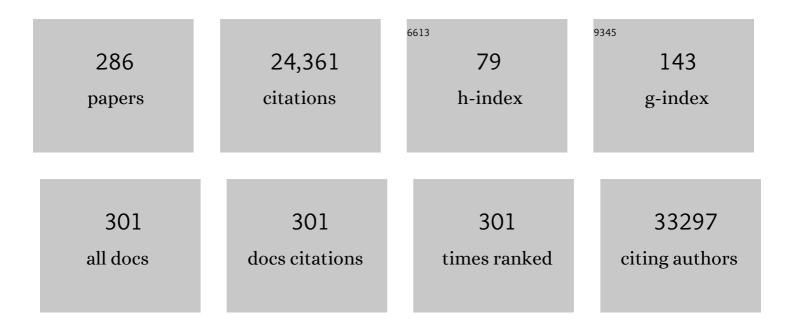
Patrick Tan

List of Publications by Year in descending order

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ΔΑΤΡΙCK ΤΑΝ

#	Article	IF	CITATIONS
1	Molecular analysis of gastric cancer identifies subtypes associated with distinct clinical outcomes. Nature Medicine, 2015, 21, 449-456.	30.7	1,592
2	Genomic Loss of microRNA-101 Leads to Overexpression of Histone Methyltransferase EZH2 in Cancer. Science, 2008, 322, 1695-1699.	12.6	995
3	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. Cancer Discovery, 2017, 7, 1116-1135.	9.4	637
4	A comprehensive survey of genomic alterations in gastric cancer reveals systematic patterns of molecular exclusivity and co-occurrence among distinct therapeutic targets. Gut, 2012, 61, 673-684.	12.1	562
5	Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. Nature Genetics, 2012, 44, 570-574.	21.4	560
6	A common BIM deletion polymorphism mediates intrinsic resistance and inferior responses to tyrosine kinase inhibitors in cancer. Nature Medicine, 2012, 18, 521-528.	30.7	510
7	Complications of Cholecystectomy: Risks of the Laparoscopic Approach and Protective Effects of Operative Cholangiography. Annals of Surgery, 1999, 229, 449-457.	4.2	456
8	Rearrangements of the RAF kinase pathway in prostate cancer, gastric cancer and melanoma. Nature Medicine, 2010, 16, 793-798.	30.7	436
9	Exome sequencing identifies distinct mutational patterns in liver fluke–related and non-infection-related bile duct cancers. Nature Genetics, 2013, 45, 1474-1478.	21.4	426
10	Exome sequencing of liver fluke–associated cholangiocarcinoma. Nature Genetics, 2012, 44, 690-693.	21.4	412
11	Identification of Molecular Subtypes of Gastric Cancer With Different Responses to PI3-Kinase Inhibitors and 5-Fluorouracil. Gastroenterology, 2013, 145, 554-565.	1.3	381
12	Genetics and Molecular Pathogenesis of Gastric Adenocarcinoma. Gastroenterology, 2015, 149, 1153-1162.e3.	1.3	355
13	Oncogenic Pathway Combinations Predict Clinical Prognosis in Gastric Cancer. PLoS Genetics, 2009, 5, e1000676.	3.5	354
14	"Fluorescent Timer": Protein That Changes Color with Time. Science, 2000, 290, 1585-1588.	12.6	347
15	Profiling MicroRNA Expression in Hepatocellular Carcinoma Reveals MicroRNA-224 Up-regulation and Apoptosis Inhibitor-5 as a MicroRNA-224-specific Target. Journal of Biological Chemistry, 2008, 283, 13205-13215.	3.4	341
16	Intrinsic Subtypes of Gastric Cancer, Based on Gene Expression Pattern, Predict Survival and Respond Differently to Chemotherapy. Gastroenterology, 2011, 141, 476-485.e11.	1.3	304
17	Integrative Analysis of Head and Neck Cancer Identifies Two Biologically Distinct HPV and Three Non-HPV Subtypes. Clinical Cancer Research, 2015, 21, 870-881.	7.0	303
18	Paradoxical Relationship between Chromosomal Instability and Survival Outcome in Cancer. Cancer Research, 2011, 71, 3447-3452.	0.9	296

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19	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	27.8	280
20	Aristolochic acids and their derivatives are widely implicated in liver cancers in Taiwan and throughout Asia. Science Translational Medicine, 2017, 9, .	12.4	272
21	STAT3-Driven Upregulation of TLR2 Promotes Gastric Tumorigenesis Independent of Tumor Inflammation. Cancer Cell, 2012, 22, 466-478.	16.8	245
22	Janus Kinase 3–Activating Mutations Identified in Natural Killer/T-cell Lymphoma. Cancer Discovery, 2012, 2, 591-597.	9.4	236
23	Genome-Wide Mutational Signatures of Aristolochic Acid and Its Application as a Screening Tool. Science Translational Medicine, 2013, 5, 197ra101.	12.4	233
24	Molecular classification of gastric cancer. Annals of Oncology, 2016, 27, 763-769.	1.2	215
25	Lethal-7 is down-regulated by the hepatitis B virus x protein and targets signal transducer and activator of transcription 3. Journal of Hepatology, 2010, 53, 57-66.	3.7	212
26	Triple-negative breast cancer: clinicopathological characteristics and relationship with basal-like breast cancer. Modern Pathology, 2010, 23, 123-133.	5.5	209
27	Biological heterogeneity and versatility of cancer-associated fibroblasts in the tumor microenvironment. Oncogene, 2019, 38, 4887-4901.	5.9	205
28	Genomic Loss of <i>miR-486</i> Regulates Tumor Progression and the <i>OLFM4</i> Antiapoptotic Factor in Gastric Cancer. Clinical Cancer Research, 2011, 17, 2657-2667.	7.0	200
29	Meta-analysis of microsatellite instability in relation to clinicopathological characteristics and overall survival in gastric cancer. British Journal of Surgery, 2018, 105, 159-167.	0.3	199
30	Signatures of tumour immunity distinguish Asian and non-Asian gastric adenocarcinomas. Gut, 2015, 64, 1721-1731.	12.1	197
31	Genomic and Epigenomic Profiling of High-Risk Intestinal Metaplasia Reveals Molecular Determinants of Progression to Gastric Cancer. Cancer Cell, 2018, 33, 137-150.e5.	16.8	175
32	Exome sequencing identifies highly recurrent MED12 somatic mutations in breast fibroadenoma. Nature Genetics, 2014, 46, 877-880.	21.4	172
33	Workshop on Treatment of and Postexposure Prophylaxis for <i>Burkholderia pseudomallei</i> and <i>B. mallei</i> Infection, 2010. Emerging Infectious Diseases, 2012, 18, e2-e2.	4.3	170
34	Enabling Technologies for Personalized and Precision Medicine. Trends in Biotechnology, 2020, 38, 497-518.	9.3	169
35	Genomic landscapes of breast fibroepithelial tumors. Nature Genetics, 2015, 47, 1341-1345.	21.4	167
36	Loss of tumor suppressor KDM6A amplifies PRC2-regulated transcriptional repression in bladder cancer and can be targeted through inhibition of EZH2. Science Translational Medicine, 2017, 9, .	12.4	165

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37	Single-Cell Atlas of Lineage States, Tumor Microenvironment, and Subtype-Specific Expression Programs in Gastric Cancer. Cancer Discovery, 2022, 12, 670-691.	9.4	165
38	STAT5 programs a distinct subset of GM-CSF-producing T helper cells that is essential for autoimmune neuroinflammation. Cell Research, 2014, 24, 1387-1402.	12.0	164
39	Methylation Subtypes and Large-Scale Epigenetic Alterations in Gastric Cancer. Science Translational Medicine, 2012, 4, 156ra140.	12.4	163
40	Genomic patterns of pathogen evolution revealed by comparison of Burkholderia pseudomallei, the causative agent of melioidosis, to avirulent Burkholderia thailandensis. BMC Microbiology, 2006, 6, 46.	3.3	158
41	Activation of Transforming Growth Factor Beta 1 Signaling in Gastric Cancer-associated Fibroblasts Increases Their Motility, via Expression of Rhomboid 5 Homolog 2, and Ability to Induce Invasiveness of Gastric Cancer Cells. Gastroenterology, 2017, 153, 191-204.e16.	1.3	158
42	Unmet needs and challenges in gastric cancer: The way forward. Cancer Treatment Reviews, 2014, 40, 692-700.	7.7	156
43	Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. BMC Biology, 2009, 7, 78.	3.8	155
44	Regulatory crosstalk between lineage-survival oncogenes <i>KLF5, GATA4</i> and <i>GATA6</i> cooperatively promotes gastric cancer development. Gut, 2015, 64, 707-719.	12.1	148
45	The Opisthorchis viverrini genome provides insights into life in the bile duct. Nature Communications, 2014, 5, 4378.	12.8	144
46	CXCL12/CXCR4 activation by cancerâ€associated fibroblasts promotes integrin β1 clustering and invasiveness in gastric cancer. International Journal of Cancer, 2016, 138, 1207-1219.	5.1	144
47	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. Cell, 2019, 178, 1465-1477.e17.	28.9	144
48	Management of Accidental Laboratory Exposure to <i>Burkholderia pseudomallei</i> and <i>B. mallei</i> . Emerging Infectious Diseases, 2008, 14, e2-e2.	4.3	140
49	Comprehensive genomic meta-analysis identifies intra-tumoural stroma as a predictor of survival in patients with gastric cancer. Gut, 2013, 62, 1100-1111.	12.1	139
50	VHL substrate transcription factor ZHX2 as an oncogenic driver in clear cell renal cell carcinoma. Science, 2018, 361, 290-295.	12.6	134
51	JAK-STAT and G-protein-coupled receptor signaling pathways are frequently altered in epitheliotropic intestinal T-cell lymphoma. Leukemia, 2016, 30, 1311-1319.	7.2	130
52	ADAR-Mediated RNA Editing Predicts Progression and Prognosis of Gastric Cancer. Gastroenterology, 2016, 151, 637-650.e10.	1.3	127
53	How to stomach an epigenetic insult: the gastric cancer epigenome. Nature Reviews Gastroenterology and Hepatology, 2017, 14, 467-478.	17.8	126
54	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	28.9	126

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55	Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. Nature Communications, 2016, 7, 12983.	12.8	123
56	A Genomic Survey of Positive Selection in Burkholderia pseudomallei Provides Insights into the Evolution of Accidental Virulence. PLoS Pathogens, 2010, 6, e1000845.	4.7	116
57	MSIseq: Software for Assessing Microsatellite Instability from Catalogs of Somatic Mutations. Scientific Reports, 2015, 5, 13321.	3.3	113
58	Conservation of Breast Cancer Molecular Subtypes and Transcriptional Patterns of Tumor Progression Across Distinct Ethnic Populations. Clinical Cancer Research, 2004, 10, 5508-5517.	7.0	112
59	Immunohistochemical detection of Ki67 in breast cancer correlates with transcriptional regulation of genes related to apoptosis and cell death. Modern Pathology, 2005, 18, 374-381.	5.5	112
60	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. Cell Reports, 2015, 12, 272-285.	6.4	112
61	<i>VHL</i> Deficiency Drives Enhancer Activation of Oncogenes in Clear Cell Renal Cell Carcinoma. Cancer Discovery, 2017, 7, 1284-1305.	9.4	111
62	Mutation hotspots at CTCF binding sites coupled to chromosomal instability in gastrointestinal cancers. Nature Communications, 2018, 9, 1520.	12.8	109
63	A <i>Burkholderia pseudomallei</i> Toxin Inhibits Helicase Activity of Translation Factor eIF4A. Science, 2011, 334, 821-824.	12.6	107
64	Continuing Evolution of Burkholderia mallei Through Genome Reduction and Large-Scale Rearrangements. Genome Biology and Evolution, 2010, 2, 102-116.	2.5	106
65	A combined comparative genomic hybridization and expression microarray analysis of gastric cancer reveals novel molecular subtypes. Cancer Research, 2003, 63, 3309-16.	0.9	106
66	Inhibition of Gastric Cancer Invasion and Metastasis by <i>PLA2G2A</i> , a Novel β-Catenin/TCF Target Gene. Cancer Research, 2008, 68, 4277-4286.	0.9	103
67	Genetic blueprint of the zoonotic pathogen Toxocara canis. Nature Communications, 2015, 6, 6145.	12.8	103
68	Characterization of Burkholderia pseudomallei infection and identification of novel virulence factors using a Caenorhabditis elegans host system. Molecular Microbiology, 2002, 44, 1185-1197.	2.5	99
69	Molecular subtypes in cancers of the gastrointestinal tract. Nature Reviews Gastroenterology and Hepatology, 2017, 14, 333-342.	17.8	99
70	Triple Negative Breast Cancer: Outcome Correlation With Immunohistochemical Detection of Basal Markers. American Journal of Surgical Pathology, 2010, 34, 956-964.	3.7	98
71	Antimicrobial resistance to ceftazidime involving loss of penicillin-binding protein 3 in <i>Burkholderia pseudomallei</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17165-17170.	7.1	98
72	Nanostring-Based Multigene Assay to Predict Recurrence for Gastric Cancer Patients after Surgery. PLoS ONE, 2014, 9, e90133.	2.5	96

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73	Tissue Microbiome Profiling Identifies an Enrichment of Specific Enteric Bacteria in Opisthorchis viverrini Associated Cholangiocarcinoma. EBioMedicine, 2016, 8, 195-202.	6.1	94
74	Extracellular Vesicles from Cancer-Associated Fibroblasts Containing Annexin A6 Induces FAK-YAP Activation by Stabilizing β1 Integrin, Enhancing Drug Resistance. Cancer Research, 2020, 80, 3222-3235.	0.9	94
75	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
76	Integrative Genomics Identifies <i>RAB23</i> as an Invasion Mediator Gene in Diffuse-Type Gastric Cancer. Cancer Research, 2008, 68, 4623-4630.	0.9	93
77	Genome-scale mutational signatures of aflatoxin in cells, mice, and human tumors. Genome Research, 2017, 27, 1475-1486.	5.5	90
78	AQP5 enriches for stem cells and cancer origins in the distal stomach. Nature, 2020, 578, 437-443.	27.8	89
79	mTORC1 inhibition restricts inflammation-associated gastrointestinal tumorigenesis in mice. Journal of Clinical Investigation, 2013, 123, 767-81.	8.2	89
80	Integrated epigenomics identifies <i>BMP4</i> as a modulator of cisplatin sensitivity in gastric cancer. Gut, 2013, 62, 22-33.	12.1	88
81	Mutation signatures implicate aristolochic acid in bladder cancer development. Genome Medicine, 2015, 7, 38.	8.2	87
82	Topological and Functional Discovery in a Gene Coexpression Meta-Network of Gastric Cancer. Cancer Research, 2006, 66, 232-241.	0.9	83
83	The Condition-Dependent Transcriptional Landscape of Burkholderia pseudomallei. PLoS Genetics, 2013, 9, e1003795.	3.5	81
84	Development of a Comprehensive Sequencing Assay for Inherited Cardiac Condition Genes. Journal of Cardiovascular Translational Research, 2016, 9, 3-11.	2.4	80
85	Gastric Cancer Pathology and Underlying Molecular Mechanisms. Digestive Surgery, 2013, 30, 150-158.	1.2	79
86	Aberrant enhancer hypomethylation contributes to hepatic carcinogenesis through global transcriptional reprogramming. Nature Communications, 2019, 10, 335.	12.8	77
87	KRAS and BRAF mutations are rare and related to DNA mismatch repair deficiency in gastric cancer from the East and the West: Results from a large international multicentre study. British Journal of Cancer, 2013, 108, 1495-1501.	6.4	76
88	Using Whole Genome Amplification (WGA) of Low-Volume Biopsies to Assess the Prognostic Role of EGFR, KRAS, p53, and CMET Mutations in Advanced-Stage Non-small Cell Lung Cancer (NSCLC). Journal of Thoracic Oncology, 2009, 4, 12-21.	1.1	75
89	Mutation signatures of carcinogen exposure: genome-wide detection and new opportunities for cancer prevention. Genome Medicine, 2014, 6, 24.	8.2	75
90	Phenotype-driven precision oncology as a guide for clinical decisions one patient at a time. Nature Communications, 2017, 8, 435.	12.8	75

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91	Genetic and Structural Variation in the Gastric Cancer Kinome Revealed through Targeted Deep Sequencing. Cancer Research, 2011, 71, 29-39.	0.9	74
92	Mutational landscapes of tongue carcinoma reveal recurrent mutations in genes of therapeutic and prognostic relevance. Genome Medicine, 2015, 7, 98.	8.2	74
93	RUNX3 is a novel negative regulator of oncogenic TEAD–YAP complex in gastric cancer. Oncogene, 2016, 35, 2664-2674.	5.9	74
94	Nanoscale chromatin profiling of gastric adenocarcinoma reveals cancer-associated cryptic promoters and somatically acquired regulatory elements. Nature Communications, 2014, 5, 4361.	12.8	72
95	Anti-tumor efficacy of Selinexor (KPT-330) in gastric cancer is dependent on nuclear accumulation of p53 tumor suppressor. Scientific Reports, 2018, 8, 12248.	3.3	72
96	Mapping the genomic diaspora of gastric cancer. Nature Reviews Cancer, 2022, 22, 71-84.	28.4	72
97	The Core and Accessory Genomes of Burkholderia pseudomallei: Implications for Human Melioidosis. PLoS Pathogens, 2008, 4, e1000178.	4.7	71
98	Genomic acquisition of a capsular polysaccharide virulence cluster by non-pathogenic Burkholderia isolates. Genome Biology, 2010, 11, R89.	9.6	70
99	An 18-gene signature (ColoPrint®) for colon cancer prognosis. Nature Reviews Clinical Oncology, 2011, 8, 131-133.	27.6	67
100	Genomic Profiles Specific to Patient Ethnicity in Lung Adenocarcinoma. Clinical Cancer Research, 2011, 17, 3542-3550.	7.0	65
101	<i>TP53</i> Genomic Status Regulates Sensitivity of Gastric Cancer Cells to the Histone Methylation Inhibitor 3-Deazaneplanocin A (DZNep). Clinical Cancer Research, 2012, 18, 4201-4212.	7.0	65
102	Dissection of gastric cancer heterogeneity for precision oncology. Cancer Science, 2019, 110, 3405-3414.	3.9	65
103	Cross-species chromatin interactions drive transcriptional rewiring in Epstein–Barr virus–positive gastric adenocarcinoma. Nature Genetics, 2020, 52, 919-930.	21.4	65
104	Inflammation-driven senescence-associated secretory phenotype in cancer-associated fibroblasts enhances peritoneal dissemination. Cell Reports, 2021, 34, 108779.	6.4	64
105	A Molecular Signature of the Nottingham Prognostic Index in Breast Cancer. Cancer Research, 2004, 64, 2962-2968.	0.9	63
106	Evidence for Selective Expression of the p53 Codon 72 Polymorphs: Implications in Cancer Development. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2245-2252.	2.5	63
107	Individualised multiplexed circulating tumour DNA assays for monitoring of tumour presence in patients after colorectal cancer surgery. Scientific Reports, 2017, 7, 40737.	3.3	62
108	<i>Burkholderia pseudomallei</i> sequencing identifies genomic clades with distinct recombination, accessory, and epigenetic profiles. Genome Research, 2015, 25, 129-141.	5.5	61

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109	Patterns of large-scale genomic variation in virulent and avirulent Burkholderia species. Genome Research, 2004, 14, 2295-2307.	5.5	60
110	A Signature Predicting Poor Prognosis in Gastric and Ovarian Cancer Represents a Coordinated Macrophage and Stromal Response. Clinical Cancer Research, 2014, 20, 2761-2772.	7.0	60
111	Genomic and functional characterizations of phosphodiesterase subtype 4D in human cancers. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6109-6114.	7.1	59
112	A selective HDAC8 inhibitor potentiates antitumor immunity and efficacy of immune checkpoint blockade in hepatocellular carcinoma. Science Translational Medicine, 2021, 13, .	12.4	59
113	Integrated Molecular Profiling of Human Gastric Cancer Identifies DDR2 as a Potential Regulator of Peritoneal Dissemination. Scientific Reports, 2016, 6, 22371.	3.3	58
114	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. Journal of Clinical Investigation, 2020, 130, 5833-5846.	8.2	58
115	Beyond fitness tracking: The use of consumer-grade wearable data from normal volunteers in cardiovascular and lipidomics research. PLoS Biology, 2018, 16, e2004285.	5.6	57
116	SOX7 is down-regulated in lung cancer. Journal of Experimental and Clinical Cancer Research, 2013, 32, 17.	8.6	56
117	Tumour expression of leptin is associated with chemotherapy resistance and therapy-independent prognosis in gastro-oesophageal adenocarcinomas. British Journal of Cancer, 2014, 110, 1525-1534.	6.4	56
118	Exome-wide Sequencing Shows Low Mutation Rates and Identifies Novel Mutated Genes in Seminomas. European Urology, 2015, 68, 77-83.	1.9	56
119	Identification of a TLR2-regulated gene signature associated with tumor cell growth in gastric cancer. Oncogene, 2017, 36, 5134-5144.	5.9	56
120	OCT1 is a determinant of synbindin-related ERK signalling with independent prognostic significance in gastric cancer. Gut, 2015, 64, 37-48.	12.1	55
121	<i>CD44-SLC1A2</i> Gene Fusions in Gastric Cancer. Science Translational Medicine, 2011, 3, 77ra30.	12.4	54
122	Translating gastric cancer genomics into targeted therapies. Critical Reviews in Oncology/Hematology, 2016, 100, 141-146.	4.4	52
123	Germline Mutations in Cancer Predisposition Genes are Frequent in Sporadic Sarcomas. Scientific Reports, 2017, 7, 10660.	3.3	52
124	<i>TP53</i> intron 1 hotspot rearrangements are specific to sporadic osteosarcoma and can cause Li-Fraumeni syndrome. Oncotarget, 2015, 6, 7727-7740.	1.8	51
125	Mutually exclusive FGFR2, HER2, and KRAS gene amplifications in gastric cancer revealed by multicolour FISH. Cancer Letters, 2014, 353, 167-175.	7.2	50
126	Development and Validation of Burkholderia pseudomallei-Specific Real-Time PCR Assays for Clinical, Environmental or Forensic Detection Applications. PLoS ONE, 2012, 7, e37723.	2.5	50

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127	<i>SETD2</i> histone modifier loss in aggressive GI stromal tumours. Gut, 2016, 65, 1960-1972.	12.1	49
128	An integrative model of pathway convergence in genetically heterogeneous blast crisis chronic myeloid leukemia. Blood, 2020, 135, 2337-2353.	1.4	49
129	Novel Breast Cancer Biomarkers Identified by Integrative Proteomic and Gene Expression Mapping. Journal of Proteome Research, 2008, 7, 1518-1528.	3.7	48
130	Prediction of Clinical Outcome in Multiple Lung Cancer Cohorts by Integrative Genomics: Implications for Chemotherapy Selection. Cancer Research, 2009, 69, 1055-1062.	0.9	48
131	Epigenomic Promoter Alterations Amplify Gene Isoform and Immunogenic Diversity in Gastric Adenocarcinoma. Cancer Discovery, 2017, 7, 630-651.	9.4	48
132	Identification of a regulatory cascade controlling Type III Secretion System 3 gene expression in Burkholderia pseudomallei. Molecular Microbiology, 2010, 76, 677-689.	2.5	46
133	Clinical Utility of a STAT3-Regulated miRNA-200 Family Signature with Prognostic Potential in Early Gastric Cancer. Clinical Cancer Research, 2018, 24, 1459-1472.	7.0	46
134	Long-read transcriptome sequencing reveals abundant promoter diversity in distinct molecular subtypes of gastric cancer. Genome Biology, 2021, 22, 44.	8.8	46
135	Molecular classification of breast phyllodes tumors: validation of the histologic grading scheme and insights into malignant progression. Breast Cancer Research and Treatment, 2011, 129, 319-329.	2.5	45
136	Classifying the estrogen receptor status of breast cancers by expression profiles reveals a poor prognosis subpopulation exhibiting high expression of the ERBB2 receptor. Human Molecular Genetics, 2003, 12, 3245-3258.	2.9	44
137	Epigenomic promoter alterations predict for benefit from immune checkpoint inhibition in metastatic gastric cancer. Annals of Oncology, 2019, 30, 424-430.	1.2	44
138	A Densely Interconnected Genome-Wide Network of MicroRNAs and Oncogenic Pathways Revealed Using Gene Expression Signatures. PLoS Genetics, 2011, 7, e1002415.	3.5	42
139	High-depth sequencing of over 750 genes supports linear progression of primary tumors and metastases in most patients with liver-limited metastatic colorectal cancer. Genome Biology, 2015, 16, 32.	8.8	42
140	Acquired Resistance to FGFR Inhibitor in Diffuse-Type Gastric Cancer through an AKT-Independent PKC-Mediated Phosphorylation of GSK3β. Molecular Cancer Therapeutics, 2018, 17, 232-242.	4.1	42
141	Intertumor heterogeneity of nonâ€smallâ€cell lung carcinomas revealed by multiplexed mutation profiling and integrative genomics. International Journal of Cancer, 2014, 135, 1092-1100.	5.1	41
142	Colorectal Cancer Stem Cells Acquire Chemoresistance Through the Upregulation of F-Box/WD Repeat-Containing Protein 7 and the Consequent Degradation of c-Myc. Stem Cells, 2017, 35, 2027-2036.	3.2	41
143	New insights into the inflamed tumor immune microenvironment of gastric cancer with lymphoid stroma: from morphology and digital analysis to gene expression. Gastric Cancer, 2019, 22, 77-90.	5.3	41
144	Quantitative Profiling of Drug-Associated Proteomic Alterations by Combined 2-Nitrobenzenesulfenyl Chloride (NBS) Isotope Labeling and 2DE/MS Identification. Journal of Proteome Research, 2006, 5, 2194-2206.	3.7	40

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145	Global Map of Growth-Regulated Gene Expression in Burkholderia pseudomallei , the Causative Agent of Melioidosis. Journal of Bacteriology, 2006, 188, 8178-8188.	2.2	40
146	A Modular Analysis of Breast Cancer Reveals a Novel Low-Grade Molecular Signature in Estrogen Receptor–Positive Tumors. Clinical Cancer Research, 2006, 12, 3288-3296.	7.0	40
147	Whole-Genome Sequencing of Asian Lung Cancers: Second-Hand Smoke Unlikely to Be Responsible for Higher Incidence of Lung Cancer among Asian Never-Smokers. Cancer Research, 2014, 74, 6071-6081.	0.9	40
148	A randomized controlled trial of WATAAP to promote physical activity in colorectal and endometrial cancer survivors. Psycho-Oncology, 2019, 28, 1420-1429.	2.3	40
149	Regulation of cellular sphingosine-1-phosphate by sphingosine kinase 1 and sphingosine-1-phopshate lyase determines chemotherapy resistance in gastroesophageal cancer. BMC Cancer, 2015, 15, 762.	2.6	38
150	Multiregion ultraâ€deep sequencing reveals early intermixing and variable levels of intratumoral heterogeneity in colorectal cancer. Molecular Oncology, 2017, 11, 124-139.	4.6	38
151	HoxC5 and miR-615-3p target newly evolved genomic regions to repress hTERT and inhibit tumorigenesis. Nature Communications, 2018, 9, 100.	12.8	38
152	Spatial profiling of gastric cancer patient-matched primary and locoregional metastases reveals principles of tumour dissemination. Gut, 2021, 70, 1823-1832.	12.1	38
153	Mapping genomic and epigenomic evolution in cancer ecosystems. Science, 2021, 373, 1474-1479.	12.6	38
154	Tollâ€like receptor 2 regulates metabolic reprogramming in gastric cancer <i>via</i> superoxide dismutase 2. International Journal of Cancer, 2019, 144, 3056-3069.	5.1	37
155	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent <i>CCNE1</i> and <i>IGF2</i> enhancer hijacking in primary gastric adenocarcinoma. Gut, 2020, 69, 1039-1052.	12.1	36
156	Integrative Genomic, Transcriptional, and Proteomic Diversity in Natural Isolates of the Human Pathogen <i>Burkholderia pseudomallei</i> . Journal of Bacteriology, 2005, 187, 4276-4285.	2.2	35
157	Targets of genome copy number reduction in primary breast cancers identified by integrative genomics. Genes Chromosomes and Cancer, 2007, 46, 288-301.	2.8	35
158	Understanding the genetic basis of gastric cancer: recent advances. Expert Review of Gastroenterology and Hepatology, 2012, 6, 335-341.	3.0	35
159	Protection against Experimental Melioidosis following Immunization with Live Burkholderia thailandensis Expressing a <i>manno</i> -Heptose Capsule. Vaccine Journal, 2013, 20, 1041-1047.	3.1	35
160	Massively Parallel Sequencing of Patients with Intellectual Disability, Congenital Anomalies and/or Autism Spectrum Disorders with a Targeted Gene Panel. PLoS ONE, 2014, 9, e93409.	2.5	35
161	Lack of Targetable FGFR2 Fusions in Endemic Fluke-Associated Cholangiocarcinoma. JCO Global Oncology, 2020, 6, 628-638.	1.8	35
162	Pathogenesis of cholangiocarcinoma: From genetics to signalling pathways. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2015, 29, 233-244.	2.4	34

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163	Digital phenotyping by consumer wearables identifies sleep-associated markers of cardiovascular disease risk and biological aging. Communications Biology, 2019, 2, 361.	4.4	34
164	A tumour-resident Lgr5+ stem-cell-like pool drives the establishment and progression of advanced gastric cancers. Nature Cell Biology, 2021, 23, 1299-1313.	10.3	34
165	Exploring molecular variation in Schistosoma japonicum in China. Scientific Reports, 2015, 5, 17345.	3.3	33
166	Genomic characterisation of breast fibroepithelial lesions in an international cohort. Journal of Pathology, 2019, 249, 447-460.	4.5	33
167	Fanconi anemia gene variants in therapy-related myeloid neoplasms. Blood Cancer Journal, 2015, 5, e323-e323.	6.2	32
168	A seven-Gene Signature assay improves prognostic risk stratification of perioperative chemotherapy treated gastroesophageal cancer patients from the MAGIC trial. Annals of Oncology, 2018, 29, 2356-2362.	1.2	32
169	Predictive Biomarkers of Immune Checkpoint Inhibition in Gastroesophageal Cancers. Frontiers in Oncology, 2020, 10, 763.	2.8	32
170	Current perspectives toward the identification of key players in gastric cancer micro <scp>RNA</scp> dysregulation. International Journal of Cancer, 2016, 138, 1337-1349.	5.1	31
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