

# Marc Ladanyi

## List of Publications by Year in descending order

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253  
papers

36,749  
citations

4146

87  
h-index

3650

180  
g-index

259  
all docs

259  
docs citations

259  
times ranked

38309  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tumor mutational load predicts survival after immunotherapy across multiple cancer types. <i>Nature Genetics</i> , 2019, 51, 202-206.	21.4	2,702
2	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. <i>Nature Medicine</i> , 2017, 23, 703-713.	30.7	2,473
3	Classification and diagnostic prediction of cancers using gene expression profiling and artificial neural networks. <i>Nature Medicine</i> , 2001, 7, 673-679.	30.7	2,352
4	Efficacy of Larotrectinib in <i>TRK</i> -Positive Cancers in Adults and Children. <i>New England Journal of Medicine</i> , 2018, 378, 731-739.	27.0	2,036
5	Memorial Sloan Kettering-Integrated Mutation Profiling of Actionable Cancer Targets (MSK-IMPACT). <i>Journal of Molecular Diagnostics</i> , 2015, 17, 251-264.	2.8	1,566
6	OncoKB: A Precision Oncology Knowledge Base. <i>JCO Precision Oncology</i> , 2017, 2017, 1-16.	3.0	1,266
7	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.4	801
8	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. <i>Cancer Cell</i> , 2018, 34, 427-438.e6.	16.8	633
9	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. <i>Cancer Cell</i> , 2018, 33, 125-136.e3.	16.8	589
10	Therapy-Related Clonal Hematopoiesis in Patients with Non-hematologic Cancers Is Common and Associated with Adverse Clinical Outcomes. <i>Cell Stem Cell</i> , 2017, 21, 374-382.e4.	11.1	578
11	The <i>der(17)t(X;17)(p11;q25)</i> of human alveolar soft part sarcoma fuses the TFE3 transcription factor gene to ASPL, a novel gene at 17q25. <i>Oncogene</i> , 2001, 20, 48-57.	5.9	562
12	Response to MET Inhibitors in Patients with Stage IV Lung Adenocarcinomas Harboring <i>MET</i> Mutations Causing Exon 14 Skipping. <i>Cancer Discovery</i> , 2015, 5, 842-849.	9.4	514
13	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. <i>Cancer Discovery</i> , 2017, 7, 596-609.	9.4	490
14	High-intensity sequencing reveals the sources of plasma circulating cell-free DNA variants. <i>Nature Medicine</i> , 2019, 25, 1928-1937.	30.7	485
15	Optimization of Dosing for EGFR-Mutant Non-Small Cell Lung Cancer with Evolutionary Cancer Modeling. <i>Science Translational Medicine</i> , 2011, 3, 90ra59.	12.4	457
16	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018, 8, 1548-1565.	9.4	422
17	Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. <i>Journal of Clinical Oncology</i> , 2019, 37, 286-295.	1.6	397
18	Impact of SYT-SSX fusion type on the clinical behavior of synovial sarcoma: a multi-institutional retrospective study of 243 patients. <i>Cancer Research</i> , 2002, 62, 135-40.	0.9	390

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19	NTRK fusion detection across multiple assays and 33,997 cases: diagnostic implications and pitfalls. <i>Modern Pathology</i> , 2020, 33, 38-46.	5.5	373
20	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. <i>Nature Genetics</i> , 2020, 52, 1219-1226.	21.4	367
21	Mutation Detection in Patients With Advanced Cancer by Universal Sequencing of Cancer-Related Genes in Tumor and Normal DNA vs Guideline-Based Germline Testing. <i>JAMA - Journal of the American Medical Association</i> , 2017, 318, 825.	7.4	366
22	Cabozantinib in patients with advanced RET -rearranged non-small-cell lung cancer: an open-label, single-centre, phase 2, single-arm trial. <i>Lancet Oncology</i> , The, 2016, 17, 1653-1660.	10.7	365
23	Next-Generation Sequencing of Pulmonary Large Cell Neuroendocrine Carcinoma Reveals Small Cell Carcinoma-like and Non-small Cell Carcinoma-like Subsets. <i>Clinical Cancer Research</i> , 2016, 22, 3618-3629.	7.0	342
24	Effects of Co-occurring Genomic Alterations on Outcomes in Patients with KRAS-Mutant Non-small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 334-340.	7.0	323
25	Lung adenocarcinoma: guiding EGFR-targeted therapy and beyond. <i>Modern Pathology</i> , 2008, 21, S16-S22.	5.5	313
26	Tumour lineage shapes BRCA-mediated phenotypes. <i>Nature</i> , 2019, 571, 576-579.	27.8	295
27	High Yield of RNA Sequencing for Targetable Kinase Fusions in Lung Adenocarcinomas with No Mitogenic Driver Alteration Detected by DNA Sequencing and Low Tumor Mutation Burden. <i>Clinical Cancer Research</i> , 2019, 25, 4712-4722.	7.0	292
28	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. <i>JCO Precision Oncology</i> , 2017, 2017, 1-16.	3.0	286
29	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
30	TFE3 Fusions Activate MET Signaling by Transcriptional Up-regulation, Defining Another Class of Tumors as Candidates for Therapeutic MET Inhibition. <i>Cancer Research</i> , 2007, 67, 919-929.	0.9	275
31	Accelerating Discovery of Functional Mutant Alleles in Cancer. <i>Cancer Discovery</i> , 2018, 8, 174-183.	9.4	275
32	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. <i>Cancer Discovery</i> , 2018, 8, 49-58.	9.4	275
33	Germline Variants in Targeted Tumor Sequencing Using Matched Normal DNA. <i>JAMA Oncology</i> , 2016, 2, 104.	7.1	270
34	Tumor Mutation Burden and Efficacy of EGFR-Tyrosine Kinase Inhibitors in Patients with EGFR-Mutant Lung Cancers. <i>Clinical Cancer Research</i> , 2019, 25, 1063-1069.	7.0	257
35	Rationale for co-targeting IGF-1R and ALK in ALK fusion-positive lung cancer. <i>Nature Medicine</i> , 2014, 20, 1027-1034.	30.7	243
36	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021, 12, 498.	12.8	237

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37	Concurrent RB1 and TP53 Alterations Define a Subset of EGFR-Mutant Lung Cancers at risk for Histologic Transformation and Inferior Clinical Outcomes. <i>Journal of Thoracic Oncology</i> , 2019, 14, 1784-1793.	1.1	232
38	Tumor Analyses Reveal Squamous Transformation and Off-Target Alterations As Early Resistance Mechanisms to First-line Osimertinib in EGFR-Mutant Lung Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 2654-2663.	7.0	230
39	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. <i>Cell</i> , 2022, 185, 563-575.e11.	28.9	223
40	Acquired Resistance of EGFR-Mutant Lung Cancer to a T790M-Specific EGFR Inhibitor. <i>JAMA Oncology</i> , 2015, 1, 982.	7.1	214
41	Pretreatment neutrophil-to-lymphocyte ratio and mutational burden as biomarkers of tumor response to immune checkpoint inhibitors. <i>Nature Communications</i> , 2021, 12, 729.	12.8	212
42	Fusions of the SYT and SSX genes in synovial sarcoma. <i>Oncogene</i> , 2001, 20, 5755-5762.	5.9	204
43	Oncogene Mutation Profiling of Pediatric Solid Tumors Reveals Significant Subsets of Embryonal Rhabdomyosarcoma and Neuroblastoma with Mutated Genes in Growth Signaling Pathways. <i>Clinical Cancer Research</i> , 2012, 18, 748-757.	7.0	203
44	Concurrent Alterations in EGFR-Mutant Lung Cancers Associated with Resistance to EGFR Kinase Inhibitors and Characterization of MTOR as a Mediator of Resistance. <i>Clinical Cancer Research</i> , 2018, 24, 3108-3118.	7.0	200
45	Merlin/NF2 Loss-Driven Tumorigenesis Linked to CRL4DCAF1-Mediated Inhibition of the Hippo Pathway Kinases Lats1 and 2 in the Nucleus. <i>Cancer Cell</i> , 2014, 26, 48-60.	16.8	198
46	Skeletal and extraskeletal myxoid chondrosarcoma. <i>Cancer</i> , 1998, 83, 1504-1521.	4.1	194
47	Alternative transcription initiation leads to expression of a novel ALK isoform in cancer. <i>Nature</i> , 2015, 526, 453-457.	27.8	191
48	Monophasic and biphasic synovial sarcomas abundantly express cancer/testis antigen ny-eso-1 but not mage-a1 or ct7. <i>International Journal of Cancer</i> , 2001, 94, 252-256.	5.1	182
49	Polymorphous low-grade neuroepithelial tumor of the young (PLNTY): an epileptogenic neoplasm with oligodendroglioma-like components, aberrant CD34 expression, and genetic alterations involving the MAP kinase pathway. <i>Acta Neuropathologica</i> , 2017, 133, 417-429.	7.7	172
50	SMARCA4-Deficient Thoracic Sarcomatoid Tumors Represent Primarily Smoking-Related Undifferentiated Carcinomas Rather Than Primary Thoracic Sarcomas. <i>Journal of Thoracic Oncology</i> , 2020, 15, 231-247.	1.1	172
51	Identification of KIF5B-RET and GOPC-ROS1 Fusions in Lung Adenocarcinomas through a Comprehensive mRNA-Based Screen for Tyrosine Kinase Fusions. <i>Clinical Cancer Research</i> , 2012, 18, 6599-6608.	7.0	169
52	The EWS-WT1 translocation product induces PDGFA in desmoplastic small round-cell tumour. <i>Nature Genetics</i> , 1997, 17, 309-313.	21.4	166
53	Epidermal growth factor receptor exon 20 insertions in advanced lung adenocarcinomas: Clinical outcomes and response to erlotinib. <i>Cancer</i> , 2015, 121, 3212-3220.	4.1	160
54	A recurrent neomorphic mutation in MYOD1 defines a clinically aggressive subset of embryonal rhabdomyosarcoma associated with PI3K-AKT pathway mutations. <i>Nature Genetics</i> , 2014, 46, 595-600.	21.4	152

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55	Resistance to TRK inhibition mediated by convergent MAPK pathway activation. <i>Nature Medicine</i> , 2019, 25, 1422-1427.	30.7	144
56	A Novel Crizotinib-Resistant Solvent-Front Mutation Responsive to Cabozantinib Therapy in a Patient with <i>ROS1</i> -Rearranged Lung Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 2351-2358.	7.0	141
57	Prevalence of Clonal Hematopoiesis Mutations in Tumor-Only Clinical Genomic Profiling of Solid Tumors. <i>JAMA Oncology</i> , 2018, 4, 1589.	7.1	139
58	The association between tumor mutational burden and prognosis is dependent on treatment context. <i>Nature Genetics</i> , 2021, 53, 11-15.	21.4	139
59	Prognostic impact of P53 status in Ewing sarcoma. <i>Cancer</i> , 2000, 89, 783-792.	4.1	138
60	Clinical heterogeneity of Xp11 translocation renal cell carcinoma: impact of fusion subtype, age, and stage. <i>Modern Pathology</i> , 2014, 27, 875-886.	5.5	136
61	Precision medicine at Memorial Sloan Kettering Cancer Center: clinical next-generation sequencing enabling next-generation targeted therapy trials. <i>Drug Discovery Today</i> , 2015, 20, 1422-1428.	6.4	136
62	Synovial Sarcoma: Recent Discoveries as a Roadmap to New Avenues for Therapy. <i>Cancer Discovery</i> , 2015, 5, 124-134.	9.4	135
63	The Genomic Landscape of <i>SMARCA4</i> Alterations and Associations with Outcomes in Patients with Lung Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 5701-5708.	7.0	133
64	Prevalence of Germline Mutations in Cancer Susceptibility Genes in Patients With Advanced Renal Cell Carcinoma. <i>JAMA Oncology</i> , 2018, 4, 1228.	7.1	132
65	ZC3H7B-BCOR high-grade endometrial stromal sarcomas: a report of 17 cases of a newly defined entity. <i>Modern Pathology</i> , 2018, 31, 674-684.	5.5	130
66	Next-Generation Sequencing of Stage IV Squamous Cell Lung Cancers Reveals an Association of PI3K Aberrations and Evidence of Clonal Heterogeneity in Patients with Brain Metastases. <i>Cancer Discovery</i> , 2015, 5, 610-621.	9.4	129
67	MYOD1-mutant spindle cell and sclerosing rhabdomyosarcoma: an aggressive subtype irrespective of age. A reappraisal for molecular classification and risk stratification. <i>Modern Pathology</i> , 2019, 32, 27-36.	5.5	126
68	p53 and MDM2 alterations in osteosarcomas. , 1997, 79, 1541-1547.		125
69	<i>MAP2K1</i> ( <i>MEK1</i> ) Mutations Define a Distinct Subset of Lung Adenocarcinoma Associated with Smoking. <i>Clinical Cancer Research</i> , 2015, 21, 1935-1943.	7.0	124
70	Activating mutations in CSF1R and additional receptor tyrosine kinases in histiocytic neoplasms. <i>Nature Medicine</i> , 2019, 25, 1839-1842.	30.7	122
71	The epigenomics of sarcoma. <i>Nature Reviews Cancer</i> , 2020, 20, 608-623.	28.4	121
72	BCOR is a robust diagnostic immunohistochemical marker of genetically diverse high-grade endometrial stromal sarcoma, including tumors exhibiting variant morphology. <i>Modern Pathology</i> , 2017, 30, 1251-1261.	5.5	112

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73	Diagnosis of known sarcoma fusions and novel fusion partners by targeted RNA sequencing with identification of a recurrent ACTB-FOSB fusion in pseudomyogenic hemangioendothelioma. <i>Modern Pathology</i> , 2019, 32, 609-620.	5.5	112
74	Colorectal Carcinomas Containing Hypermethylated MLH1 Promoter and Wild-Type BRAF/KRAS Are Enriched for Targetable Kinase Fusions. <i>Cancer Research</i> , 2019, 79, 1047-1053.	0.9	112
75	CDK4 gene amplification in osteosarcoma: Reciprocal relationship withINK4A gene alterations and mapping of 12q13 amplicons. , 1999, 80, 199-204.		111
76	Comprehensive detection of germline variants by MSK-IMPACT, a clinical diagnostic platform for solid tumor molecular oncology and concurrent cancer predisposition testing. <i>BMC Medical Genomics</i> , 2017, 10, 33.	1.5	111
77	Improved prediction of immune checkpoint blockade efficacy across multiple cancer types. <i>Nature Biotechnology</i> , 2022, 40, 499-506.	17.5	110
78	Leukemic differentiation of a mediastinal germ cell tumor. <i>Genes Chromosomes and Cancer</i> , 1989, 1, 83-87.	2.8	109
79	The Precrystalline Cytoplasmic Granules of Alveolar Soft Part Sarcoma Contain Monocarboxylate Transporter 1 and CD147. <i>American Journal of Pathology</i> , 2002, 160, 1215-1221.	3.8	109
80	Genomic Correlates of Disease Progression and Treatment Response in Prospectively Characterized Gliomas. <i>Clinical Cancer Research</i> , 2019, 25, 5537-5547.	7.0	107
81	SFK/FAK Signaling Attenuates Osimertinib Efficacy in Both Drug-Sensitive and Drug-Resistant Models of EGFR-Mutant Lung Cancer. <i>Cancer Research</i> , 2017, 77, 2990-3000.	0.9	106
82	Precision medicine in non-small cell lung cancer: Current applications and future directions. <i>Seminars in Cancer Biology</i> , 2022, 84, 184-198.	9.6	106
83	Massively parallel sequencing of phyllodes tumours of the breast reveals actionable mutations, and <i>TERT</i> promoter hotspot mutations and <i>TERT</i> gene amplification as likely drivers of progression. <i>Journal of Pathology</i> , 2016, 238, 508-518.	4.5	102
84	Clinical Utility of Prospective Molecular Characterization in Advanced Endometrial Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 5939-5947.	7.0	100
85	The SS18-SSX Oncoprotein Hijacks KDM2B-PRC1.1 to Drive Synovial Sarcoma. <i>Cancer Cell</i> , 2018, 33, 527-541.e8.	16.8	99
86	Prognostic impact of INK4A deletion in Ewing sarcoma. <i>Cancer</i> , 2000, 89, 793-799.	4.1	98
87	Next-Generation Assessment of Human Epidermal Growth Factor Receptor 2 (ERBB2) Amplification Status. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 244-254.	2.8	96
88	A Prospective Study of Circulating Tumor DNA to Guide Matched Targeted Therapy in Lung Cancers. <i>Journal of the National Cancer Institute</i> , 2019, 111, 575-583.	6.3	96
89	Effect of Osimertinib and Bevacizumab on Progression-Free Survival for Patients With Metastatic EGFR-Mutant Lung Cancers. <i>JAMA Oncology</i> , 2020, 6, 1048.	7.1	96
90	MDM2 andCDK4 gene amplification in Ewing's sarcoma. <i>Journal of Pathology</i> , 1995, 175, 211-217.	4.5	95

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91	<i>EGFR</i> Kinase Domain Duplication ( <i>EGFR</i> -KDD) Is a Novel Oncogenic Driver in Lung Cancer That Is Clinically Responsive to Afatinib. <i>Cancer Discovery</i> , 2015, 5, 1155-1163.	9.4	94
92	Activation of KRAS Mediates Resistance to Targeted Therapy in MET Exon 14 mutant Non-small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 1248-1260.	7.0	92
93	Bronchiolar Adenoma. <i>American Journal of Surgical Pathology</i> , 2018, 42, 1010-1026.	3.7	91
94	Overcoming MET-Dependent Resistance to Selective RET Inhibition in Patients with RET Fusion Positive Lung Cancer by Combining Selpercatinib with Crizotinib. <i>Clinical Cancer Research</i> , 2021, 27, 34-42.	7.0	87
95	Therapeutic Implications of Germline Testing in Patients With Advanced Cancers. <i>Journal of Clinical Oncology</i> , 2021, 39, 2698-2709.	1.6	83
96	DNA methylation-based classification of sinonasal undifferentiated carcinoma. <i>Modern Pathology</i> , 2019, 32, 1447-1459.	5.5	82
97	Clonal hematopoiesis is associated with risk of severe Covid-19. <i>Nature Communications</i> , 2021, 12, 5975.	12.8	81
98	New Strategies in Pleural Mesothelioma: BAP1 and NF2 as Novel Targets for Therapeutic Development and Risk Assessment. <i>Clinical Cancer Research</i> , 2012, 18, 4485-4490.	7.0	77
99	Clinical Genomic Sequencing of Pediatric and Adult Osteosarcoma Reveals Distinct Molecular Subsets with Potentially Targetable Alterations. <i>Clinical Cancer Research</i> , 2019, 25, 6346-6356.	7.0	75
100	Prospective pan-cancer germline testing using MSK-IMPACT informs clinical translation in 751 patients with pediatric solid tumors. <i>Nature Cancer</i> , 2021, 2, 357-365.	13.2	74
101	Clinical and Molecular Predictors of Response to Immune Checkpoint Inhibitors in Patients with Advanced Esophagogastric Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 6160-6169.	7.0	73
102	Acquired BRAF Rearrangements Induce Secondary Resistance to EGFR therapy in EGFR-Mutated Lung Cancers. <i>Journal of Thoracic Oncology</i> , 2019, 14, 802-815.	1.1	71
103	Implications of P16/CDKN2A deletion in pleural mesotheliomas. <i>Lung Cancer</i> , 2005, 49, S95-S98.	2.0	69
104	Comprehensive Next-Generation Sequencing Unambiguously Distinguishes Separate Primary Lung Carcinomas From Intrapulmonary Metastases: Comparison with Standard Histopathologic Approach. <i>Clinical Cancer Research</i> , 2019, 25, 7113-7125.	7.0	69
105	Benign metastasizing giant cell tumors of bone. A DNA flow cytometric study. <i>Cancer</i> , 1989, 64, 1521-1526.	4.1	68
106	PDGF Receptor Alpha Is an Alternative Mediator of Rapamycin-Induced Akt Activation: Implications for Combination Targeted Therapy of Synovial Sarcoma. <i>Cancer Research</i> , 2012, 72, 4515-4525.	0.9	68
107	Enhanced specificity of clinical high-sensitivity tumor mutation profiling in cell-free DNA via paired normal sequencing using MSK-ACCESS. <i>Nature Communications</i> , 2021, 12, 3770.	12.8	68
108	Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. <i>JAMA Oncology</i> , 2020, 6, 84.	7.1	66

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109	V-domain Ig-containing suppressor of T-cell activation (VISTA), a potentially targetable immune checkpoint molecule, is highly expressed in epithelioid malignant pleural mesothelioma. <i>Modern Pathology</i> , 2020, 33, 303-311.	5.5	65
110	Treatment Outcomes and Clinical Characteristics of Patients with KRAS-G12Câ€“Mutant Nonâ€“Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 2209-2215.	7.0	65
111	Clinical sequencing of soft tissue and bone sarcomas delineates diverse genomic landscapes and potential therapeutic targets. <i>Nature Communications</i> , 2022, 13, .	12.8	63
112	Expanding the Molecular Characterization of Thoracic Inflammatory Myofibroblastic Tumors beyond ALK Gene Rearrangements. <i>Journal of Thoracic Oncology</i> , 2019, 14, 825-834.	1.1	62
113	Antitumor Activity of RXDX-105 in Multiple Cancer Types with <i>RET</i> Rearrangements or Mutations. <i>Clinical Cancer Research</i> , 2017, 23, 2981-2990.	7.0	61
114	Undifferentiated Uterine Sarcomas Represent Under-Recognized High-grade Endometrial Stromal Sarcomas. <i>American Journal of Surgical Pathology</i> , 2019, 43, 662-669.	3.7	61
115	Genomic Profiling Identifies Association of <i>IDH1/IDH2</i> Mutation with Longer Relapse-Free and Metastasis-Free Survival in High-Grade Chondrosarcoma. <i>Clinical Cancer Research</i> , 2020, 26, 419-427.	7.0	60
116	Zenocutuzumab, a HER2xHER3 Bispecific Antibody, Is Effective Therapy for Tumors Driven by <i>NRG1</i> Gene Rearrangements. <i>Cancer Discovery</i> , 2022, 12, 1233-1247.	9.4	60
117	Combining integrated genomics and functional genomics to dissect the biology of a cancer-associated, aberrant transcription factor, the <i>ASPSCR1</i> - <i>TFE3</i> fusion oncoprotein. <i>Journal of Pathology</i> , 2013, 229, 743-754.	4.5	58
118	Genomic aberrations frequently alter chromatin regulatory genes in chordoma. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 591-600.	2.8	58
119	Stage IV lung carcinoids: spectrum and evolution of proliferation rate, focusing on variants with elevated proliferation indices. <i>Modern Pathology</i> , 2019, 32, 1106-1122.	5.5	58
120	Retained mismatch repair protein expression occurs in approximately 6% of microsatellite instability-high cancers and is associated with missense mutations in mismatch repair genes. <i>Modern Pathology</i> , 2020, 33, 871-879.	5.5	58
121	<i>RASA1</i> and <i>NF1</i> are Preferentially Co-Mutated and Define A Distinct Genetic Subset of Smoking-Associated Nonâ€“Small Cell Lung Carcinomas Sensitive to MEK Inhibition. <i>Clinical Cancer Research</i> , 2018, 24, 1436-1447.	7.0	56
122	The second European interdisciplinary Ewing sarcoma research summit - A joint effort to deconstructing the multiple layers of a complex disease. <i>Oncotarget</i> , 2016, 7, 8613-8624.	1.8	55
123	JAK2 inhibition sensitizes resistant EGFR-mutant lung adenocarcinoma to tyrosine kinase inhibitors. <i>Science Signaling</i> , 2016, 9, ra33.	3.6	54
124	MAX inactivation is an early event in GIST development that regulates p16 and cell proliferation. <i>Nature Communications</i> , 2017, 8, 14674.	12.8	53
125	Novel PLAG1 Gene Rearrangement Distinguishes a Subset of Uterine Myxoid Leiomyosarcoma From Other Uterine Myxoid Mesenchymal Tumors. <i>American Journal of Surgical Pathology</i> , 2019, 43, 382-388.	3.7	53
126	Clinical genomic profiling in the management of patients with soft tissue and bone sarcoma. <i>Nature Communications</i> , 2022, 13, .	12.8	51



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127	Immunohistochemical, molecular, and cytogenetic analysis of a consecutive series of 20 peripheral t-cell lymphomas and lymphomas of uncertain lineage, including 12 Ki-I positive lymphomas. <i>Genes Chromosomes and Cancer</i> , 1990, 2, 27-35.	2.8	50
128	The molecular pathology of cancer: from pan-genomics to post-genomics. <i>Journal of Pathology</i> , 2018, 244, 509-511.	4.5	50
129	Pulmonary large cell neuroendocrine carcinoma with adenocarcinoma-like features: napsin A expression and genomic alterations. <i>Modern Pathology</i> , 2018, 31, 111-121.	5.5	50
130	Integrating Genomics Into Clinical Pediatric Oncology Using the Molecular Tumor Board at the Memorial Sloan Kettering Cancer Center. <i>Pediatric Blood and Cancer</i> , 2016, 63, 1368-1374.	1.5	49
131	JAK2/PD-L1/PD-L2 (9p24.1) amplifications in renal cell carcinomas with sarcomatoid transformation: implications for clinical management. <i>Modern Pathology</i> , 2019, 32, 1344-1358.	5.5	49
132	Clinicopathologic and Genomic Analysis of TP53-Mutated Endometrial Carcinomas. <i>Clinical Cancer Research</i> , 2021, 27, 2613-2623.	7.0	49
133	The evolution of RET inhibitor resistance in RET-driven lung and thyroid cancers. <i>Nature Communications</i> , 2022, 13, 1450.	12.8	47
134	Identification of Targetable Kinase Alterations in Patients with Colorectal Carcinoma That are Preferentially Associated with Wild-Type RAS/RAF. <i>Molecular Cancer Research</i> , 2016, 14, 296-301.	3.4	46
135	Comprehensive Molecular and Clinicopathologic Analysis of 200 Pulmonary Invasive Mucinous Adenocarcinomas Identifies Distinct Characteristics of Molecular Subtypes. <i>Clinical Cancer Research</i> , 2021, 27, 4066-4076.	7.0	45
136	Consistent copy number changes and recurrent PRKAR1A mutations distinguish melanotic schwannomas from melanomas: SNP array and next generation sequencing analysis. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 463-471.	2.8	44
137	YES1 amplification is a mechanism of acquired resistance to EGFR inhibitors identified by transposon mutagenesis and clinical genomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6030-E6038.	7.1	44
138	The context-specific role of germline pathogenicity in tumorigenesis. <i>Nature Genetics</i> , 2021, 53, 1577-1585.	21.4	44
139	Rare but Recurrent ROS1 Fusions Resulting From Chromosome 6q22 Microdeletions are Targetable Oncogenes in Glioma. <i>Clinical Cancer Research</i> , 2018, 24, 6471-6482.	7.0	42
140	Response to Standard Therapies and Comprehensive Genomic Analysis for Patients with Lung Adenocarcinoma with EGFR Exon 20 Insertions. <i>Clinical Cancer Research</i> , 2021, 27, 2920-2927.	7.0	42
141	A Performance Comparison of Commonly Used Assays to Detect RET Fusions. <i>Clinical Cancer Research</i> , 2021, 27, 1316-1328.	7.0	39
142	Current state of pediatric sarcoma biology and opportunities for future discovery: A report from the sarcoma translational research workshop. <i>Cancer Genetics</i> , 2016, 209, 182-194.	0.4	38
143	DNA Methylation-Based Classifier for Accurate Molecular Diagnosis of Bone Sarcomas. <i>JCO Precision Oncology</i> , 2017, 2017, 1-11.	3.0	37
144	Clonal cytogenetic abnormalities in Hodgkin's disease. <i>Genes Chromosomes and Cancer</i> , 1991, 3, 294-299.	2.8	36

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