

Rameen Beroukhim

List of Publications by Citations

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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.

145
papers

51,790
citations

88
h-index

153
g-index

153
ext. papers

67,132
ext. citations

24.5
avg, IF

6.14
L-index

#	Paper	IF	Citations
145	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900
144	The landscape of somatic copy-number alteration across human cancers. <i>Nature</i> , 2010 , 463, 899-905	50.4	2590
143	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
142	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807
141	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
140	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
139	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
138	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
137	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012 , 30, 413-21	44.5	1229
136	Molecular determinants of the response of glioblastomas to EGFR kinase inhibitors. <i>New England Journal of Medicine</i> , 2005 , 353, 2012-24	59.2	1211
135	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013 , 45, 1134-40	36.3	1198
134	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
133	Molecular definition of breast tumor heterogeneity. <i>Cancer Cell</i> , 2007 , 11, 259-73	24.3	1135
132	Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. <i>Nature</i> , 2005 , 436, 117-22	50.4	1127
131	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
130	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
129	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072

128	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
127	Molecular characterization of the tumor microenvironment in breast cancer. <i>Cancer Cell</i> , 2004 , 6, 17-32	24.3	1038
126	Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007 , 450, 893-8	50.4	900
125	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13	56.2	13896
124	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	56.2	888
123	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
122	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
121	Phosphoglycerate dehydrogenase diverts glycolytic flux and contributes to oncogenesis. <i>Nature Genetics</i> , 2011 , 43, 869-74	36.3	788
120	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
119	Frequent and focal FGFR1 amplification associates with therapeutically tractable FGFR1 dependency in squamous cell lung cancer. <i>Science Translational Medicine</i> , 2010 , 2, 62ra93	17.5	646
118	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012 , 488, 49-56	50.4	596
117	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015 , 5, 1164-1177	24.4	581
116	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
115	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
114	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017 , 547, 311-317	50.4	472
113	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
112	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
111	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405

110	The histone methyltransferase SETDB1 is recurrently amplified in melanoma and accelerates its onset. <i>Nature</i> , 2011 , 471, 513-7	50.4	405
109	Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. <i>Nature Genetics</i> , 2013 , 45, 285-9	36.3	397
108	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
107	Patient-derived xenografts undergo mouse-specific tumor evolution. <i>Nature Genetics</i> , 2017 , 49, 1567-1573.e7	36.3	384
106	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018 , 560, 325-330	50.4	379
105	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
104	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366
103	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
102	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736.e3	24.3	324
101	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
100	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. <i>Nature</i> , 2012 , 487, 491-5	50.4	294
99	Genetic and functional studies implicate HIF1 α as a 14q kidney cancer suppressor gene. <i>Cancer Discovery</i> , 2011 , 1, 222-35	24.4	283
98	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
97	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	24.3	275
96	Modeling genomic diversity and tumor dependency in malignant melanoma. <i>Cancer Research</i> , 2008 , 68, 664-73	10.1	248
95	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794	10.6	247
94	Epidermal growth factor receptor activation in glioblastoma through novel missense mutations in the extracellular domain. <i>PLoS Medicine</i> , 2006 , 3, e485	11.6	242
93	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228

92	BET bromodomain inhibition of MYC-amplified medulloblastoma. <i>Clinical Cancer Research</i> , 2014 , 20, 912-925	22.9	227
91	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
90	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
89	Gastrointestinal adenocarcinomas of the esophagus, stomach, and colon exhibit distinct patterns of genome instability and oncogenesis. <i>Cancer Research</i> , 2012 , 72, 4383-93	10.1	204
88	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406	10.6	200
87	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
86	Mechanisms and therapeutic implications of hypermutation in gliomas. <i>Nature</i> , 2020 , 580, 517-523	50.4	172
85	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020 , 52, 331-341	36.3	168
84	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. <i>Nature Genetics</i> , 2017 , 49, 10-16	36.3	167
83	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
82	Cancer vulnerabilities unveiled by genomic loss. <i>Cell</i> , 2012 , 150, 842-54	56.2	163
81	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	10.6	159
80	Genomic analysis of diffuse pediatric low-grade gliomas identifies recurrent oncogenic truncating rearrangements in the transcription factor MYBL1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 8188-93	11.5	156
79	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. <i>Cell</i> , 2018 , 174, 433-447.e19	56.2	155
78	MYB-QKI rearrangements in angiocentric glioma drive tumorigenicity through a tripartite mechanism. <i>Nature Genetics</i> , 2016 , 48, 273-82	36.3	154
77	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018 , 25, 1304-1317.e5	10.6	152
76	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019 , 576, 112-120	50.4	151
75	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150

74	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018 , 28, 581-591	9.7	149
73	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, 359-72	24.3	148
72	Recurrent hemizygous deletions in cancers may optimize proliferative potential. <i>Science</i> , 2012 , 337, 104-9	33.3	148
71	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	10.6	147
70	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
69	Overexpression, amplification, and androgen regulation of TPD52 in prostate cancer. <i>Cancer Research</i> , 2004 , 64, 3814-22	10.1	136
68	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. <i>Nature Genetics</i> , 2016 , 48, 848-55	36.3	135
67	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
66	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020 , 52, 306-319	36.3	122
65	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
64	SGK3 mediates INPP4B-dependent PI3K signaling in breast cancer. <i>Molecular Cell</i> , 2014 , 56, 595-607	17.6	105
63	Genomic evolution of cancer models: perils and opportunities. <i>Nature Reviews Cancer</i> , 2019 , 19, 97-109	31.3	104
62	Genomic evolution and chemoresistance in germ-cell tumours. <i>Nature</i> , 2016 , 540, 114-118	50.4	100
61	ERG rearrangement is specific to prostate cancer and does not occur in any other common tumor. <i>Modern Pathology</i> , 2010 , 23, 1061-7	9.8	97
60	ATARiS: computational quantification of gene suppression phenotypes from multisample RNAi screens. <i>Genome Research</i> , 2013 , 23, 665-78	9.7	93
59	Allele-specific amplification in cancer revealed by SNP array analysis. <i>PLoS Computational Biology</i> , 2005 , 1, e65	5	92
58	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	10.6	85
57	Genomic landscape of high-grade meningiomas. <i>Npj Genomic Medicine</i> , 2017 , 2,	6.2	78

56	Single nucleotide polymorphism array analysis of cancer. <i>Current Opinion in Oncology</i> , 2007 , 19, 43-9	4.2	78
55	The genomic landscape of schwannoma. <i>Nature Genetics</i> , 2016 , 48, 1339-1348	36.3	74
54	Distinct genomic aberrations associated with ERG rearranged prostate cancer. <i>Genes Chromosomes and Cancer</i> , 2009 , 48, 366-80	5	72
53	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
52	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	2.2	64
51	Landscape of Genomic Alterations in Pituitary Adenomas. <i>Clinical Cancer Research</i> , 2017 , 23, 1841-1851	12.9	64
50	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. <i>Neuro-Oncology</i> , 2018 , 20, 873-884	1	63
49	Genomic landscape of intracranial meningiomas. <i>Journal of Neurosurgery</i> , 2016 , 125, 525-35	3.2	62
48	Germline and somatic BAP1 mutations in high-grade rhabdoid meningiomas. <i>Neuro-Oncology</i> , 2017 , 19, 535-545	1	60
47	Systematic interrogation of 3q26 identifies TLOC1 and SKIL as cancer drivers. <i>Cancer Discovery</i> , 2013 , 3, 1044-57	24.4	59
46	ARID1A and TERT promoter mutations in dedifferentiated meningioma. <i>Cancer Genetics</i> , 2015 , 208, 345-50	5.9	57
45	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021 , 184, 2239-2254.e39	56.2	57
44	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
43	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	26.3	56
42	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	3.7	56
41	SNP panel identification assay (SPIA): a genetic-based assay for the identification of cell lines. <i>Nucleic Acids Research</i> , 2008 , 36, 2446-56	20.1	54
40	MicroRNA Signatures and Molecular Subtypes of Glioblastoma: The Role of Extracellular Transfer. <i>Stem Cell Reports</i> , 2017 , 8, 1497-1505	8	49
39	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

38	Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. <i>Oncotarget</i> , 2014 , 5, 8083-92	3.3	46
37	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020 , 183, 197-210.e32	56.2	45
36	Clinical Identification of Oncogenic Drivers and Copy-Number Alterations in Pituitary Tumors. <i>Endocrinology</i> , 2017 , 158, 2284-2291	4.8	42
35	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. <i>Neuro-Oncology</i> , 2015 , 17, 1344-55	1	39
34	The whole-genome panorama of cancer drivers		38
33	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
32	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. <i>Nature</i> , 2021 , 590, 486-491	50.4	34
31	Genomic profile of human meningioma cell lines. <i>PLoS ONE</i> , 2017 , 12, e0178322	3.7	30
30	Molecular profiling and targeted therapy in pediatric gliomas: review and consensus recommendations. <i>Neuro-Oncology</i> , 2019 , 21, 968-980	1	26
29	Copy number alterations unmasked as enhancer hijackers. <i>Nature Genetics</i> , 2016 , 49, 5-6	36.3	25
28	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes		25
27	Genomic and Epigenomic Landscape in Meningioma. <i>Neurosurgery Clinics of North America</i> , 2016 , 27, 167-79	4	24
26	MAPK activation and HRAS mutation identified in pituitary spindle cell oncocytoma. <i>Oncotarget</i> , 2016 , 7, 37054-37063	3.3	24
25	Pan-Cancer Analysis Links PARK2 to BCL-XL-Dependent Control of Apoptosis. <i>Neoplasia</i> , 2017 , 19, 75-83	6.4	23
24	Somatic copy number alterations in gastric adenocarcinomas among Asian and Western patients. <i>PLoS ONE</i> , 2017 , 12, e0176045	3.7	22
23	Genomic Heterogeneity and Exceptional Response to Dual Pathway Inhibition in Anaplastic Thyroid Cancer. <i>Clinical Cancer Research</i> , 2017 , 23, 2367-2373	12.9	22
22	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities. <i>Nature Communications</i> , 2020 , 11, 2517	17.4	21
21	Selective and mechanistic sources of recurrent rearrangements across the cancer genome		20

20	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
19	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. <i>Nature Communications</i> , 2019 , 10, 3731	17.4	17
18	Leveraging molecular datasets for biomarker-based clinical trial design in glioblastoma. <i>Neuro-Oncology</i> , 2017 , 19, 908-917	1	14
17	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
16	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
15	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020 , 11, 4748	17.4	10
14	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
13	Novel patterns of complex structural variation revealed across thousands of cancer genome graphs		8
12	Case Report: Next generation sequencing identifies a NAB2-STAT6 fusion in Glioblastoma. <i>Diagnostic Pathology</i> , 2016 , 11, 13	3	8
11	SvABA: Genome-wide detection of structural variants and indels by local assembly		5
10	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	11.5	4
9	Selective vulnerability of aneuploid human cancer cells to inhibition of the spindle assembly checkpoint		4
8	Quantification of aneuploidy in targeted sequencing data using ASCETS. <i>Bioinformatics</i> , 2021 , 37, 2461-2463	4.63	4
7	Patient-derived xenografts undergo murine-specific tumor evolution		3
6	The Tangent copy-number inference pipeline for cancer genome analyses		3
5	Amplification of phosphoglycerate dehydrogenase diverts glycolytic flux and contributes to oncogenesis. <i>BMC Proceedings</i> , 2012 , 6,	2.3	2
4	MCL1 and DEDD Promote Urothelial Carcinoma Progression. <i>Molecular Cancer Research</i> , 2019 , 17, 1294-1304	13.04	2
3	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities		1

- 2 PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation.. *Nature Communications*, **2022**, 13, 604 17.4 ○
- 1 Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. *STAR Protocols*, **2021**, 2, 100483 1.4 ○