

Marco A Marra

List of Publications by Year in descending order

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Version: 2024-02-01

513
papers

222,497
citations

120

166
h-index

28

446
g-index

533
all docs

533
docs citations

533
times ranked

208092
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimization of magnetic bead-based nucleic acid extraction for SARS-CoV-2 testing using readily available reagents. <i>Journal of Virological Methods</i> , 2022, 299, 114339.	1.0	4
2	Early-stage economic analysis of research-based comprehensive genomic sequencing for advanced cancer care. <i>Journal of Community Genetics</i> , 2022, 13, 523-538.	0.5	4
3	Integrative multi-omic analysis reveals neurodevelopmental gene dysregulation in <i>CIC</i> knockout and <i>IDH1</i> mutant cells. <i>Journal of Pathology</i> , 2022, 256, 297-309.	2.1	5
4	ICGC-ARGO precision medicine: familial matters in pancreatic cancer. <i>Lancet Oncology</i> , The, 2022, 23, 25-26.	5.1	6
5	A platform for oncogenomic reporting and interpretation. <i>Nature Communications</i> , 2022, 13, 756.	5.8	7
6	Cost-Effectiveness of Molecularly Guided Treatment in Diffuse Large B-Cell Lymphoma (DLBCL) in Patients under 60. <i>Cancers</i> , 2022, 14, 908.	1.7	0
7	The Neoantigen Landscape of the Coding and Noncoding Cancer Genome Space. <i>Journal of Molecular Diagnostics</i> , 2022, , .	1.2	0
8	Single-cell landscapes of primary glioblastomas and matched explants and cell lines show variable retention of inter- and intratumor heterogeneity. <i>Cancer Cell</i> , 2022, 40, 379-392.e9.	7.7	54
9	The impact of whole genome and transcriptome analysis (WGTA) on predictive biomarker discovery and diagnostic accuracy of advanced malignancies. <i>Journal of Pathology: Clinical Research</i> , 2022, 8, 395-407.	1.3	3
10	Combinatorial and Machine Learning Approaches for Improved Somatic Variant Calling From Formalin-Fixed Paraffin-Embedded Genome Sequence Data. <i>Frontiers in Genetics</i> , 2022, 13, 834764.	1.1	1
11	Whole-genome and transcriptome analysis of advanced adrenocortical cancer highlights multiple alterations affecting epigenome and DNA repair pathways. <i>Cold Spring Harbor Molecular Case Studies</i> , 2022, 8, .	0.7	2
12	Impact of MYC and BCL2 structural variants in tumors of DLBCL morphology and mechanisms of false-negative MYC IHC. <i>Blood</i> , 2021, 137, 2196-2208.	0.6	18
13	Uncovering Clinically Relevant Gene Fusions with Integrated Genomic and Transcriptomic Profiling of Metastatic Cancers. <i>Clinical Cancer Research</i> , 2021, 27, 522-531.	3.2	14
14	Whole-slide laser microdissection for tumour enrichment. <i>Journal of Pathology</i> , 2021, 253, 225-233.	2.1	4
15	Delving into Early-onset Pancreatic Ductal Adenocarcinoma: How Does Age Fit In?. <i>Clinical Cancer Research</i> , 2021, 27, 246-254.	3.2	16
16	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. <i>Clinical Cancer Research</i> , 2021, 27, 202-212.	3.2	50
17	Subtype-Discordant Pancreatic Ductal Adenocarcinoma Tumors Show Intermediate Clinical and Molecular Characteristics. <i>Clinical Cancer Research</i> , 2021, 27, 150-157.	3.2	24
18	Matching methods in precision oncology: An introduction and illustrative example. <i>Molecular Genetics & Genomic Medicine</i> , 2021, 9, e1554.	0.6	13

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19	Molecular attributes underlying central nervous system and systemic relapse in diffuse large B-cell lymphoma. <i>Haematologica</i> , 2021, 106, 1466-1471.	1.7	9
20	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. <i>Nature Cancer</i> , 2021, 2, 157-173.	5.7	147
21	NTRK2 Fusion driven pediatric glioblastoma: Identification of oncogenic Drivers via integrative Genome and transcriptome profiling. <i>Clinical Case Reports (discontinued)</i> , 2021, 9, 1472-1477.	0.2	3
22	Megabase-scale methylation phasing using nanopore long reads and NanoMethPhase. <i>Genome Biology</i> , 2021, 22, 68.	3.8	36
23	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021, 12, 1749.	5.8	47
24	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2474.	5.8	49
25	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. <i>Developmental Cell</i> , 2021, 56, 1238-1252.e5.	3.1	29
26	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. <i>Frontiers in Genetics</i> , 2021, 12, 665888.	1.1	2
27	Clinical and cost outcomes following genomics-informed treatment for advanced cancers. <i>Cancer Medicine</i> , 2021, 10, 5131-5140.	1.3	8
28	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021, 595, 585-590.	13.7	71
29	Tumor infiltrating neutrophils and gland formation predict overall survival and molecular subgroups in pancreatic ductal adenocarcinoma. <i>Cancer Medicine</i> , 2021, 10, 1155-1165.	1.3	9
30	Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. <i>Cell Reports</i> , 2021, 37, 109817.	2.9	14
31	Rearrangement-mediated cis-regulatory alterations in advanced patient tumors reveal interactions with therapy. <i>Cell Reports</i> , 2021, 37, 110023.	2.9	8
32	Clinical response to nivolumab in an INI1-deficient pediatric chordoma correlates with immunogenic recognition of brachyury. <i>Npj Precision Oncology</i> , 2021, 5, 103.	2.3	18
33	Altered Gene Expression along the Glycolysis-Cholesterol Synthesis Axis Is Associated with Outcome in Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 135-146.	3.2	121
34	Establishing a Framework for the Clinical Translation of Germline Findings in Precision Oncology. <i>JNCI Cancer Spectrum</i> , 2020, 4, pkaa045.	1.4	6
35	Clioma-derived IL-33 orchestrates an inflammatory brain tumor microenvironment that accelerates glioma progression. <i>Nature Communications</i> , 2020, 11, 4997.	5.8	109
36	Epigenomic programming in early fetal brain development. <i>Epigenomics</i> , 2020, 12, 1053-1070.	1.0	9

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37	Analysis of Ugandan cervical carcinomas identifies human papillomavirus clade-specific epigenome and transcriptome landscapes. <i>Nature Genetics</i> , 2020, 52, 800-810.	9.4	40
38	Single-cell analysis of ROR1 [±] tracer mouse lung reveals ILC progenitors and effector ILC2 subsets. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	74
39	TRIM25 promotes Capicua degradation independently of ERK in the absence of ATXN1L. <i>BMC Biology</i> , 2020, 18, 154.	1.7	7
40	Evaluating genomic biomarkers associated with resistance or sensitivity to chemotherapy in patients with advanced breast and colorectal cancer. <i>Journal of Oncology Pharmacy Practice</i> , 2020, 27, 107815522095184.	0.5	2
41	Validation of the RHL30 digital gene expression assay as a prognostic biomarker for relapsed Hodgkin lymphoma. <i>British Journal of Haematology</i> , 2020, 190, 864-868.	1.2	5
42	Endogenous Retrovirus Transcript Levels Are Associated with Immunogenic Signatures in Multiple Metastatic Cancer Types. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 1889-1897.	1.9	10
43	Genetic and evolutionary patterns of treatment resistance in relapsed B-cell lymphoma. <i>Blood Advances</i> , 2020, 4, 2886-2898.	2.5	59
44	Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing. <i>Genetics in Medicine</i> , 2020, 22, 1892-1897.	1.1	42
45	Integration of Whole-Genome Sequencing With Circulating Tumor DNA Analysis Captures Clonal Evolution and Tumor Heterogeneity in Non-V600 BRAF Mutant Colorectal Cancer. <i>Clinical Colorectal Cancer</i> , 2020, 19, 132-136.e3.	1.0	1
46	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. <i>Nature Medicine</i> , 2020, 26, 577-588.	15.2	46
47	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , 2020, 52, 231-240.	9.4	365
48	Fluorouracil sensitivity in a head and neck squamous cell carcinoma with a somatic DPYD structural variant. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a004713.	0.5	5
49	Patient selection for a developmental therapeutics program using whole genome and Transcriptome analysis. <i>Investigational New Drugs</i> , 2020, 38, 1601-1604.	1.2	0
50	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
51	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. <i>Nature Cancer</i> , 2020, 1, 452-468.	5.7	103
52	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. <i>Blood</i> , 2020, 136, 572-584.	0.6	44
53	Integrative Analysis of Single-Cell RNA-Seq and ATAC-Seq Data across Treatment Time Points in Pediatric AML. <i>Blood</i> , 2020, 136, 29-29.	0.6	1
54	Abstract PR-009: Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. , 2020, , .		0

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55	Transcriptomic analysis of CIC and ATXN1L reveal a functional relationship exploited by cancer. <i>Oncogene</i> , 2019, 38, 273-290.	2.6	32
56	The pivotal role of sampling recurrent tumors in the precision care of patients with tumors of the central nervous system. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004143.	0.5	4
57	The Genome of the Steller Sea Lion (<i>Eumetopias jubatus</i>). <i>Genes</i> , 2019, 10, 486.	1.0	4
58	Integrative genomic analysis identifies key pathogenic mechanisms in primary mediastinal large B-cell lymphoma. <i>Blood</i> , 2019, 134, 802-813.	0.6	96
59	High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. <i>Genome Research</i> , 2019, 29, 1211-1222.	2.4	52
60	Therapeutic Implication of Genomic Landscape of Adult Metastatic Sarcoma. <i>JCO Precision Oncology</i> , 2019, 3, 1-25.	1.5	12
61	Comparative Tumor RNA Sequencing Analysis for Difficult-to-Treat Pediatric and Young Adult Patients With Cancer. <i>JAMA Network Open</i> , 2019, 2, e1913968.	2.8	38
62	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. <i>PLoS ONE</i> , 2019, 14, e0224578.	1.1	12
63	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. <i>Cell Reports</i> , 2019, 29, 2338-2354.e7.	2.9	74
64	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22.	13.5	162
65	Comprehensive genomic profiling of glioblastoma tumors, BTICs, and xenografts reveals stability and adaptation to growth environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19098-19108.	3.3	42
66	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. <i>Cancer Discovery</i> , 2019, 9, 546-563.	7.7	213
67	A distinct neurodevelopmental syndrome with intellectual disability, autism spectrum disorder, characteristic facies, and macrocephaly is caused by defects in CHD8. <i>Journal of Human Genetics</i> , 2019, 64, 271-280.	1.1	35
68	Integrative genomic analysis of matched primary and metastatic pediatric osteosarcoma. <i>Journal of Pathology</i> , 2019, 249, 319-331.	2.1	36
69	Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003814.	0.5	17
70	<i>NRG1</i> Gene Fusions Are Recurrent, Clinically Actionable Gene Rearrangements in <i>KRAS</i> Wild-Type Pancreatic Ductal Adenocarcinoma. <i>Clinical Cancer Research</i> , 2019, 25, 4674-4681.	3.2	121
71	Capicua regulates neural stem cell proliferation and lineage specification through control of Ets factors. <i>Nature Communications</i> , 2019, 10, 2000.	5.8	34
72	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. <i>Nature</i> , 2019, 572, 67-73.	13.7	293

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73	Application of a Neural Network Whole Transcriptome-Based Pan-Cancer Method for Diagnosis of Primary and Metastatic Cancers. <i>JAMA Network Open</i> , 2019, 2, e192597.	2.8	67
74	Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. <i>Cancer Research</i> , 2019, 79, 2111-2123.	0.4	28
75	Base excision repair deficiency signatures implicate germline and somatic <i>MUTYH</i> aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003681.	0.5	33
76	Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2019, 37, 190-201.	0.8	257
77	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. <i>BioTechniques</i> , 2019, 66, 85-92.	0.8	13
78	Recurrent noncoding U1 snRNA mutations drive cryptic splicing in SHH medulloblastoma. <i>Nature</i> , 2019, 574, 707-711.	13.7	129
79	Sources of erroneous sequences and artifact chimeric reads in next generation sequencing of genomic DNA from formalin-fixed paraffin-embedded samples. <i>Nucleic Acids Research</i> , 2019, 47, e12-e12.	6.5	50
80	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. <i>Blood</i> , 2019, 133, 1313-1324.	0.6	172
81	Clinical outcomes after whole-genome sequencing in patients with metastatic non-small-cell lung cancer. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a002659.	0.5	3
82	Abstract B56: Endogenous retrovirus transcript levels are associated with immunogenic signatures in multiple metastatic cancer types. , 2019, , .		0
83	Abstract 3480: <i>TMEM30A</i> loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. , 2019, , .		0
84	A Hematogenous Route for Medulloblastoma Leptomeningeal Metastases. <i>Cell</i> , 2018, 172, 1050-1062.e14.	13.5	85
85	Molecular characterization of <i>ERBB2</i> -amplified colorectal cancer identifies potential mechanisms of resistance to targeted therapies: a report of two instructive cases. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002535.	0.5	16
86	Assessment of Capture and Amplicon-Based Approaches for the Development of a Targeted Next-Generation Sequencing Pipeline to Personalize Lymphoma Management. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 203-214.	1.2	58
87	Application of genomics to identify therapeutic targets in recurrent pediatric papillary thyroid carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002568.	0.5	14
88	Personalized oncogenomic analysis of metastatic adenoid cystic carcinoma: using whole-genome sequencing to inform clinical decision-making. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002626.	0.5	18
89	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	13.5	2,277
90	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670

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91	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	13.5	1,718
92	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	13.5	228
93	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
94	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
95	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
96	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	13.5	620
97	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	2.9	333
98	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	407
99	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	245
100	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018, 23, 297-312.e12.	2.9	205
101	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	523
102	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	2.9	683
103	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
104	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	2.9	119
105	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
106	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
107	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
108	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	2.9	177

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109	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
110	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
111	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	2.9	284
112	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018, 33, 706-720.e9.	7.7	400
113	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
114	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
115	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
116	Whole genome and whole transcriptome genomic profiling of a metastatic eccrine porocarcinoma. <i>Npj Precision Oncology</i> , 2018, 2, 8.	2.3	15
117	Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. <i>Developmental Cell</i> , 2018, 44, 709-724.e6.	3.1	35
118	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. <i>Nature Medicine</i> , 2018, 24, 103-112.	15.2	525
119	Molecular characterization of metastatic pancreatic neuroendocrine tumors (PNETs) using whole-genome and transcriptome sequencing. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002329.	0.5	30
120	High-resolution architecture and partner genes of MYC rearrangements in lymphoma with DLBCL morphology. <i>Blood Advances</i> , 2018, 2, 2755-2765.	2.5	74
121	Temporal Dynamics of Genomic Alterations in a BRCA1 Germline-“Mutated Pancreatic Cancer With Low Genomic Instability Burden but Exceptional Response to Fluorouracil, Oxaliplatin, Leucovorin, and Irinotecan. <i>JCO Precision Oncology</i> , 2018, 2, 1-8.	1.5	1
122	Comparative RNA-Sequencing Analysis Benefits a Pediatric Patient With Relapsed Cancer. <i>JCO Precision Oncology</i> , 2018, 2, 1-16.	1.5	12
123	Whole-genome and transcriptome profiling of a metastatic thyroid-like follicular renal cell carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a003137.	0.5	15
124	The Genome of the North American Brown Bear or Grizzly: <i>Ursus arctos</i> ssp. <i>horribilis</i> . <i>Genes</i> , 2018, 9, 598.	1.0	34
125	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , 2018, 9, 4001.	5.8	102
126	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	2.9	134

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127	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018, 8, 1548-1565.	7.7	422
128	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	2.9	329
129	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , 2018, 562, 373-379.	13.7	236
130	ABT-888 restores sensitivity in temozolomide resistant glioma cells and xenografts. <i>PLoS ONE</i> , 2018, 13, e0202860.	1.1	28
131	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
132	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology</i> , The, 2018, 19, 785-798.	5.1	268
133	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
134	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	13.7	1,158
135	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	532
136	Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , 2017, 49, 780-788.	9.4	112
137	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. <i>Nature Genetics</i> , 2017, 49, 856-865.	9.4	220
138	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
139	Genomic profiling of pelvic genital type leiomyosarcoma in a woman with a germline CHEK2:c.1100delC mutation and a concomitant diagnosis of metastatic invasive ductal breast carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2017, 3, a001628.	0.5	8
140	Pyruvate Kinase Inhibits Proliferation during Postnatal Cerebellar Neurogenesis and Suppresses Medulloblastoma Formation. <i>Cancer Research</i> , 2017, 77, 3217-3230.	0.4	45
141	Whole-genome analysis reveals unexpected dynamics of mutant subclone development in a patient with JAK2-V617F-positive chronic myeloid leukemia. <i>Experimental Hematology</i> , 2017, 53, 48-58.	0.2	15
142	Genetic profiling of MYC and BCL2 in diffuse large B-cell lymphoma determines cell-of-origin-specific clinical impact. <i>Blood</i> , 2017, 129, 2760-2770.	0.6	112
143	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
144	Comparative transcriptome analysis of isogenic cell line models and primary cancers links capicua (CIC) loss to activation of the MAPK signalling cascade. <i>Journal of Pathology</i> , 2017, 242, 206-220.	2.1	31

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145	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	416
146	The cost and cost trajectory of whole-genome analysis guiding treatment of patients with advanced cancers. <i>Molecular Genetics & Genomic Medicine</i> , 2017, 5, 251-260.	0.6	40
147	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , 2017, 541, 169-175.	13.7	1,448
148	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
149	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. <i>Nature Genetics</i> , 2017, 49, 1487-1494.	9.4	255
150	Clonal expansion and epigenetic reprogramming following deletion or amplification of mutant <i>IDH1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10743-10748.	3.3	109
151	Identification of GPC2 as an Oncoprotein and Candidate Immunotherapeutic Target in High-Risk Neuroblastoma. <i>Cancer Cell</i> , 2017, 32, 295-309.e12.	7.7	148
152	Detection and genomic characterization of a mammary-like adenocarcinoma. <i>Journal of Physical Education and Sports Management</i> , 2017, 3, a002170.	0.5	13
153	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
154	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
155	Characterization of the human thyroid epigenome. <i>Journal of Endocrinology</i> , 2017, 235, 153-165.	1.2	8
156	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
157	Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 7521-7530.	3.2	144
158	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
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