

# Marco A Marra

## List of Publications by Year in Descending Order

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**Version:** 2024-04-10

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

510 papers	162,332 citations	152 h-index	402 g-index
533 ext. papers	198,899 ext. citations	15.5 avg, IF	9.33 L-index

#	Paper	IF	Citations
510	A platform for oncogenomic reporting and interpretation.. <i>Nature Communications</i> , <b>2022</b> , 13, 756	17.4	1
509	ICGC-ARGO precision medicine: familial matters in pancreatic cancer.. <i>Lancet Oncology</i> , <b>2022</b> , 23, 25-26	21.7	2
508	Optimization of magnetic bead-based nucleic acid extraction for SARS-CoV-2 testing using readily available reagents. <i>Journal of Virological Methods</i> , <b>2022</b> , 299, 114339	2.6	3
507	Combinatorial and Machine Learning Approaches for Improved Somatic Variant Calling From Formalin-Fixed Paraffin-Embedded Genome Sequence Data.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 834764	4.5	
506	Clinical response to nivolumab in an INI1-deficient pediatric chordoma correlates with immunogenic recognition of brachyury.. <i>Npj Precision Oncology</i> , <b>2021</b> , 5, 103	9.8	2
505	Early-stage economic analysis of research-based comprehensive genomic sequencing for advanced cancer care. <i>Journal of Community Genetics</i> , <b>2021</b> , 1	2.5	1
504	Integrative multi-omic analysis reveals neurodevelopmental gene dysregulation in CIC-knockout and IDH1 mutant cells. <i>Journal of Pathology</i> , <b>2021</b> ,	9.4	1
503	Rearrangement-mediated cis-regulatory alterations in advanced patient tumors reveal interactions with therapy. <i>Cell Reports</i> , <b>2021</b> , 37, 110023	10.6	0
502	Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. <i>Cell Reports</i> , <b>2021</b> , 37, 109817	10.6	3
501	The impact of MYC and BCL2 structural variants in tumors of DLBCL morphology and mechanisms of false-negative MYC IHC. <i>Blood</i> , <b>2021</b> , 137, 2196-2208	2.2	5
500	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> , <b>2021</b> , 27, 1371-1381	1.7	1
499	The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , <b>2021</b> , 12, 1749	17.4	7
498	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , <b>2021</b> , 12, 2474	17.4	10
497	Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. <i>Developmental Cell</i> , <b>2021</b> , 56, 1238-1252.e5	10.2	7
496	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 665888	4.5	1
495	Clinical and cost outcomes following genomics-informed treatment for advanced cancers. <i>Cancer Medicine</i> , <b>2021</b> , 10, 5131-5140	4.8	3
494	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , <b>2021</b> , 595, 585-590	59.4	10

493	Uncovering Clinically Relevant Gene Fusions with Integrated Genomic and Transcriptomic Profiling of Metastatic Cancers. <i>Clinical Cancer Research</i> , <b>2021</b> , 27, 522-531	12.9	4
492	Whole-slide laser microdissection for tumour enrichment. <i>Journal of Pathology</i> , <b>2021</b> , 253, 225-233	9.4	1
491	Delving into Early-onset Pancreatic Ductal Adenocarcinoma: How Does Age Fit In?. <i>Clinical Cancer Research</i> , <b>2021</b> , 27, 246-254	12.9	4
490	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. <i>Clinical Cancer Research</i> , <b>2021</b> , 27, 202-212	12.9	19
489	Subtype-Discordant Pancreatic Ductal Adenocarcinoma Tumors Show Intermediate Clinical and Molecular Characteristics. <i>Clinical Cancer Research</i> , <b>2021</b> , 27, 150-157	12.9	8
488	Matching methods in precision oncology: An introduction and illustrative example. <i>Molecular Genetics &amp; Genomic Medicine</i> , <b>2021</b> , 9, e1554	2.3	3
487	Molecular attributes underlying central nervous system and systemic relapse in diffuse large B-cell lymphoma. <i>Haematologica</i> , <b>2021</b> , 106, 1466-1471	6.6	4
486	Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity.. <i>Nature Cancer</i> , <b>2021</b> , 2, 157-173	15.4	31
485	NTRK2 Fusion driven pediatric glioblastoma: Identification of oncogenic Drivers via integrative Genome and transcriptome profiling. <i>Clinical Case Reports (discontinued)</i> , <b>2021</b> , 9, 1472-1477	0.7	2
484	Megabase-scale methylation phasing using nanopore long reads and NanoMethPhase. <i>Genome Biology</i> , <b>2021</b> , 22, 68	18.3	9
483	Tumor infiltrating neutrophils and gland formation predict overall survival and molecular subgroups in pancreatic ductal adenocarcinoma. <i>Cancer Medicine</i> , <b>2021</b> , 10, 1155-1165	4.8	3
482	Tumor necrosis factor overcomes immune evasion in p53-mutant medulloblastoma. <i>Nature Neuroscience</i> , <b>2020</b> , 23, 842-853	25.5	22
481	Validation of the RHL30 digital gene expression assay as a prognostic biomarker for relapsed Hodgkin lymphoma. <i>British Journal of Haematology</i> , <b>2020</b> , 190, 864-868	4.5	2
480	Endogenous Retrovirus Transcript Levels Are Associated with Immunogenic Signatures in Multiple Metastatic Cancer Types. <i>Molecular Cancer Therapeutics</i> , <b>2020</b> , 19, 1889-1897	6.1	3
479	Genetic and evolutionary patterns of treatment resistance in relapsed B-cell lymphoma. <i>Blood Advances</i> , <b>2020</b> , 4, 2886-2898	7.8	24
478	Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing. <i>Genetics in Medicine</i> , <b>2020</b> , 22, 1892-1897	8.1	15
477	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> , <b>2020</b> , 19, 132-136.e3	3.8	1
476	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. <i>Nature Medicine</i> , <b>2020</b> , 26, 577-588	50.5	22

475	Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , <b>2020</b> , 52, 231-240	36.3	148
474	Fluorouracil sensitivity in a head and neck squamous cell carcinoma with a somatic structural variant. <i>Journal of Physical Education and Sports Management</i> , <b>2020</b> , 6,	2.8	3
473	Patient selection for a developmental therapeutics program using whole genome and Transcriptome analysis. <i>Investigational New Drugs</i> , <b>2020</b> , 38, 1601-1604	4.3	
472	Pan-cancer analysis of whole genomes. <i>Nature</i> , <b>2020</b> , 578, 82-93	50.4	840
471	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes.. <i>Nature Cancer</i> , <b>2020</b> , 1, 452-468	15.4	34
470	Integrative Analysis of Single-Cell RNA-Seq and ATAC-Seq Data across Treatment Time Points in Pediatric AML. <i>Blood</i> , <b>2020</b> , 136, 29-29	2.2	0
469	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. <i>Blood</i> , <b>2020</b> , 136, 572-584	2.2	19
468	Altered Gene Expression along the Glycolysis-Cholesterol Synthesis Axis Is Associated with Outcome in Pancreatic Cancer. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 135-146	12.9	61
467	Establishing a Framework for the Clinical Translation of Germline Findings in Precision Oncology. <i>JNCI Cancer Spectrum</i> , <b>2020</b> , 4, pkaa045	4.6	0
466	Glioma-derived IL-33 orchestrates an inflammatory brain tumor microenvironment that accelerates glioma progression. <i>Nature Communications</i> , <b>2020</b> , 11, 4997	17.4	42
465	Epigenomic programming in early fetal brain development. <i>Epigenomics</i> , <b>2020</b> , 12, 1053-1070	4.4	2
464	Analysis of Ugandan cervical carcinomas identifies human papillomavirus clade-specific epigenome and transcriptome landscapes. <i>Nature Genetics</i> , <b>2020</b> , 52, 800-810	36.3	17
463	Single-cell analysis of ROR1 <sup>tracer</sup> mouse lung reveals ILC progenitors and effector ILC2 subsets. <i>Journal of Experimental Medicine</i> , <b>2020</b> , 217,	16.6	37
462	TRIM25 promotes Capicua degradation independently of ERK in the absence of ATXN1L. <i>BMC Biology</i> , <b>2020</b> , 18, 154	7.3	1
461	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> , <b>2019</b> , 116, 19098-19108	11.5	23
460	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. <i>Cancer Discovery</i> , <b>2019</b> , 9, 546-563	24.4	123
459	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> , <b>2019</b> , 64, 271-280	4.3	20
458	Integrative genomic analysis of matched primary and metastatic pediatric osteosarcoma. <i>Journal of Pathology</i> , <b>2019</b> , 249, 319-331	9.4	19

457	Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. <i>Journal of Physical Education and Sports Management</i> , <b>2019</b> , 5,	2.8	8
456	Gene Fusions Are Recurrent, Clinically Actionable Gene Rearrangements in Wild-Type Pancreatic Ductal Adenocarcinoma. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 4674-4681	12.9	63
455	Capicua regulates neural stem cell proliferation and lineage specification through control of Ets factors. <i>Nature Communications</i> , <b>2019</b> , 10, 2000	17.4	20
454	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. <i>Nature</i> , <b>2019</b> , 572, 67-73	50.4	149
453	Application of a Neural Network Whole Transcriptome-Based Pan-Cancer Method for Diagnosis of Primary and Metastatic Cancers. <i>JAMA Network Open</i> , <b>2019</b> , 2, e192597	10.4	25
452	Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. <i>Cancer Research</i> , <b>2019</b> , 79, 2111-2123	10.1	14
451	Base excision repair deficiency signatures implicate germline and somatic aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. <i>Journal of Physical Education and Sports Management</i> , <b>2019</b> , 5,	2.8	17
450	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> , <b>2019</b> , 37, 190-201	2.2	137
449	A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. <i>BioTechniques</i> , <b>2019</b> , 66, 85-92	2.5	7
448	Transcriptomic analysis of CIC and ATXN1L reveal a functional relationship exploited by cancer. <i>Oncogene</i> , <b>2019</b> , 38, 273-290	9.2	23
447	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> , <b>2019</b> , 5,	2.8	4
446	The Genome of the Steller Sea Lion (). <i>Genes</i> , <b>2019</b> , 10,	4.2	3
445	Integrative genomic analysis identifies key pathogenic mechanisms in primary mediastinal large B-cell lymphoma. <i>Blood</i> , <b>2019</b> , 134, 802-813	2.2	41
444	High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. <i>Genome Research</i> , <b>2019</b> , 29, 1211-1222	9.7	31
443	Therapeutic Implication of Genomic Landscape of Adult Metastatic Sarcoma.. <i>JCO Precision Oncology</i> , <b>2019</b> , 3, 1-25	3.6	5
442	Comparative Tumor RNA Sequencing Analysis for Difficult-to-Treat Pediatric and Young Adult Patients With Cancer. <i>JAMA Network Open</i> , <b>2019</b> , 2, e1913968	10.4	22
441	Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. <i>PLoS ONE</i> , <b>2019</b> , 14, e0224578	3.7	6
440	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. <i>Cell Reports</i> , <b>2019</b> , 29, 2338-2354.e7	10.6	40

439	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , <b>2019</b> , 179, 1207-1221.e22	56.2	73
438	Recurrent noncoding U1 snRNA mutations drive cryptic splicing in SHH medulloblastoma. <i>Nature</i> , <b>2019</b> , 574, 707-711	50.4	78
437	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> , <b>2019</b> , 47, e12	20.1	33
436	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. <i>Blood</i> , <b>2019</b> , 133, 1313-1324	2.2	75
435	Clinical outcomes after whole-genome sequencing in patients with metastatic non-small-cell lung cancer. <i>Journal of Physical Education and Sports Management</i> , <b>2019</b> , 5,	2.8	2
434	A Hematogenous Route for Medulloblastoma Leptomeningeal Metastases. <i>Cell</i> , <b>2018</b> , 172, 1050-1062.e14	56.2	46
433	Molecular characterization of -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> , <b>2018</b> , 4,	2.8	9
432	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> , <b>2018</b> , 20, 203-214	5.1	42
431	Application of genomics to identify therapeutic targets in recurrent pediatric papillary thyroid carcinoma. <i>Journal of Physical Education and Sports Management</i> , <b>2018</b> , 4,	2.8	13
430	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> , <b>2018</b> , 4,	2.8	14
429	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , <b>2018</b> , 173, 400-416.e11	56.2	1072
428	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , <b>2018</b> , 173, 371-385.e18	56.2	854
427	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , <b>2018</b> , 173, 291-304.e6	56.2	888
426	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , <b>2018</b> , 173, 386-399.e12	56.2	133
425	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , <b>2018</b> , 173, 305-320.e10	56.2	166
424	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , <b>2018</b> , 173, 338-354.e15	56.2	560
423	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , <b>2018</b> , 173, 321-337.e10	56.2	1124
422	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , <b>2018</b> , 173, 355-370.e14	56.2	342

421	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , <b>2018</b> , 23, 282-296.e4	10.6	188
420	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , <b>2018</b> , 23, 227-238.e3	10.6	235
419	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , <b>2018</b> , 23, 194-212.e6	10.6	146
418	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , <b>2018</b> , 23, 297-312.e12	10.6	147
417	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , <b>2018</b> , 23, 313-326.e5	10.6	295
416	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , <b>2018</b> , 23, 181-193.e7	10.6	366
415	The Immune Landscape of Cancer. <i>Immunity</i> , <b>2018</b> , 48, 812-830.e14	32.3	1754
414	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 172-180.e3	10.6	66
413	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , <b>2018</b> , 23, 213-226.e3	10.6	56
412	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 239-254.e6	10.6	405
411	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , <b>2018</b> , 23, 255-269.e4	10.6	112
410	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , <b>2018</b> , 23, 270-281.e3	10.6	121
409	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , <b>2018</b> , 33, 244-258.e10	24.3	150
408	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , <b>2018</b> , 6, 271-281.e7	10.6	320
407	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , <b>2018</b> , 6, 282-300.e2	10.6	159
406	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> , <b>2018</b> , 33, 706-720.e9	24.3	275
405	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , <b>2018</b> , 33, 676-689.e3	24.3	377
404	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , <b>2018</b> , 33, 721-735.e8	24.3	228



403	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , <b>2018</b> , 33, 690-705.e9	24.3	277
402	Whole genome and whole transcriptome genomic profiling of a metastatic eccrine porocarcinoma. <i>Npj Precision Oncology</i> , <b>2018</b> , 2, 8	9.8	11
401	Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. <i>Developmental Cell</i> , <b>2018</b> , 44, 709-724.e6	10.2	25
400	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , <b>2018</b> , 34, 211-224.e6	24.3	327
399	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology</i> , <b>2018</b> , 19, 785-798	21.7	159
398	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , <b>2018</b> , 23, 3392-3406	10.6	200
397	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. <i>Nature Medicine</i> , <b>2018</b> , 24, 103-112	50.5	272
396	Molecular characterization of metastatic pancreatic neuroendocrine tumors (PNETs) using whole-genome and transcriptome sequencing. <i>Journal of Physical Education and Sports Management</i> , <b>2018</b> , 4,	2.8	20
395	High-resolution architecture and partner genes of rearrangements in lymphoma with DLBCL morphology. <i>Blood Advances</i> , <b>2018</b> , 2, 2755-2765	7.8	38
394	Temporal Dynamics of Genomic Alterations in a Germline-Mutated Pancreatic Cancer With Low Genomic Instability Burden but Exceptional Response to Fluorouracil, Oxaliplatin, Leucovorin, and Irinotecan. <i>JCO Precision Oncology</i> , <b>2018</b> , 2,	3.6	0
393	Comparative RNA-Sequencing Analysis Benefits a Pediatric Patient With Relapsed Cancer. <i>JCO Precision Oncology</i> , <b>2018</b> , 2,	3.6	6
392	Whole-genome and transcriptome profiling of a metastatic thyroid-like follicular renal cell carcinoma. <i>Journal of Physical Education and Sports Management</i> , <b>2018</b> , 4,	2.8	10
391	The Genome of the North American Brown Bear or Grizzly: <i>Ursus arctos</i> ssp. <i>horribilis</i> . <i>Genes</i> , <b>2018</b> , 9,	4.2	13
390	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , <b>2018</b> , 9, 4001	17.4	64
389	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. <i>Cell Systems</i> , <b>2018</b> , 7, 422-437.e7	10.6	85
388	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , <b>2018</b> , 8, 1548-1565	24.4	258
387	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , <b>2018</b> , 25, 1304-1317.e5	10.6	152
386	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , <b>2018</b> , 562, 373-379	50.4	140



385	ABT-888 restores sensitivity in temozolomide resistant glioma cells and xenografts. <i>PLoS ONE</i> , <b>2018</b> , 13, e0202860	3.7	18
384	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , <b>2017</b> , 543, 378-384	50.4	755
383	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , <b>2017</b> , 31, 181-193	24.3	350
382	Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , <b>2017</b> , 49, 780-788	36.3	80
381	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. <i>Nature Genetics</i> , <b>2017</b> , 49, 856-865	36.3	141
380	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , <b>2017</b> , 169, 1327-1341.e23	56.2	1125
379	Genomic profiling of pelvic genital type leiomyosarcoma in a woman with a germline :c.1100delC mutation and a concomitant diagnosis of metastatic invasive ductal breast carcinoma. <i>Journal of Physical Education and Sports Management</i> , <b>2017</b> , 3,	2.8	6
378	Pyruvate Kinase Inhibits Proliferation during Postnatal Cerebellar Neurogenesis and Suppresses Medulloblastoma Formation. <i>Cancer Research</i> , <b>2017</b> , 77, 3217-3230	10.1	32
377	Whole-genome analysis reveals unexpected dynamics of mutant subclone development in a patient with JAK2-V617F-positive chronic myeloid leukemia. <i>Experimental Hematology</i> , <b>2017</b> , 53, 48-58	3.1	13
376	Genetic profiling of and in diffuse large B-cell lymphoma determines cell-of-origin-specific clinical impact. <i>Blood</i> , <b>2017</b> , 129, 2760-2770	2.2	82
375	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , <b>2017</b> , 31, 411-423	24.3	210
374	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> , <b>2017</b> , 242, 206-220	9.4	22
373	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , <b>2017</b> , 18, 2780-2794	10.6	247
372	The cost and cost trajectory of whole-genome analysis guiding treatment of patients with advanced cancers. <i>Molecular Genetics &amp; Genomic Medicine</i> , <b>2017</b> , 5, 251-260	2.3	30
371	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , <b>2017</b> , 541, 169-175	50.4	965
370	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , <b>2017</b> , 171, 540-556.e25	50.2	961
369	Carcinoma ex pleomorphic adenoma: case report and options for systemic therapy. <i>Current Oncology</i> , <b>2017</b> , 24, e251-e254	2.8	8
368	MicroRNA Expression-Based Model Indicates Event-Free Survival in Pediatric Acute Myeloid Leukemia. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, 3964-3977	2.2	31

367	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. <i>Nature Genetics</i> , <b>2017</b> , 49, 1487-1494	36.3	160
366	Clonal expansion and epigenetic reprogramming following deletion or amplification of mutant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 10743-10748	11.5	78
365	Identification of GPC2 as an Oncoprotein and Candidate Immunotherapeutic Target in High-Risk Neuroblastoma. <i>Cancer Cell</i> , <b>2017</b> , 32, 295-309.e12	24.3	100
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