

Rameen Beroukhim

List of Publications by Year in Descending Order

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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.

133
papers

25,865
citations

64
h-index

147
g-index

147
ext. papers

33,397
ext. citations

16.9
avg, IF

6.11
L-index

#	Paper	IF	Citations
133	PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation.. <i>Nature Communications</i> , 2022 , 13, 604	17.4	0
132	DNA-based copy number analysis confirms genomic evolution of PDX models.. <i>Npj Precision Oncology</i> , 2022 , 6, 30	9.8	1
131	LGG-58. Understanding the transcriptional heterogeneity of pediatric low-grade gliomas and its implication for tumor pathophysiology. <i>Neuro-Oncology</i> , 2022 , 24, i101-i102	1	
130	RARE-22 Characterizing the landscape of structural variants in adamantinomatous craniopharyngioma. <i>Neuro-Oncology</i> , 2022 , 24, i14-i14	1	
129	LGG-45. Genetic dependencies inMYB/MYBL1-driven pediatric low-grade glioma models. <i>Neuro-Oncology</i> , 2022 , 24, i98-i98	1	
128	Quantification of aneuploidy in targeted sequencing data using ASCETS. <i>Bioinformatics</i> , 2021 , 37, 2461-2463	4.6	4
127	Activity of PD-1 blockade with Nivolumab among patients with recurrent atypical/anaplastic meningioma: Phase II trial results. <i>Neuro-Oncology</i> , 2021 ,	1	7
126	TIRR inhibits the 53BP1-p53 complex to alter cell-fate programs. <i>Molecular Cell</i> , 2021 , 81, 2583-2595.e6	17.6	3
125	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. <i>STAR Protocols</i> , 2021 , 2, 100483	1.4	0
124	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. <i>Nature</i> , 2021 , 590, 486-491	50.4	34
123	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021 , 34, 108707	10.6	7
122	Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. <i>Genome Medicine</i> , 2021 , 13, 114	14.4	2
121	A Molecularly Integrated Grade for Meningioma. <i>Neuro-Oncology</i> , 2021 ,	1	7
120	Clinical utility of targeted next generation sequencing assay in IDH-wildtype glioblastoma for therapy decision-making. <i>Neuro-Oncology</i> , 2021 ,	1	3
119	MR Imaging Correlates for Molecular and Mutational Analyses in Children with Diffuse Intrinsic Pontine Glioma. <i>American Journal of Neuroradiology</i> , 2020 , 41, 874-881	4.4	10
118	Cas9 activates the p53 pathway and selects for p53-inactivating mutations. <i>Nature Genetics</i> , 2020 , 52, 662-668	36.3	69
117	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities. <i>Nature Communications</i> , 2020 , 11, 2517	17.4	21

116	Tumor Interferon Signaling Is Regulated by a lncRNA INCR1 Transcribed from the PD-L1 Locus. <i>Molecular Cell</i> , 2020 , 78, 1207-1223.e8	17.6	18
115	Treatment-Induced Tumor Dormancy through YAP-Mediated Transcriptional Reprogramming of the Apoptotic Pathway. <i>Cancer Cell</i> , 2020 , 37, 104-122.e12	24.3	107
114	Patterns of somatic structural variation in human cancer genomes. <i>Nature</i> , 2020 , 578, 112-121	50.4	232
113	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020 , 52, 294-305	36.3	81
112	Early TP53 alterations engage environmental exposures to promote gastric premalignancy in an integrative mouse model. <i>Nature Genetics</i> , 2020 , 52, 219-230	36.3	15
111	Targeting Cancer Gene Dependencies with Anthrax-Mediated Delivery of Peptide Nucleic Acids. <i>ACS Chemical Biology</i> , 2020 , 15, 1358-1369	4.9	8
110	RARE-07. THE LANDSCAPE OF GENOMIC ALTERATIONS IN ADAMANTINOMATOUS CRANIOPHARYNGIOMAS. <i>Neuro-Oncology</i> , 2020 , 22, iii443-iii443	1	78
109	LGG-35. FUNCTIONAL GENOMIC APPROACHES TO IDENTIFY THERAPEUTIC TARGETS IN MYB AND MYBL1 EXPRESSING PEDIATRIC LOW-GRADE GLIOMAS. <i>Neuro-Oncology</i> , 2020 , 22, iii373-iii373	1	78
108	HGG-41. STRUCTURAL VARIANT DRIVERS IN PEDIATRIC HIGH-GRADE GLIOMA. <i>Neuro-Oncology</i> , 2020 , 22, iii351-iii351	1	1
107	DIPG-53. CHARACTERIZING THE ROLE OF PPM1D MUTATIONS IN THE PATHOGENESIS OF DIFFUSE INTRINSIC PONTINE GLIOMAS (DIPGS). <i>Neuro-Oncology</i> , 2020 , 22, iii297-iii297	1	78
106	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020 , 37, 639-654.e6	24.3	56
105	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020 , 183, 197-210.e32	56.2	45
104	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. <i>Cell</i> , 2020 , 183, 1617-1633.e22	56.2	29
103	CloneSifter: enrichment of rare clones from heterogeneous cell populations. <i>BMC Biology</i> , 2020 , 18, 1777.3		3
102	Mechanisms and therapeutic implications of hypermutation in gliomas. <i>Nature</i> , 2020 , 580, 517-523	50.4	172
101	DIPG-12. CHARACTERIZING THE ROLE OF PPM1D MUTATIONS IN THE PATHOGENESIS OF DIFFUSE INTRINSIC PONTINE GLIOMAS (DIPGs). <i>Neuro-Oncology</i> , 2019 , 21, ii70-ii71	1	78
100	Neuronal differentiation and cell-cycle programs mediate response to BET-bromodomain inhibition in MYC-driven medulloblastoma. <i>Nature Communications</i> , 2019 , 10, 2400	17.4	18
99	LGG-04. CLINICO-HISTO-MOLECULAR LANDSCAPE OF EIGHTY-TWO PEDIATRIC AND YOUNG ADULT DYSEMBRYOPLASTIC NEUROEPITHELIAL TUMORS. <i>Neuro-Oncology</i> , 2019 , 21, ii99-ii99	1	78

98	Histone demethylase KDM6A directly senses oxygen to control chromatin and cell fate. <i>Science</i> , 2019 , 363, 1217-1222	33.3	165
97	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. <i>Nature Communications</i> , 2019 , 10, 3731	17.4	17
96	MEDU-36. BCL2 FAMILY MEMBERS ATTENUATE RESPONSE OF MYC-DRIVEN MEDULLOBLASTOMAS TO BET-BROMODOMAIN INHIBITION. <i>Neuro-Oncology</i> , 2019 , 21, ii110-ii111	1	78
95	Renal medullary carcinomas depend upon loss and are sensitive to proteasome inhibition. <i>ELife</i> , 2019 , 8,	8.9	20
94	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019 , 576, 112-120	50.4	151
93	miR-4516 predicts poor prognosis and functions as a novel oncogene via targeting PTPN14 in human glioblastoma. <i>Oncogene</i> , 2019 , 38, 2923-2936	9.2	36
92	Genomic evolution of cancer models: perils and opportunities. <i>Nature Reviews Cancer</i> , 2019 , 19, 97-109	31.3	104
91	Amplification Associates with Aggressive Phenotype but Not Markers of AKT-MTOR Signaling in Endometrial Carcinoma. <i>Clinical Cancer Research</i> , 2019 , 25, 334-345	12.9	9
90	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018 , 360, 331-335	33.3	255
89	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
88	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018 , 24, 679-690	50.5	659
87	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
86	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
85	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
84	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018 , 28, 581-591	9.7	149
83	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018 , 560, 325-330	50.4	379
82	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. <i>Cell</i> , 2018 , 174, 433-447.e19	56.2	155
81	TMOD-14. A PATIENT-DERIVED CANCER CELL LINE ATLAS OF PRIMARY AND METASTATIC CENTRAL NERVOUS SYSTEM TUMORS. <i>Neuro-Oncology</i> , 2018 , 20, vi271-vi271	1	78

80	PDTM-06. ALK AMPLIFICATION AND REARRANGEMENTS ARE RECURRENT TARGETABLE EVENTS IN GLIOBLASTOMA. <i>Neuro-Oncology</i> , 2018 , 20, vi204-vi205	1	2
79	INN-22. LIQUID BIOPSY DETECTION OF GENOMIC ALTERATIONS IN PEDIATRIC BRAIN TUMORS FROM CELL FREE DNA IN PERIPHERAL BLOOD, CSF, AND URINE. <i>Neuro-Oncology</i> , 2018 , 20, vi142-vi143	1	78
78	PATH-16. MOLECULAR PATHOLOGY AND CLINICAL CHARACTERISTICS OF MMR DEFICIENCY (MMRd) IN DIFFUSE GLIOMAS. <i>Neuro-Oncology</i> , 2018 , 20, vi161-vi161	1	78
77	DRES-05. MOLECULAR EVOLUTION OF DIFFUSE GLIOMAS AND THE GLIOMA LONGITUDINAL ANALYSIS CONSORTIUM. <i>Neuro-Oncology</i> , 2018 , 20, vi76-vi76	1	78
76	Resistance to Epigenetic-Targeted Therapy Engenders Tumor Cell Vulnerabilities Associated with Enhancer Remodeling. <i>Cancer Cell</i> , 2018 , 34, 922-938.e7	24.3	31
75	Targeting wild-type KRAS-amplified gastroesophageal cancer through combined MEK and SHP2 inhibition. <i>Nature Medicine</i> , 2018 , 24, 968-977	50.5	126
74	Clinical targeted exome-based sequencing in combination with genome-wide copy number profiling: precision medicine analysis of 203 pediatric brain tumors. <i>Neuro-Oncology</i> , 2017 , 19, 986-996	1	39
73	Clinical Identification of Oncogenic Drivers and Copy-Number Alterations in Pituitary Tumors. <i>Endocrinology</i> , 2017 , 158, 2284-2291	4.8	42
72	MicroRNA Signatures and Molecular Subtypes of Glioblastoma: The Role of Extracellular Transfer. <i>Stem Cell Reports</i> , 2017 , 8, 1497-1505	8	49
71	Genomic landscape of high-grade meningiomas. <i>Npj Genomic Medicine</i> , 2017 , 2,	6.2	78
70	Leveraging molecular datasets for biomarker-based clinical trial design in glioblastoma. <i>Neuro-Oncology</i> , 2017 , 19, 908-917	1	14
69	Pan-Cancer Analysis Links PARK2 to BCL-XL-Dependent Control of Apoptosis. <i>Neoplasia</i> , 2017 , 19, 75-836.4		23
68	Patient-derived xenografts undergo mouse-specific tumor evolution. <i>Nature Genetics</i> , 2017 , 49, 1567-1576.3	36.3	384
67	Somatic copy number alterations in gastric adenocarcinomas among Asian and Western patients. <i>PLoS ONE</i> , 2017 , 12, e0176045	3.7	22
66	Genomic profile of human meningioma cell lines. <i>PLoS ONE</i> , 2017 , 12, e0178322	3.7	30
65	Germline and somatic BAP1 mutations in high-grade rhabdoid meningiomas. <i>Neuro-Oncology</i> , 2017 , 19, 535-545	1	60
64	Landscape of Genomic Alterations in Pituitary Adenomas. <i>Clinical Cancer Research</i> , 2017 , 23, 1841-1851	12.9	64
63	Tyrosine receptor kinase B is a drug target in astrocytomas. <i>Neuro-Oncology</i> , 2017 , 19, 22-30	1	26

62	Radiographic prediction of meningioma grade by semantic and radiomic features. <i>PLoS ONE</i> , 2017 , 12, e0187908	3.7	66
61	Copy-number and gene dependency analysis reveals partial copy loss of wild-type SF3B1 as a novel cancer vulnerability. <i>ELife</i> , 2017 , 6,	8.9	49
60	SeqLib: a C ++ API for rapid BAM manipulation, sequence alignment and sequence assembly. <i>Bioinformatics</i> , 2017 , 33, 751-753	7.2	5
59	Myxopapillary ependymomas in children: imaging, treatment and outcomes. <i>Journal of Neuro-Oncology</i> , 2016 , 126, 165-174	4.8	28
58	Copy number alterations unmasked as enhancer hijackers. <i>Nature Genetics</i> , 2016 , 49, 5-6	36.3	25
57	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	4.9	11
56	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. <i>Nature Genetics</i> , 2016 , 48, 848-55	36.3	135
55	Genomic landscape of intracranial meningiomas. <i>Journal of Neurosurgery</i> , 2016 , 125, 525-35	3.2	62
54	CANCER. The oncogene makes its escape. <i>Science</i> , 2016 , 351, 1398-9	33.3	2
53	Genomic and Epigenomic Landscape in Meningioma. <i>Neurosurgery Clinics of North America</i> , 2016 , 27, 167-79	4	24
52	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
51	MYB-QKI rearrangements in angiocentric glioma drive tumorigenicity through a tripartite mechanism. <i>Nature Genetics</i> , 2016 , 48, 273-82	36.3	154
50	Oncogenic PI3K mutations are as common as AKT1 and SMO mutations in meningioma. <i>Neuro-Oncology</i> , 2016 , 18, 649-55	1	144
49	VariantBam: filtering and profiling of next-generational sequencing data using region-specific rules. <i>Bioinformatics</i> , 2016 , 32, 2029-31	7.2	14
48	MECP2 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	24.4	35
47	MAPK activation and HRAS mutation identified in pituitary spindle cell oncocytoma. <i>Oncotarget</i> , 2016 , 7, 37054-37063	3.3	24
46	Case Report: Next generation sequencing identifies a NAB2-STAT6 fusion in Glioblastoma. <i>Diagnostic Pathology</i> , 2016 , 11, 13	3	8
45	Disseminated glioneuronal tumors occurring in childhood: treatment outcomes and BRAF alterations including V600E mutation. <i>Journal of Neuro-Oncology</i> , 2016 , 128, 293-302	4.8	36

44	The genomic landscape of schwannoma. <i>Nature Genetics</i> , 2016 , 48, 1339-1348	36.3	74
43	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
42	ARID1A and TERT promoter mutations in dedifferentiated meningioma. <i>Cancer Genetics</i> , 2015 , 208, 345-50	57	
41	Predicting clinical response to anticancer drugs using an ex vivo platform that captures tumour heterogeneity. <i>Nature Communications</i> , 2015 , 6, 6169	17.4	185
40	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. <i>Neuro-Oncology</i> , 2015 , 17, 1344-55	1	39
39	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015 , 5, 1164-1177	24.4	581
38	Structure and mechanism of activity-based inhibition of the EGF receptor by Mig6. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 703-711	17.6	56
37	Extent of resection and overall survival for patients with atypical and malignant meningioma. <i>Cancer</i> , 2015 , 121, 4376-81	6.4	105
36	Expression profiles of 151 pediatric low-grade gliomas reveal molecular differences associated with location and histological subtype. <i>Neuro-Oncology</i> , 2015 , 17, 1486-96	1	33
35	Phase II study of panobinostat in combination with bevacizumab for recurrent glioblastoma and anaplastic glioma. <i>Neuro-Oncology</i> , 2015 , 17, 862-7	1	84
34	An in-tumor genetic screen reveals that the BET bromodomain protein, BRD4, is a potential therapeutic target in ovarian carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 232-7	11.5	112
33	Phase II study of monthly pasireotide LAR (SOM230C) for recurrent or progressive meningioma. <i>Neurology</i> , 2015 , 84, 280-6	6.5	62
32	Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothed inhibition. <i>Cancer Cell</i> , 2014 , 25, 393-405	24.3	469
31	Pan-cancer genetic analysis identifies PARK2 as a master regulator of G1/S cyclins. <i>Nature Genetics</i> , 2014 , 46, 588-94	36.3	124
30	Long-term outcome of 4,040 children diagnosed with pediatric low-grade gliomas: an analysis of the Surveillance Epidemiology and End Results (SEER) database. <i>Pediatric Blood and Cancer</i> , 2014 , 61, 1173-9	3	158
29	Pediatric low-grade gliomas: how modern biology reshapes the clinical field. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2014 , 1845, 294-307	11.2	28
28	BET bromodomain inhibition of MYC-amplified medulloblastoma. <i>Clinical Cancer Research</i> , 2014 , 20, 912-25	227	
27	SGK3 mediates INPP4B-dependent PI3K signaling in breast cancer. <i>Molecular Cell</i> , 2014 , 56, 595-607	17.6	105

26	Retrospective study of carmustine or lomustine with bevacizumab in recurrent glioblastoma patients who have failed prior bevacizumab. <i>Neuro-Oncology</i> , 2014 , 16, 1523-9	1	19
25	Epigenetic targeting of Hedgehog pathway transcriptional output through BET bromodomain inhibition. <i>Nature Medicine</i> , 2014 , 20, 732-40	50.5	213
24	Adjuvant radiation therapy, local recurrence, and the need for salvage therapy in atypical meningioma. <i>Neuro-Oncology</i> , 2014 , 16, 1547-53	1	61
23	Tumor associated seizures in glioblastomas are influenced by survival gene expression in a region-specific manner: a gene expression imaging study. <i>Epilepsy Research</i> , 2014 , 108, 843-52	3	13
22	AT-36PANOBINOSTAT IN COMBINATION WITH BEVACIZUMAB FOR RECURRENT GLIOBLASTOMA AND ANAPLASTIC GLIOMA. <i>Neuro-Oncology</i> , 2014 , 16, v16-v16	1	78
21	Angiomatous meningiomas have a distinct genetic profile with multiple chromosomal polysomies including polysomy of chromosome 5. <i>Oncotarget</i> , 2014 , 5, 10596-606	3.3	46
20	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. <i>Genes and Development</i> , 2014 , 28, 1957-75	12.6	66
19	Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. <i>Oncotarget</i> , 2014 , 5, 8083-92	3.3	46
18	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900
17	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013 , 45, 1134-40	36.3	1198
16	SQSTM1 is a pathogenic target of 5q copy number gains in kidney cancer. <i>Cancer Cell</i> , 2013 , 24, 738-50	24.3	111
15	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. <i>Nature Genetics</i> , 2013 , 45, 478-86	36.3	558
14	Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. <i>Genome Research</i> , 2013 , 23, 228-35	9.7	109
13	Cancer vulnerabilities unveiled by genomic loss. <i>Cell</i> , 2012 , 150, 842-54	56.2	163
12	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012 , 30, 413-21	44.5	1229
11	Chemical genomics identifies small-molecule MCL1 repressors and BCL-xL as a predictor of MCL1 dependency. <i>Cancer Cell</i> , 2012 , 21, 547-62	24.3	145
10	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	18.3	1614
9	The landscape of somatic copy-number alteration across human cancers. <i>Nature</i> , 2010 , 463, 899-905	50.4	2590

8	Patterns of gene expression and copy-number alterations in von-hippel lindau disease-associated and sporadic clear cell carcinoma of the kidney. <i>Cancer Research</i> , 2009 , 69, 4674-81	10.1	327
7	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, 20380-5	11.5	424
6	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, 20007-12	11.5	812
5	Inferring loss-of-heterozygosity from unpaired tumors using high-density oligonucleotide SNP arrays. <i>PLoS Computational Biology</i> , 2006 , 2, e41	5	124
4	SvABA: Genome-wide detection of structural variants and indels by local assembly		5
3	Selective and mechanistic sources of recurrent rearrangements across the cancer genome		20
2	The Tangent copy-number inference pipeline for cancer genome analyses		3
1	Novel patterns of complex structural variation revealed across thousands of cancer genome graphs		8