

Marco A Marra

List of Publications by Year in descending order

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Version: 2024-02-01

513
papers

222,497
citations

97

166
h-index

21

447
g-index

533
all docs

533
docs citations

533
times ranked

191014
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. | 2.1 | 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. | 1.2 | 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. | 4.5 | 5 |
| 4 | ICGC-ARGO precision medicine: familial matters in pancreatic cancer. <i>Lancet Oncology</i> , The, 2022, 23, 25-26. | 10.7 | 6 |
| 5 | A platform for oncogenomic reporting and interpretation. <i>Nature Communications</i> , 2022, 13, 756. | 12.8 | 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. | 3.7 | 0 |
| 7 | The Neoantigen Landscape of the Coding and Noncoding Cancer Genome Space. <i>Journal of Molecular Diagnostics</i> , 2022, , . | 2.8 | 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. | 16.8 | 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. | 3.0 | 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. | 2.3 | 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, . | 1.0 | 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. | 1.4 | 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. | 7.0 | 14 |
| 14 | Whole-slide laser microdissection for tumour enrichment. <i>Journal of Pathology</i> , 2021, 253, 225-233. | 4.5 | 4 |
| 15 | Delving into Early-onset Pancreatic Ductal Adenocarcinoma: How Does Age Fit In?. <i>Clinical Cancer Research</i> , 2021, 27, 246-254. | 7.0 | 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. | 7.0 | 50 |
| 17 | Subtype-Discordant Pancreatic Ductal Adenocarcinoma Tumors Show Intermediate Clinical and Molecular Characteristics. <i>Clinical Cancer Research</i> , 2021, 27, 150-157. | 7.0 | 24 |
| 18 | Matching methods in precision oncology: An introduction and illustrative example. <i>Molecular Genetics & Genomic Medicine</i> , 2021, 9, e1554. | 1.2 | 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. | 3.5 | 9 |
| 20 | Gradient of Developmental and Injury Response transcriptional states defines functional vulnerabilities underpinning glioblastoma heterogeneity. <i>Nature Cancer</i> , 2021, 2, 157-173. | 13.2 | 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. | 0.5 | 3 |
| 22 | Megabase-scale methylation phasing using nanopore long reads and NanoMethPhase. <i>Genome Biology</i> , 2021, 22, 68. | 8.8 | 36 |
| 23 | The transcriptional landscape of Shh medulloblastoma. <i>Nature Communications</i> , 2021, 12, 1749. | 12.8 | 47 |
| 24 | A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2474. | 12.8 | 49 |
| 25 | Human placental cytotrophoblast epigenome dynamics over gestation and alterations in placental disease. <i>Developmental Cell</i> , 2021, 56, 1238-1252.e5. | 7.0 | 29 |
| 26 | A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. <i>Frontiers in Genetics</i> , 2021, 12, 665888. | 2.3 | 2 |
| 27 | Clinical and cost outcomes following genomics-informed treatment for advanced cancers. <i>Cancer Medicine</i> , 2021, 10, 5131-5140. | 2.8 | 8 |
| 28 | Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021, 595, 585-590. | 27.8 | 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. | 2.8 | 9 |
| 30 | Proteotranscriptomic classification and characterization of pancreatic neuroendocrine neoplasms. <i>Cell Reports</i> , 2021, 37, 109817. | 6.4 | 14 |
| 31 | Rearrangement-mediated cis-regulatory alterations in advanced patient tumors reveal interactions with therapy. <i>Cell Reports</i> , 2021, 37, 110023. | 6.4 | 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. | 5.4 | 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. | 7.0 | 121 |
| 34 | Establishing a Framework for the Clinical Translation of Germline Findings in Precision Oncology. <i>JNCI Cancer Spectrum</i> , 2020, 4, pkaa045. | 2.9 | 6 |
| 35 | Glioma-derived IL-33 orchestrates an inflammatory brain tumor microenvironment that accelerates glioma progression. <i>Nature Communications</i> , 2020, 11, 4997. | 12.8 | 109 |
| 36 | Epigenomic programming in early fetal brain development. <i>Epigenomics</i> , 2020, 12, 1053-1070. | 2.1 | 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. | 21.4 | 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, . | 8.5 | 74 |
| 39 | TRIM25 promotes Capicua degradation independently of ERK in the absence of ATXN1L. <i>BMC Biology</i> , 2020, 18, 154. | 3.8 | 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. | 0.9 | 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. | 2.5 | 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. | 4.1 | 10 |
| 43 | Genetic and evolutionary patterns of treatment resistance in relapsed B-cell lymphoma. <i>Blood Advances</i> , 2020, 4, 2886-2898. | 5.2 | 59 |
| 44 | Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing. <i>Genetics in Medicine</i> , 2020, 22, 1892-1897. | 2.4 | 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. | 2.3 | 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. | 30.7 | 46 |
| 47 | Transcription phenotypes of pancreatic cancer are driven by genomic events during tumor evolution. <i>Nature Genetics</i> , 2020, 52, 231-240. | 21.4 | 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. | 1.2 | 5 |
| 49 | Patient selection for a developmental therapeutics program using whole genome and Transcriptome analysis. <i>Investigational New Drugs</i> , 2020, 38, 1601-1604. | 2.6 | 0 |
| 50 | Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93. | 27.8 | 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. | 13.2 | 103 |
| 52 | Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. <i>Blood</i> , 2020, 136, 572-584. | 1.4 | 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. | 1.4 | 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. | 5.9 | 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. | 1.2 | 4 |
| 57 | The Genome of the Steller Sea Lion (<i>Eumetopias jubatus</i>). <i>Genes</i> , 2019, 10, 486. | 2.4 | 4 |
| 58 | Integrative genomic analysis identifies key pathogenic mechanisms in primary mediastinal large B-cell lymphoma. <i>Blood</i> , 2019, 134, 802-813. | 1.4 | 96 |
| 59 | High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. <i>Genome Research</i> , 2019, 29, 1211-1222. | 5.5 | 52 |
| 60 | Therapeutic Implication of Genomic Landscape of Adult Metastatic Sarcoma. <i>JCO Precision Oncology</i> , 2019, 3, 1-25. | 3.0 | 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. | 5.9 | 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. | 2.5 | 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. | 6.4 | 74 |
| 64 | Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22. | 28.9 | 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. | 7.1 | 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. | 9.4 | 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. | 2.3 | 35 |
| 68 | Integrative genomic analysis of matched primary and metastatic pediatric osteosarcoma. <i>Journal of Pathology</i> , 2019, 249, 319-331. | 4.5 | 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. | 1.2 | 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. | 7.0 | 121 |
| 71 | Capicua regulates neural stem cell proliferation and lineage specification through control of Ets factors. <i>Nature Communications</i> , 2019, 10, 2000. | 12.8 | 34 |
| 72 | Childhood cerebellar tumours mirror conserved fetal transcriptional programs. <i>Nature</i> , 2019, 572, 67-73. | 27.8 | 293 |

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|----|---|------|-----------|
| 73 | Application of a Neural Network Whole Transcriptome-Based Pan-Cancer Method for Diagnosis of Primary and Metastatic Cancers. JAMA Network Open, 2019, 2, e192597. | 5.9 | 67 |
| 74 | Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. Cancer Research, 2019, 79, 2111-2123. | 0.9 | 28 |
| 75 | Base excision repair deficiency signatures implicate germline and somatic <i>MUTYH</i> aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. Journal of Physical Education and Sports Management, 2019, 5, a003681. | 1.2 | 33 |
| 76 | Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2019, 37, 190-201. | 1.6 | 257 |
| 77 | A high-throughput protocol for isolating cell-free circulating tumor DNA from peripheral blood. BioTechniques, 2019, 66, 85-92. | 1.8 | 13 |
| 78 | Recurrent noncoding U1 snRNA mutations drive cryptic splicing in SHH medulloblastoma. Nature, 2019, 574, 707-711. | 27.8 | 129 |
| 79 | Sources of erroneous sequences and artifact chimeric reads in next generation sequencing of genomic DNA from formalin-fixed paraffin-embedded samples. Nucleic Acids Research, 2019, 47, e12-e12. | 14.5 | 50 |
| 80 | Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. Blood, 2019, 133, 1313-1324. | 1.4 | 172 |
| 81 | Clinical outcomes after whole-genome sequencing in patients with metastatic non-small-cell lung cancer. Journal of Physical Education and Sports Management, 2019, 5, a002659. | 1.2 | 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. Cell, 2018, 172, 1050-1062.e14. | 28.9 | 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. Journal of Physical Education and Sports Management, 2018, 4, a002535. | 1.2 | 16 |
| 86 | Assessment of Capture and Amplicon-Based Approaches for the Development of a Targeted Next-Generation Sequencing Pipeline to Personalize Lymphoma Management. Journal of Molecular Diagnostics, 2018, 20, 203-214. | 2.8 | 58 |
| 87 | Application of genomics to identify therapeutic targets in recurrent pediatric papillary thyroid carcinoma. Journal of Physical Education and Sports Management, 2018, 4, a002568. | 1.2 | 14 |
| 88 | Personalized oncogenomic analysis of metastatic adenoid cystic carcinoma: using whole-genome sequencing to inform clinical decision-making. Journal of Physical Education and Sports Management, 2018, 4, a002626. | 1.2 | 18 |
| 89 | An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11. | 28.9 | 2,277 |
| 90 | Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18. | 28.9 | 1,670 |

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|-----|---|------|-----------|
| 91 | Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6. | 28.9 | 1,718 |
| 92 | A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12. | 28.9 | 228 |
| 93 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10. | 28.9 | 272 |
| 94 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15. | 28.9 | 1,417 |
| 95 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10. | 28.9 | 2,111 |
| 96 | Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14. | 28.9 | 620 |
| 97 | Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4. | 6.4 | 333 |
| 98 | Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3. | 6.4 | 407 |
| 99 | Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6. | 6.4 | 245 |
| 100 | Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12. | 6.4 | 205 |
| 101 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5. | 6.4 | 523 |
| 102 | Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7. | 6.4 | 683 |
| 103 | The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14. | 14.3 | 3,706 |
| 104 | Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3. | 6.4 | 119 |
| 105 | Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3. | 6.4 | 83 |
| 106 | Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6. | 6.4 | 801 |
| 107 | Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4. | 6.4 | 204 |
| 108 | Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3. | 6.4 | 177 |

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|-----|---|------|-----------|
| 109 | The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10. | 16.8 | 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. | 6.2 | 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. | 6.2 | 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. | 16.8 | 400 |
| 113 | Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3. | 16.8 | 750 |
| 114 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8. | 16.8 | 396 |
| 115 | A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9. | 16.8 | 478 |
| 116 | Whole genome and whole transcriptome genomic profiling of a metastatic eccrine porocarcinoma. <i>Npj Precision Oncology</i> , 2018, 2, 8. | 5.4 | 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. | 7.0 | 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. | 30.7 | 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. | 1.2 | 30 |
| 120 | High-resolution architecture and partner genes of MYC rearrangements in lymphoma with DLBCL morphology. <i>Blood Advances</i> , 2018, 2, 2755-2765. | 5.2 | 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. | 3.0 | 1 |
| 122 | Comparative RNA-Sequencing Analysis Benefits a Pediatric Patient With Relapsed Cancer. <i>JCO Precision Oncology</i> , 2018, 2, 1-16. | 3.0 | 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. | 1.2 | 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. | 2.4 | 34 |
| 125 | Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , 2018, 9, 4001. | 12.8 | 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. | 6.2 | 134 |

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|-----|---|------|-----------|
| 127 | Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565. | 9.4 | 422 |
| 128 | Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5. | 6.4 | 329 |
| 129 | The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 2018, 562, 373-379. | 27.8 | 236 |
| 130 | ABT-888 restores sensitivity in temozolomide resistant glioma cells and xenografts. PLoS ONE, 2018, 13, e0202860. | 2.5 | 28 |
| 131 | Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6. | 16.8 | 623 |
| 132 | Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798. | 10.7 | 268 |
| 133 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406. | 6.4 | 324 |
| 134 | Integrated genomic and molecular characterization of cervical cancer. Nature, 2017, 543, 378-384. | 27.8 | 1,158 |
| 135 | Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193. | 16.8 | 532 |
| 136 | Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788. | 21.4 | 112 |
| 137 | Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. Nature Genetics, 2017, 49, 856-865. | 21.4 | 220 |
| 138 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23. | 28.9 | 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. Journal of Physical Education and Sports Management, 2017, 3, a001628. | 1.2 | 8 |
| 140 | Pyruvate Kinase Inhibits Proliferation during Postnatal Cerebellar Neurogenesis and Suppresses Medulloblastoma Formation. Cancer Research, 2017, 77, 3217-3230. | 0.9 | 45 |
| 141 | Whole-genome analysis reveals unexpected dynamics of mutant subclone development in a patient with JAK2-V617F-positive chronic myeloid leukemia. Experimental Hematology, 2017, 53, 48-58. | 0.4 | 15 |
| 142 | Genetic profiling of MYC and BCL2 in diffuse large B-cell lymphoma determines cell-of-origin-specific clinical impact. Blood, 2017, 129, 2760-2770. | 1.4 | 112 |
| 143 | Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423. | 16.8 | 309 |
| 144 | Comparative transcriptome analysis of isogenic cell line models and primary cancers links capicua (CIC) loss to activation of the MAPK signalling cascade. Journal of Pathology, 2017, 242, 206-220. | 4.5 | 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. | 6.4 | 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. | 1.2 | 40 |
| 147 | Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , 2017, 541, 169-175. | 27.8 | 1,448 |
| 148 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25. | 28.9 | 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. | 21.4 | 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. | 7.1 | 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. | 16.8 | 148 |
| 152 | Detection and genomic characterization of a mammary-like adenocarcinoma. <i>Journal of Physical Education and Sports Management</i> , 2017, 3, a002170. | 1.2 | 13 |
| 153 | The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317. | 27.8 | 787 |
| 154 | Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15. | 16.8 | 642 |
| 155 | Characterization of the human thyroid epigenome. <i>Journal of Endocrinology</i> , 2017, 235, 153-165. | 2.6 | 8 |
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