrenocortical Carcinoma. PLoS ONE, 2014, 9, e103744.	2.5	40
74	An ANOCEF genomic and transcriptomic microarray study of the response to radiotherapy or to alkylating first-line chemotherapy in glioblastoma patients. Molecular Cancer, 2010, 9, 234.	19.2	37
75	Molecular Subtypes of Clear Cell Renal Cell Carcinoma Are Associated With Outcome During Pazopanib Therapy in the Metastatic Setting. Clinical Genitourinary Cancer, 2018, 16, e605-e612.	1.9	37
76	Pre-TCR expression cooperates with TEL-JAK2 to transform immature thymocytes and induce T-cell leukemia. Blood, 2007, 109, 3972-3981.	1.4	36
77	Clearance of PML/RARA-bound promoters suffice to initiate APL differentiation. Blood, 2014, 124, 3772-3780.	1.4	36
78	Colorectal Cancer Subtyping Consortium (CRCSC) identification of a consensus of molecular subtypes Journal of Clinical Oncology, 2014, 32, 3511-3511.	1.6	34
79	Identification of Gene Expression Profiles Associated With Cortisol Secretion in Adrenocortical Adenomas. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E1109-E1121.	3.6	33
80	<i>KRAS</i> Mutation Signature in Colorectal Tumors Significantly Overlaps With the Cetuximab Response Signature. Journal of Clinical Oncology, 2008, 26, 2228-2230.	1.6	32
81	Mutational Profile of Aggressive, Localised Prostate Cancer from African Caribbean Men Versus European Ancestry Men. European Urology, 2019, 75, 11-15.	1.9	32
82	Prognostic Biomarkers in Pancreatic Cancer: Avoiding Errata When Using the TCGA Dataset. Cancers, 2019, 11, 126.	3.7	29
83	PD-1 Blockade in Solid Tumors with Defects in Polymerase Epsilon. Cancer Discovery, 2022, 12, 1435-1448.	9.4	28
84	The RhoE/ROCK/ARHGAP25 signaling pathway controls cell invasion by inhibition of Rac activity. Molecular Biology of the Cell, 2016, 27, 2653-2661.	2.1	27
85	The cellular prion protein controls the mesenchymal-like molecular subtype and predicts disease outcome in colorectal cancer. EBioMedicine, 2019, 46, 94-104.	6.1	24
86	Clinical utility of colon cancer molecular subtypes: Validation of two main colorectal molecular classifications on the PETACC-8 phase III trial cohort Journal of Clinical Oncology, 2017, 35, 3509-3509.	1.6	24
87	Assessing reproducibility of matrix factorization methods in independent transcriptomes. Bioinformatics, 2019, 35, 4307-4313.	4.1	23
88	Extensive characterization of sphere models established from colorectal cancer cell lines. Cellular and Molecular Life Sciences, 2013, 70, 729-742.	5.4	21
89	Deletion of Chromosomes 13q and 14q Is a Common Feature of Tumors with BRCA2 Mutations. PLoS ONE, 2012, 7, e52079.	2.5	20
90	Preferential Response of Basal-Like Head and Neck Squamous Cell Carcinoma Cell Lines to EGFR-Targeted Therapy Depending on EREG-Driven Oncogenic Addiction. Cancers, 2019, 11, 795.	3.7	17

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91	ROQUIN/RC3H1 Alterations Are Not Found in Angioimmunoblastic T-Cell Lymphoma. PLoS ONE, 2013, 8, e64536.	2.5	15
92	Identification of Positively and Negatively Selected Driver GeneÂMutations Associated With Colorectal Cancer With Microsatellite Instability. Cellular and Molecular Gastroenterology and Hepatology, 2018, 6, 277-300.	4.5	15
93	An array CCH based genomic instability index (C2I) is predictive of clinical outcome in breast cancer and reveals a subset of tumors without lymph node involvement but with poor prognosis. BMC Medical Genomics, 2012, 5, 54.	1.5	14
94	Receptor-Independent Ectopic Activity of <i>Prolactin</i> Predicts Aggressive Lung Tumors and Indicates HDACi-Based Therapeutic Strategies. Antioxidants and Redox Signaling, 2015, 23, 1-14.	5.4	12
95	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
96	Identity by Descent Mapping of Founder Mutations in Cancer Using High-Resolution Tumor SNP Data. PLoS ONE, 2012, 7, e35897.	2.5	8
97	Unraveling the cellular heterogeneity of malignant pleural mesothelioma through a deconvolution approach. Molecular and Cellular Oncology, 2019, 6, 1610322.	0.7	8
98	The PAX-FOXO1s trigger fast trans-differentiation of chick embryonic neural cells into alveolar rhabdomyosarcoma with tissue invasive properties limited by S phase entry inhibition. PLoS Genetics, 2020, 16, e1009164.	3.5	8
99	Machine Learning for Better Prognostic Stratification and Driver Gene Identification Using Somatic Copy Number Variations in Anaplastic Oligodendroglioma. Oncologist, 2018, 23, 1500-1510.	3.7	6
100	Combined tumor genomic profiling and exome sequencing in a breast cancer family implicates <i>ATM</i> in tumorigenesis: A proof of principle study. Genes Chromosomes and Cancer, 2017, 56, 788-799.	2.8	5
101	High-resolution analysis of DNA copy number alterations in rectal cancer. Strahlentherapie Und Onkologie, 2014, 190, 1028-1036.	2.0	4
102	Reply to J.R. Anderson et al. Journal of Clinical Oncology, 2010, 28, e589-e590.	1.6	2
103	Integrating tumor microenvironment with cancer molecular classifications. Genome Medicine, 2015, 7, 115.	8.2	2
104	Abstract 4045: A novel transcriptomic-based immune classification of soft tissue sarcoma (STS) and its association with molecular characteristics, clinical outcome and response to therapy. , 2018, , .		2
105	Abstract 1690: A tumor deconvolution DREAM Challenge: Inferring immune infiltration from bulk gene expression data. , 2019, , .		2
106	Identification of targeted therapy for an aggressive subgroup of muscle-invasive bladder cancers. Molecular and Cellular Oncology, 2015, 2, e999507.	0.7	1
107	Abstract 4603: Clinical application and potential usefulness of targeted next-generation sequencing on resected pancreatic ductal adenocarcinoma. , 2018, , .		1
108	Immuno-molecular characterization of colorectal cancer tumors and its clinical implications. Translational Cancer Research, 2016, 5, S368-S370.	1.0	1

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109	Distinct Expression Patterns of microRNAs in Activated B Cell (ABC) and Germinal Center B (GC) Subtypes of Diffuse Large B Cell Lymphoma (DLBLC) Blood, 2007, 110, 562-562.	1.4	0
110	Abstract 1075: Molecular determinants of colon and renal cancers' immune contextures. , 2014, , .		0
111	Abstract 603: Consensus molecular subtyping through a community of experts advances unsupervised gene expression-based disease classification and facilitates clinical translation. , 2015, , .		0
112	Abstract IA20: Cancer subtypes and their immune microenvironments. , 2016, , .		0
113	Abstract IA10: Tumor microenvironments: Prognostic and theranostic impacts. , 2016, , .		0
114	Abstract A48: Multi-omics characterization of PDAC subtypes using PDX reveals that epigenetic but not genetic analysis permit a clinically relevant classification. , 2016, , .		0
115	Abstract B72: Pancreatic cancer cell drives stroma composition. , 2016, , .		0
116	Metastatic clear cell renal cell carcinoma: Proangiogenic gene expression and outcome on sunitinib Journal of Clinical Oncology, 2017, 35, e16085-e16085.	1.6	0
117	Abstract 4396: Multiomics assessment of the cancer and stromal compartments of patient-derived pancreatic xenografts reveals clinically-relevant subtypes and novel targeted therapies. , 2017, , .		0
118	Title is missing!. , 2020, 16, e1009164.		0
119	Title is missing!. , 2020, 16, e1009164.		0
120	Title is missing!. , 2020, 16, e1009164.		0
121	Title is missing!. , 2020, 16, e1009164.		0
122	Title is missing!. , 2020, 16, e1009164.		0
123	Title is missing!. , 2020, 16, e1009164.		0