Rameen Beroukhim

List of Publications by Year
in descending order

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139 papers	77,906 citations	2669 95 h-index	10127 140 g-index
153 all docs	153 docs citations	153 times ranked	82772 citing authors

#	Article	IF	Citations
1	PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. Nature Communications, 2022, 13, 604.	5.8	22
2	Genomic Correlates of Outcome in Tumor-Infiltrating Lymphocyte Therapy for Metastatic Melanoma. Clinical Cancer Research, 2022, 28, 1911-1924.	3.2	3
3	Structural variations in cancer and the 3D genome. Nature Reviews Cancer, 2022, 22, 533-546.	12.8	27
4	Structural variants shape driver combinations and outcomes in pediatric high-grade glioma. Nature Cancer, 2022, 3, 994-1011.	5.7	20
5	Quantification of aneuploidy in targeted sequencing data using ASCETS. Bioinformatics, 2021, 37, 2461-2463.	1.8	21
6	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. Nature, 2021, 590, 486-491.	13.7	135
7	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
8	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. STAR Protocols, 2021, 2, 100483.	0.5	2
9	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. Cell, 2020, 183, 197-210.e32.	13.5	141
10	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
11	Loss of heterozygosity of essential genes represents a widespread class of potential cancer vulnerabilities. Nature Communications, 2020, 11, 2517.	5.8	60
12	Tumor Interferon Signaling Is Regulated by a lncRNA INCR1 Transcribed from the PD-L1 Locus. Molecular Cell, 2020, 78, 1207-1223.e8.	4.5	43
13	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
14	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
15	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
16	Mechanisms and therapeutic implications of hypermutation in gliomas. Nature, 2020, 580, 517-523.	13.7	374
17	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. Nature Communications, 2019, 10, 3731.	5.8	45
18	Buparlisib in Patients With Recurrent Glioblastoma Harboring Phosphatidylinositol 3-Kinase Pathway Activation: An Open-Label, Multicenter, Multi-Arm, Phase II Trial. Journal of Clinical Oncology, 2019, 37, 741-750.	0.8	103

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19	Molecular profiling and targeted therapy in pediatric gliomas: review and consensus recommendations. Neuro-Oncology, 2019, 21, 968-980.	0.6	52
20	MCL1 and DEDD Promote Urothelial Carcinoma Progression. Molecular Cancer Research, 2019, 17, 1294-1304.	1.5	4
21	Longitudinal molecular trajectories of diffuse glioma in adults. Nature, 2019, 576, 112-120.	13.7	320
22	Genomic evolution of cancer models: perils and opportunities. Nature Reviews Cancer, 2019, 19, 97-109.	12.8	158
23	PIK3CA Amplification Associates with Aggressive Phenotype but Not Markers of AKT-MTOR Signaling in Endometrial Carcinoma. Clinical Cancer Research, 2019, 25, 334-345.	3.2	17
24	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
25	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
26	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
27	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
28	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
29	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
30	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
31	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	2.9	205
32	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
33	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
34	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	2.9	83
35	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
36	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204

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37	Glioma through the looking GLASS: molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis Consortium. Neuro-Oncology, 2018, 20, 873-884.	0.6	119
38	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	7.7	270
39	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nature Medicine, 2018, 24, 679-690.	15.2	1,224
40	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
41	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	2.9	284
42	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	7.7	400
43	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
44	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
45	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
46	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	2.4	288
47	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	2.9	134
48	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	2.9	329
49	Genetic and transcriptional evolution alters cancer cell line drug response. Nature, 2018, 560, 325-330.	13.7	662
50	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	2.9	324
51	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. Cell, 2018, 174, 433-447.e19.	13.5	258
52	Germline and somatic BAP1 mutations in high-grade rhabdoid meningiomas. Neuro-Oncology, 2017, 19, now235.	0.6	99
53	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	7.7	532
54	Clinical Identification of Oncogenic Drivers and Copy-Number Alterations in Pituitary Tumors. Endocrinology, 2017, 158, 2284-2291.	1.4	53

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55	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
56	MicroRNA Signatures and Molecular Subtypes of Glioblastoma: The Role of Extracellular Transfer. Stem Cell Reports, 2017, 8, 1497-1505.	2.3	58
57	Genomic landscape of high-grade meningiomas. Npj Genomic Medicine, 2017, 2, .	1.7	130
58	Leveraging molecular datasets for biomarker-based clinical trial design in glioblastoma. Neuro-Oncology, 2017, 19, 908-917.	0.6	23
59	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	7.7	309
60	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
61	Copy number alterations unmasked as enhancer hijackers. Nature Genetics, 2017, 49, 5-6.	9.4	40
62	Pan-Cancer Analysis Links PARK2 to BCL-XL-Dependent Control of Apoptosis. Neoplasia, 2017, 19, 75-83.	2.3	27
63	Patient-derived xenografts undergo mouse-specific tumor evolution. Nature Genetics, 2017, 49, 1567-1575.	9.4	546
64	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	13.7	787
65	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	7.7	642
66	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
67	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	13.5	738
68	Genomic Heterogeneity and Exceptional Response to Dual Pathway Inhibition in Anaplastic Thyroid Cancer. Clinical Cancer Research, 2017, 23, 2367-2373.	3.2	24
69	Landscape of Genomic Alterations in Pituitary Adenomas. Clinical Cancer Research, 2017, 23, 1841-1851.	3.2	94
70	Tumor-suppressor genes that escape from X-inactivation contribute to cancer sex bias. Nature Genetics, 2017, 49, 10-16.	9.4	307
71	Somatic copy number alterations in gastric adenocarcinomas among Asian and Western patients. PLoS ONE, 2017, 12, e0176045.	1.1	28
72	Genomic profile of human meningioma cell lines. PLoS ONE, 2017, 12, e0178322.	1.1	44

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73	Copy-number and gene dependency analysis reveals partial copy loss of wild-type SF3B1 as a novel cancer vulnerability. ELife, 2017, 6, .	2.8	66
74	Genomic evolution and chemoresistance in germ-cell tumours. Nature, 2016, 540, 114-118.	13.7	139
75	Case Report: Next generation sequencing identifies a NAB2-STAT6 fusion in Glioblastoma. Diagnostic Pathology, 2016, 11, 13.	0.9	10
76	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
77	The genomic landscape of schwannoma. Nature Genetics, 2016, 48, 1339-1348.	9.4	124
78	Recurrent hormone-binding domain truncated ESR1 amplifications in primary endometrial cancers suggest their implication in hormone independent growth. Scientific Reports, 2016, 6, 25521.	1.6	13
79	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. Nature Genetics, 2016, 48, 848-855.	9.4	174
80	Genomic landscape of intracranial meningiomas. Journal of Neurosurgery, 2016, 125, 525-535.	0.9	104
81	Genomic and Epigenomic Landscape in Meningioma. Neurosurgery Clinics of North America, 2016, 27, 167-179.	0.8	31
82	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	13.5	1,695
83	MYB-QKI rearrangements in angiocentric glioma drive tumorigenicity through a tripartite mechanism. Nature Genetics, 2016, 48, 273-282.	9.4	214
84	MECP2 Is a Frequently Amplified Oncogene with a Novel Epigenetic Mechanism That Mimics the Role of Activated RAS in Malignancy. Cancer Discovery, 2016, 6, 45-58.	7.7	57
85	MAPK activation andHRASmutation identified in pituitary spindle cell oncocytoma. Oncotarget, 2016, 7, 37054-37063.	0.8	27
86	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	13.5	2,562
87	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
88	ARID1A and TERT promoter mutations in dedifferentiated meningioma. Cancer Genetics, 2015, 208, 345-350.	0.2	73
89	Clinical implementation of integrated whole-genome copy number and mutation profiling for glioblastoma. Neuro-Oncology, 2015, 17, 1344-1355.	0.6	40
90	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. Cancer Discovery, 2015, 5, 1164-1177.	7.7	821

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91	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
92	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	13.5	1,485
93	Structure and mechanism of activity-based inhibition of the EGF receptor by Mig6. Nature Structural and Molecular Biology, 2015, 22, 703-711.	3.6	72
94	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
95	Beating the odds: extreme long-term survival with glioblastoma. Neuro-Oncology, 2014, 16, 1159-1160.	0.6	63
96	Systematic screening reveals a role for BRCA1 in the response to transcription-associated DNA damage. Genes and Development, 2014, 28, 1957-1975.	2.7	86
97	Pan-cancer genetic analysis identifies PARK2 as a master regulator of G1/S cyclins. Nature Genetics, 2014, 46, 588-594.	9.4	144
98	BET Bromodomain Inhibition of MYC-Amplified Medulloblastoma. Clinical Cancer Research, 2014, 20, 912-925.	3.2	296
99	SGK3 Mediates INPP4B-Dependent PI3K Signaling in Breast Cancer. Molecular Cell, 2014, 56, 595-607.	4.5	133
100	Clinical multiplexed exome sequencing distinguishes adult oligodendroglial neoplasms from astrocytic and mixed lineage gliomas. Oncotarget, 2014, 5, 8083-8092.	0.8	55
101	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
102	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	9.4	1,616
103	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. Nature Genetics, 2013, 45, 478-486.	9.4	671
104	Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. Nature Genetics, 2013, 45, 285-289.	9.4	532
105	Systematic Interrogation of 3q26 Identifies TLOC1 and SKIL as Cancer Drivers. Cancer Discovery, 2013, 3, 1044-1057.	7.7	71
106	ATARiS: Computational quantification of gene suppression phenotypes from multisample RNAi screens. Genome Research, 2013, 23, 665-678.	2.4	110
107	Genomic analysis of diffuse pediatric low-grade gliomas identifies recurrent oncogenic truncating rearrangements in the transcription factor MYBL1. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8188-8193.	3.3	188
108	Integrated Genomic Analysis of the 8q24 Amplification in Endometrial Cancers Identifies ATAD2 as Essential to MYC-Dependent Cancers. PLoS ONE, 2013, 8, e54873.	1.1	70

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109	Gastrointestinal Adenocarcinomas of the Esophagus, Stomach, and Colon Exhibit Distinct Patterns of Genome Instability and Oncogenesis. Cancer Research, 2012, 72, 4383-4393.	0.4	242
110	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	13.7	761
111	Integrative Analysis Reveals an Outcome-Associated and Targetable Pattern of p53 and Cell Cycle Deregulation in Diffuse Large B Cell Lymphoma. Cancer Cell, 2012, 22, 359-372.	7.7	179
112	Cancer Vulnerabilities Unveiled by Genomic Loss. Cell, 2012, 150, 842-854.	13.5	209
113	Recurrent Hemizygous Deletions in Cancers May Optimize Proliferative Potential. Science, 2012, 337, 104-109.	6.0	172
114	Amplification of phosphoglycerate dehydrogenase diverts glycolytic flux and contributes to oncogenesis. BMC Proceedings, 2012, 6, .	1.8	2
115	Absolute quantification of somatic DNA alterations in human cancer. Nature Biotechnology, 2012, 30, 413-421.	9.4	1,710
116	Interpreting cancer genomes using systematic host network perturbations by tumour virus proteins. Nature, 2012, 487, 491-495.	13.7	349
117	Chemical Genomics Identifies Small-Molecule MCL1 Repressors and BCL-xL as a Predictor of MCL1 Dependency. Cancer Cell, 2012, 21, 547-562.	7.7	158
118	GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. Genome Biology, 2011, 12, R41.	3.8	2,546
119	Genetic and Functional Studies Implicate HIF1Î± as a 14q Kidney Cancer Suppressor Gene. Cancer Discovery, 2011, 1, 222-235.	7.7	347
120	The histone methyltransferase SETDB1 is recurrently amplified in melanoma and accelerates its onset. Nature, 2011, 471, 513-517.	13.7	506
121	Phosphoglycerate dehydrogenase diverts glycolytic flux and contributes to oncogenesis. Nature Genetics, 2011, 43, 869-874.	9.4	945
122	Reply to Parsons: Many tumor types follow the monoclonal model of tumor initiation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E16-E16.	3.3	6
123	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	13.7	3,331
124	Frequent and Focal FGFR1 Amplification Associates with Therapeutically Tractable FGFR1 Dependency in Squamous Cell Lung Cancer. Science Translational Medicine, 2010, 2, 62ra93.	5.8	761
125	ERG rearrangement is specific to prostate cancer and does not occur in any other common tumor. Modern Pathology, 2010, 23, 1061-1067.	2.9	114
126	Distinct genomic aberrations associated with ERG rearranged prostate cancer. Genes Chromosomes and Cancer, 2009, 48, 366-380.	1.5	86

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127	SNP panel identification assay (SPIA): a genetic-based assay for the identification of cell lines. Nucleic Acids Research, 2008, 36, 2446-2456.	6.5	68
128	Highly parallel identification of essential genes in cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20380-20385.	3.3	499
129	Modeling Genomic Diversity and Tumor Dependency in Malignant Melanoma. Cancer Research, 2008, 68, 664-673.	0.4	275
130	Assessing the significance of chromosomal aberrations in cancer: Methodology and application to glioma. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20007-20012.	3.3	927
131	Single nucleotide polymorphism array analysis of cancer. Current Opinion in Oncology, 2007, 19, 43-49.	1.1	92
132	Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898.	13.7	1,020
133	Molecular Definition of Breast Tumor Heterogeneity. Cancer Cell, 2007, 11, 259-273.	7.7	1,273
134	Epidermal Growth Factor Receptor Activation in Glioblastoma through Novel Missense Mutations in the Extracellular Domain. PLoS Medicine, 2006, 3, e485.	3.9	298
135	Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. Nature, 2005, 436, 117-122.	13.7	1,329
136	Allele-Specific Amplification in Cancer Revealed by SNP Array Analysis. PLoS Computational Biology, 2005, 1, e65.	1.5	100
137	Molecular Determinants of the Response of Glioblastomas to EGFR Kinase Inhibitors. New England Journal of Medicine, 2005, 353, 2012-2024.	13.9	1,376
138	Overexpression, Amplification, and Androgen Regulation of TPD52 in Prostate Cancer. Cancer Research, 2004, 64, 3814-3822.	0.4	145
139	Molecular characterization of the tumor microenvironment in breast cancer. Cancer Cell, 2004, 6, 17-32.	7.7	1,161