

# Rameen Beroukhim

## List of Publications by Year in descending order

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Version: 2024-02-01

139  
papers

77,906  
citations

2671

95  
h-index

10152

140  
g-index

153  
all docs

153  
docs citations

153  
times ranked

82772  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	13.5	3,979
2	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
3	The landscape of somatic copy-number alteration across human cancers. <i>Nature</i> , 2010, 463, 899-905.	13.7	3,331
4	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
5	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
6	GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. <i>Genome Biology</i> , 2011, 12, R41.	3.8	2,546
7	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435
8	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
9	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
10	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
11	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
12	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
13	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012, 30, 413-421.	9.4	1,710
14	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	13.5	1,695
15	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
16	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013, 45, 1134-1140.	9.4	1,616
17	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485
18	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428

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19	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
20	Molecular Determinants of the Response of Glioblastomas to EGFR Kinase Inhibitors. <i>New England Journal of Medicine</i> , 2005, 353, 2012-2024.	13.9	1,376
21	Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. <i>Nature</i> , 2005, 436, 117-122.	13.7	1,329
22	Molecular Definition of Breast Tumor Heterogeneity. <i>Cancer Cell</i> , 2007, 11, 259-273.	7.7	1,273
23	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018, 24, 679-690.	15.2	1,224
24	Molecular characterization of the tumor microenvironment in breast cancer. <i>Cancer Cell</i> , 2004, 6, 17-32.	7.7	1,161
25	Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007, 450, 893-898.	13.7	1,020
26	Phosphoglycerate dehydrogenase diverts glycolytic flux and contributes to oncogenesis. <i>Nature Genetics</i> , 2011, 43, 869-874.	9.4	945
27	Assessing the significance of chromosomal aberrations in cancer: Methodology and application to glioma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20007-20012.	3.3	927
28	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015, 5, 1164-1177.	7.7	821
29	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
30	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
31	Frequent and Focal <i>FGFR1</i> Amplification Associates with Therapeutically Tractable <i>FGFR1</i> Dependency in Squamous Cell Lung Cancer. <i>Science Translational Medicine</i> , 2010, 2, 62ra93.	5.8	761
32	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	13.7	761
33	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
34	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
35	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
36	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. <i>Nature Genetics</i> , 2013, 45, 478-486.	9.4	671

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37	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018, 560, 325-330.	13.7	662
38	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
39	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
40	Patient-derived xenografts undergo mouse-specific tumor evolution. <i>Nature Genetics</i> , 2017, 49, 1567-1575.	9.4	546
41	Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. <i>Nature Genetics</i> , 2013, 45, 285-289.	9.4	532
42	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	532
43	The histone methyltransferase SETDB1 is recurrently amplified in melanoma and accelerates its onset. <i>Nature</i> , 2011, 471, 513-517.	13.7	506
44	Highly parallel identification of essential genes in cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20380-20385.	3.3	499
45	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
46	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
47	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	9.4	431
48	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
49	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	416
50	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
51	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
52	Mechanisms and therapeutic implications of hypermutation in gliomas. <i>Nature</i> , 2020, 580, 517-523.	13.7	374
53	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012, 487, 491-495.	13.7	349
54	Genetic and Functional Studies Implicate HIF1 $\alpha$ as a 14q Kidney Cancer Suppressor Gene. <i>Cancer Discovery</i> , 2011, 1, 222-235.	7.7	347

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55	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
56	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	2.9	329
57	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
58	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019, 576, 112-120.	13.7	320
59	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
60	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. <i>Nature Genetics</i> , 2017, 49, 10-16.	9.4	307
61	Epidermal Growth Factor Receptor Activation in Glioblastoma through Novel Missense Mutations in the Extracellular Domain. <i>PLoS Medicine</i> , 2006, 3, e485.	3.9	298
62	BET Bromodomain Inhibition of <i>MYC</i> -Amplified Medulloblastoma. <i>Clinical Cancer Research</i> , 2014, 20, 912-925.	3.2	296
63	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018, 28, 581-591.	2.4	288
64	Pan-cancer Alterations of the <i>MYC</i> Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	2.9	284
65	Modeling Genomic Diversity and Tumor Dependency in Malignant Melanoma. <i>Cancer Research</i> , 2008, 68, 664-673.	0.4	275
66	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	9.4	275
67	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
68	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
69	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	13.5	260
70	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. <i>Cell</i> , 2018, 174, 433-447.e19.	13.5	258
71	Gastrointestinal Adenocarcinomas of the Esophagus, Stomach, and Colon Exhibit Distinct Patterns of Genome Instability and Oncogenesis. <i>Cancer Research</i> , 2012, 72, 4383-4393.	0.4	242
72	MYB-QKI rearrangements in angiocentric glioma drive tumorigenicity through a tripartite mechanism. <i>Nature Genetics</i> , 2016, 48, 273-282.	9.4	214

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73	Cancer Vulnerabilities Unveiled by Genomic Loss. <i>Cell</i> , 2012, 150, 842-854.	13.5	209
74	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
75	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
76	Genomic analysis of diffuse pediatric low-grade gliomas identifies recurrent oncogenic truncating rearrangements in the transcription factor <i>MYBL1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8188-8193.	3.3	188
77	Integrative Analysis Reveals an Outcome-Associated and Targetable Pattern of p53 and Cell Cycle Deregulation in Diffuse Large B Cell Lymphoma. <i>Cancer Cell</i> , 2012, 22, 359-372.	7.7	179
78	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. <i>Nature Genetics</i> , 2016, 48, 848-855.	9.4	174
79	Recurrent Hemizygous Deletions in Cancers May Optimize Proliferative Potential. <i>Science</i> , 2012, 337, 104-109.	6.0	172
80	Chemical Genomics Identifies Small-Molecule MCL1 Repressors and BCL-xL as a Predictor of MCL1 Dependency. <i>Cancer Cell</i> , 2012, 21, 547-562.	7.7	158
81	Genomic evolution of cancer models: perils and opportunities. <i>Nature Reviews Cancer</i> , 2019, 19, 97-109.	12.8	158
82	Overexpression, Amplification, and Androgen Regulation of TPD52 in Prostate Cancer. <i>Cancer Research</i> , 2004, 64, 3814-3822.	0.4	145
83	Pan-cancer genetic analysis identifies PARK2 as a master regulator of G1/S cyclins. <i>Nature Genetics</i> , 2014, 46, 588-594.	9.4	144
84	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020, 183, 197-210.e32.	13.5	141
85	Genomic evolution and chemoresistance in germ-cell tumours. <i>Nature</i> , 2016, 540, 114-118.	13.7	139
86	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. <i>Nature</i> , 2021, 590, 486-491.	13.7	135
87	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	2.9	134
88	SGK3 Mediates INPP4B-Dependent PI3K Signaling in Breast Cancer. <i>Molecular Cell</i> , 2014, 56, 595-607.	4.5	133
89	Genomic landscape of high-grade meningiomas. <i>Npj Genomic Medicine</i> , 2017, 2, .	1.7	130
90	The genomic landscape of schwannoma. <i>Nature Genetics</i> , 2016, 48, 1339-1348.	9.4	124

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91	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2018, 20, 873-884.	0.6	119
92	ERG rearrangement is specific to prostate cancer and does not occur in any other common tumor. <i>Modern Pathology</i> , 2010, 23, 1061-1067.	2.9	114
93	ATARIS: Computational quantification of gene suppression phenotypes from multisample RNAi screens. <i>Genome Research</i> , 2013, 23, 665-678.	2.4	110
94	Genomic landscape of intracranial meningiomas. <i>Journal of Neurosurgery</i> , 2016, 125, 525-535.	0.9	104
95	Buparlisib in Patients With Recurrent Glioblastoma Harboring Phosphatidylinositol 3-Kinase Pathway Activation: An Open-Label, Multicenter, Multi-Arm, Phase II Trial. <i>Journal of Clinical Oncology</i> , 2019, 37, 741-750.	0.8	103
96	Allele-Specific Amplification in Cancer Revealed by SNP Array Analysis. <i>PLoS Computational Biology</i> , 2005, 1, e65.	1.5	100
97	Germline and somatic BAP1 mutations in high-grade rhabdoid meningiomas. <i>Neuro-Oncology</i> , 2017, 19, now235.	0.6	99
98	Landscape of Genomic Alterations in Pituitary Adenomas. <i>Clinical Cancer Research</i> , 2017, 23, 1841-1851.	3.2	94
99	Single nucleotide polymorphism array analysis of cancer. <i>Current Opinion in Oncology</i> , 2007, 19, 43-49.	1.1	92
100	Distinct genomic aberrations associated with <i>ERG</i> rearranged prostate cancer. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 366-380.	1.5	86
101	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. <i>Genes and Development</i> , 2014, 28, 1957-1975.	2.7	86
102	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
103	ARID1A and TERT promoter mutations in dedifferentiated meningioma. <i>Cancer Genetics</i> , 2015, 208, 345-350.	0.2	73
104	Structure and mechanism of activity-based inhibition of the EGF receptor by Mig6. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 703-711.	3.6	72
105	Systematic Interrogation of 3q26 Identifies <i>TLOC1</i> and <i>SKIL</i> as Cancer Drivers. <i>Cancer Discovery</i> , 2013, 3, 1044-1057.	7.7	71
106	Integrated Genomic Analysis of the 8q24 Amplification in Endometrial Cancers Identifies ATAD2 as Essential to MYC-Dependent Cancers. <i>PLoS ONE</i> , 2013, 8, e54873.	1.1	70
107	SNP panel identification assay (SPIA): a genetic-based assay for the identification of cell lines. <i>Nucleic Acids Research</i> , 2008, 36, 2446-2456.	6.5	68
108	Copy-number and gene dependency analysis reveals partial copy loss of wild-type SF3B1 as a novel cancer vulnerability. <i>ELife</i> , 2017, 6, .	2.8	66

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109	Beating the odds: extreme long-term survival with glioblastoma. <i>Neuro-Oncology</i> , 2014, 16, 1159-1160.	0.6	63
110	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities. <i>Nature Communications</i> , 2020, 11, 2517.	5.8	60
111	MicroRNA Signatures and Molecular Subtypes of Glioblastoma: The Role of Extracellular Transfer. <i>Stem Cell Reports</i> , 2017, 8, 1497-1505.	2.3	58
112	<i>MECP2</i> Is a Frequently Amplified Oncogene with a Novel Epigenetic Mechanism That Mimics the Role of Activated RAS in Malignancy. <i>Cancer Discovery</i> , 2016, 6, 45-58.	7.7	57
113	Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. <i>Oncotarget</i> , 2014, 5, 8083-8092.	0.8	55
114	Clinical Identification of Oncogenic Drivers and Copy-Number Alterations in Pituitary Tumors. <i>Endocrinology</i> , 2017, 158, 2284-2291.	1.4	53
115	Molecular profiling and targeted therapy in pediatric gliomas: review and consensus recommendations. <i>Neuro-Oncology</i> , 2019, 21, 968-980.	0.6	52
116	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. <i>Nature Communications</i> , 2019, 10, 3731.	5.8	45
117	Genomic profile of human meningioma cell lines. <i>PLoS ONE</i> , 2017, 12, e0178322.	1.1	44
118	Tumor Interferon Signaling Is Regulated by a lncRNA INCR1 Transcribed from the PD-L1 Locus. <i>Molecular Cell</i> , 2020, 78, 1207-1223.e8.	4.5	43
119	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. <i>Neuro-Oncology</i> , 2015, 17, 1344-1355.	0.6	40
120	Copy number alterations unmasked as enhancer hijackers. <i>Nature Genetics</i> , 2017, 49, 5-6.	9.4	40
121	Genomic and Epigenomic Landscape in Meningioma. <i>Neurosurgery Clinics of North America</i> , 2016, 27, 167-179.	0.8	31
122	Somatic copy number alterations in gastric adenocarcinomas among Asian and Western patients. <i>PLoS ONE</i> , 2017, 12, e0176045.	1.1	28
123	Pan-Cancer Analysis Links PARK2 to BCL-XL-Dependent Control of Apoptosis. <i>Neoplasia</i> , 2017, 19, 75-83.	2.3	27
124	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.	5.8	27
125	MAPK activation and <i>HRAS</i> mutation identified in pituitary spindle cell oncocyoma. <i>Oncotarget</i> , 2016, 7, 37054-37063.	0.8	27
126	Structural variations in cancer and the 3D genome. <i>Nature Reviews Cancer</i> , 2022, 22, 533-546.	12.8	27



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127	Genomic Heterogeneity and Exceptional Response to Dual Pathway Inhibition in Anaplastic Thyroid Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2367-2373.	3.2	24
128	Leveraging molecular datasets for biomarker-based clinical trial design in glioblastoma. <i>Neuro-Oncology</i> , 2017, 19, 908-917.	0.6	23
129	PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. <i>Nature Communications</i> , 2022, 13, 604.	5.8	22
130	Quantification of aneuploidy in targeted sequencing data using ASCETS. <i>Bioinformatics</i> , 2021, 37, 2461-2463.	1.8	21
131	Structural variants shape driver combinations and outcomes in pediatric high-grade glioma. <i>Nature Cancer</i> , 2022, 3, 994-1011.	5.7	20
132	<i>PIK3CA</i> Amplification Associates with Aggressive Phenotype but Not Markers of AKT-MTOR Signaling in Endometrial Carcinoma. <i>Clinical Cancer Research</i> , 2019, 25, 334-345.	3.2	17
133	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. <i>Scientific Reports</i> , 2016, 6, 25521.	1.6	13
134	Case Report: Next generation sequencing identifies a NAB2-STAT6 fusion in Glioblastoma. <i>Diagnostic Pathology</i> , 2016, 11, 13.	0.9	10
135	Reply to Parsons: Many tumor types follow the monoclonal model of tumor initiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E16-E16.	3.3	6
136	MCL1 and DEDD Promote Urothelial Carcinoma Progression. <i>Molecular Cancer Research</i> , 2019, 17, 1294-1304.	1.5	4
137	Genomic Correlates of Outcome in Tumor-Infiltrating Lymphocyte Therapy for Metastatic Melanoma. <i>Clinical Cancer Research</i> , 2022, 28, 1911-1924.	3.2	3
138	Amplification of phosphoglycerate dehydrogenase diverts glycolytic flux and contributes to oncogenesis. <i>BMC Proceedings</i> , 2012, 6, .	1.8	2
139	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. <i>STAR Protocols</i> , 2021, 2, 100483.	0.5	2