

# Kristian Cibulskis

## 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.

66

papers

70,116

citations

59

h-index

66

g-index

66

ext. papers

88,102

ext. citations

34.6

avg, IF

6.63

L-index

#	Paper	IF	Citations
66	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , <b>2020</b> , 581, 459-464	50.4	53
65	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , <b>2020</b> , 581, 434-443	50.4	2278
64	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , <b>2020</b> , 581, 452-458	50.4	55
63	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , <b>2017</b> , 31, 411-423	24.3	210
62	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , <b>2017</b> , 32, 204-220.e15	24.3	391
61	Systematic genomic and translational efficiency studies of uveal melanoma. <i>PLoS ONE</i> , <b>2017</b> , 12, e0178139	13.9	21
60	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. <i>Nature Communications</i> , <b>2016</b> , 7, 11589	17.4	220
59	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , <b>2015</b> , 161, 1681-96	56.2	1807
58	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , <b>2015</b> , 372, 2481-98	59.2	1828
57	Prospective derivation of a living organoid biobank of colorectal cancer patients. <i>Cell</i> , <b>2015</b> , 161, 933-45	56.2	1215
56	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , <b>2015</b> , 5, 1164-1177	24.4	581
55	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , <b>2015</b> , 163, 1011-25	56.2	1713
54	Mutations driving CLL and their evolution in progression and relapse. <i>Nature</i> , <b>2015</b> , 526, 525-30	50.4	658
53	Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 1152-8	44.5	359
52	Widespread genetic heterogeneity in multiple myeloma: implications for targeted therapy. <i>Cancer Cell</i> , <b>2014</b> , 25, 91-101	24.3	657
51	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 479-84	44.5	434
50	Genetic and clonal dissection of murine small cell lung carcinoma progression by genome sequencing. <i>Cell</i> , <b>2014</b> , 156, 1298-1311	56.2	191

49	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. <i>Nature Medicine</i> , <b>2014</b> , 20, 682-8	50.5	406
48	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , <b>2014</b> , 506, 371-5	50.4	541
47	Integrative and comparative genomic analysis of lung squamous cell carcinomas in East Asian patients. <i>Journal of Clinical Oncology</i> , <b>2014</b> , 32, 121-8	2.2	140
46	RNF43 is frequently mutated in colorectal and endometrial cancers. <i>Nature Genetics</i> , <b>2014</b> , 46, 1264-6	36.3	287
45	Colon cancer-derived oncogenic EGFR G724S mutant identified by whole genome sequence analysis is dependent on asymmetric dimerization and sensitive to cetuximab. <i>Molecular Cancer</i> , <b>2014</b> , 13, 141	42.1	22
44	The genetic landscape of clinical resistance to RAF inhibition in metastatic melanoma. <i>Cancer Discovery</i> , <b>2014</b> , 4, 94-109	24.4	626
43	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , <b>2014</b> , 159, 676-90	56.2	1660
42	Sporadic hemangioblastomas are characterized by cryptic VHL inactivation. <i>Acta Neuropathologica Communications</i> , <b>2014</b> , 2, 167	7.3	45
41	The genomic landscape of pediatric Ewing sarcoma. <i>Cancer Discovery</i> , <b>2014</b> , 4, 1326-41	24.4	302
40	Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. <i>Blood</i> , <b>2014</b> , 124, 453-62	2.2	249
39	MAP kinase pathway alterations in BRAF-mutant melanoma patients with acquired resistance to combined RAF/MEK inhibition. <i>Cancer Discovery</i> , <b>2014</b> , 4, 61-8	24.4	351
38	The somatic genomic landscape of glioblastoma. <i>Cell</i> , <b>2013</b> , 155, 462-77	56.2	2900
37	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. <i>Nature Genetics</i> , <b>2013</b> , 45, 1483-6	36.3	219
36	Evolution and impact of subclonal mutations in chronic lymphocytic leukemia. <i>Cell</i> , <b>2013</b> , 152, 714-26	56.2	1006
35	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 213-9	44.5	2830
34	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. <i>Nature Genetics</i> , <b>2013</b> , 45, 478-86	36.3	558
33	Punctuated evolution of prostate cancer genomes. <i>Cell</i> , <b>2013</b> , 153, 666-77	56.2	862
32	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , <b>2013</b> , 499, 214-218	50.4	3616

31	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , <b>2013</b> , 45, 279-84	36.3	717
30	A homozygous missense mutation in HERC2 associated with global developmental delay and autism spectrum disorder. <i>Human Mutation</i> , <b>2012</b> , 33, 1639-46	4.7	69
29	Mapping the hallmarks of lung adenocarcinoma with massively parallel sequencing. <i>Cell</i> , <b>2012</b> , 150, 1107-20	50.4	1304
28	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. <i>Nature</i> , <b>2012</b> , 488, 106-10	50.4	552
27	Melanoma genome sequencing reveals frequent PREX2 mutations. <i>Nature</i> , <b>2012</b> , 485, 502-6	50.4	555
26	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , <b>2012</b> , 44, 1104-10	36.3	919
25	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 413-21	44.5	1229
24	Genetic mapping and exome sequencing identify variants associated with five novel diseases. <i>PLoS ONE</i> , <b>2012</b> , 7, e28936	3.7	202
23	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. <i>Nature Genetics</i> , <b>2012</b> , 44, 685-9	36.3	1079
22	A landscape of driver mutations in melanoma. <i>Cell</i> , <b>2012</b> , 150, 251-63	56.2	1799
21	Sequence analysis of mutations and translocations across breast cancer subtypes. <i>Nature</i> , <b>2012</b> , 486, 405-9	50.4	895
20	A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. <i>Journal of Clinical Investigation</i> , <b>2012</b> , 122, 2983-8	15.9	286
19	SF3B1 and other novel cancer genes in chronic lymphocytic leukemia. <i>New England Journal of Medicine</i> , <b>2011</b> , 365, 2497-506	59.2	875
18	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VT11A-TCF7L2 fusion. <i>Nature Genetics</i> , <b>2011</b> , 43, 964-968	36.3	242
17	The mutational landscape of head and neck squamous cell carcinoma. <i>Science</i> , <b>2011</b> , 333, 1157-60	33.3	1836
16	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , <b>2011</b> , 12, R84	18.3	161
15	A framework for variation discovery and genotyping using next-generation DNA sequencing data. <i>Nature Genetics</i> , <b>2011</b> , 43, 491-8	36.3	7264
14	The genomic complexity of primary human prostate cancer. <i>Nature</i> , <b>2011</b> , 470, 214-20	50.4	984

13	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , <b>2011</b> , 471, 467-72	50.4	1117
12	A scalable, fully automated process for construction of sequence-ready human exome targeted capture libraries. <i>Genome Biology</i> , <b>2011</b> , 12, R1	18.3	344
11	Temporal dissection of tumorigenesis in primary cancers. <i>Cancer Discovery</i> , <b>2011</b> , 1, 137-43	24.4	201
10	ContEst: estimating cross-contamination of human samples in next-generation sequencing data. <i>Bioinformatics</i> , <b>2011</b> , 27, 2601-2	7.2	181
9	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. <i>Nature Genetics</i> , <b>2010</b> , 42, 715-21	36.3	521
8	Targeted exon sequencing by in-solution hybrid selection. <i>Current Protocols in Human Genetics</i> , <b>2010</b> , Chapter 18, Unit 18.4	3.2	37
7	Integrative analysis of the melanoma transcriptome. <i>Genome Research</i> , <b>2010</b> , 20, 413-27	9.7	216
6	The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. <i>Genome Research</i> , <b>2010</b> , 20, 1297-303	9.7	14079
5	Exome sequencing, ANGPTL3 mutations, and familial combined hypolipidemia. <i>New England Journal of Medicine</i> , <b>2010</b> , 363, 2220-7	59.2	485
4	Somatic mutations affect key pathways in lung adenocarcinoma. <i>Nature</i> , <b>2008</b> , 455, 1069-75	50.4	2280
3	Drug-sensitive FGFR2 mutations in endometrial carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 8713-7	11.5	292
2	FireCloud, a scalable cloud-based platform for collaborative genome analysis: Strategies for reducing and controlling costs		21
1	Calling Somatic SNVs and Indels with Mutect2		83