Kristian Cibulskis

List of Publications by Citations

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	The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Research*, **2010**, 20, 1297-303	9.7	14079
65	A framework for variation discovery and genotyping using next-generation DNA sequencing data. *Nature Genetics*, **2011**, 43, 491-8	36.3	7264
64	Mutational heterogeneity in cancer and the search for new cancer-associated genes. *Nature*, **2013**, 499, 214-218	50.4	3616
63	The somatic genomic landscape of glioblastoma. *Cell*, **2013**, 155, 462-77	56.2	2900
62	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. *Nature Biotechnology*, **2013**, 31, 213-9	44.5	2830
61	Somatic mutations affect key pathways in lung adenocarcinoma. *Nature*, **2008**, 455, 1069-75	50.4	2280
60	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
59	The mutational landscape of head and neck squamous cell carcinoma. *Science*, **2011**, 333, 1157-60	33.3	1836
58	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
57	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
56	A landscape of driver mutations in melanoma. *Cell*, **2012**, 150, 251-63	56.2	1799
55	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713
54	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
53	Mapping the hallmarks of lung adenocarcinoma with massively parallel sequencing. *Cell*, **2012**, 150, 1107-20	56.2	1304
52	Absolute quantification of somatic DNA alterations in human cancer. *Nature Biotechnology*, **2012**, 30, 413-21	44.5	1229
51	Prospective derivation of a living organoid biobank of colorectal cancer patients. *Cell*, **2015**, 161, 933-45	56.2	1215
50	Initial genome sequencing and analysis of multiple myeloma. *Nature*, **2011**, 471, 467-72	50.4	1117

49	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. *Nature Genetics*, **2012**, 44, 685-9	36.3	1079
48	Evolution and impact of subclonal mutations in chronic lymphocytic leukemia. *Cell*, **2013**, 152, 714-26	56.2	1006
47	The genomic complexity of primary human prostate cancer. *Nature*, **2011**, 470, 214-20	50.4	984
46	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. *Nature Genetics*, **2012**, 44, 1104-10	36.3	919
45	Sequence analysis of mutations and translocations across breast cancer subtypes. *Nature*, **2012**, 486, 405-9	50.4	895
44	SF3B1 and other novel cancer genes in chronic lymphocytic leukemia. *New England Journal of Medicine*, **2011**, 365, 2497-506	59.2	875
43	Punctuated evolution of prostate cancer genomes. *Cell*, **2013**, 153, 666-77	56.2	862
42	The genetic landscape of high-risk neuroblastoma. *Nature Genetics*, **2013**, 45, 279-84	36.3	717
41	Mutations driving CLL and their evolution in progression and relapse. *Nature*, **2015**, 526, 525-30	50.4	658
40	Widespread genetic heterogeneity in multiple myeloma: implications for targeted therapy. *Cancer Cell*, **2014**, 25, 91-101	24.3	657
39	The genetic landscape of clinical resistance to RAF inhibition in metastatic melanoma. *Cancer Discovery*, **2014**, 4, 94-109	24.4	626
38	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. *Cancer Discovery*, **2015**, 5, 1164-1177	24.4	581
37	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. *Nature Genetics*, **2013**, 45, 478-86	36.3	558
36	Melanoma genome sequencing reveals frequent PREX2 mutations. *Nature*, **2012**, 485, 502-6	50.4	555
35	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. *Nature*, **2012**, 488, 106-10	50.4	552
34	Landscape of genomic alterations in cervical carcinomas. *Nature*, **2014**, 506, 371-5	50.4	541
33	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. *Nature Genetics*, **2010**, 42, 715-21	36.3	521
32	Exome sequencing, ANGPTL3 mutations, and familial combined hypolipidemia. *New England Journal of Medicine*, **2010**, 363, 2220-7	59.2	485

31	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. *Nature Biotechnology*, **2014**, 32, 479-84	44.5	434
30	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. *Nature Medicine*, **2014**, 20, 682-8	50.5	406
29	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. *Cancer Cell*, **2017**, 32, 204-220.e15	24.3	391
28	Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. *Nature Biotechnology*, **2015**, 33, 1152-8	44.5	359
27	MAP kinase pathway alterations in BRAF-mutant melanoma patients with acquired resistance to combined RAF/MEK inhibition. *Cancer Discovery*, **2014**, 4, 61-8	24.4	351
26	A scalable, fully automated process for construction of sequence-ready human exome targeted capture libraries. *Genome Biology*, **2011**, 12, R1	18.3	344
25	The genomic landscape of pediatric Ewing sarcoma. *Cancer Discovery*, **2014**, 4, 1326-41	24.4	302
24	Drug-sensitive FGFR2 mutations in endometrial carcinoma. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 8713-7	11.5	292
23	RNF43 is frequently mutated in colorectal and endometrial cancers. *Nature Genetics*, **2014**, 46, 1264-6	36.3	287
22	A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. *Journal of Clinical Investigation*, **2012**, 122, 2983-8	15.9	286
21	Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. *Blood*, **2014**, 124, 453-62	2.2	249
20	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. *Nature Genetics*, **2011**, 43, 964-968	36.3	242
19	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. *Nature Communications*, **2016**, 7, 11589	17.4	220
18	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. *Nature Genetics*, **2013**, 45, 1483-6	36.3	219
17	Integrative analysis of the melanoma transcriptome. *Genome Research*, **2010**, 20, 413-27	9.7	216
16	Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, **2017**, 31, 411-423	24.3	210
15	Genetic mapping and exome sequencing identify variants associated with five novel diseases. *PLoS ONE*, **2012**, 7, e28936	3.7	202
14	Temporal dissection of tumorigenesis in primary cancers. *Cancer Discovery*, **2011**, 1, 137-43	24.4	201

13	Genetic and clonal dissection of murine small cell lung carcinoma progression by genome sequencing. *Cell*, **2014**, 156, 1298-1311	56.2	191
12	ContEst: estimating cross-contamination of human samples in next-generation sequencing data. *Bioinformatics*, **2011**, 27, 2601-2	7.2	181
11	The functional spectrum of low-frequency coding variation. *Genome Biology*, **2011**, 12, R84	18.3	161
10	Integrative and comparative genomic analysis of lung squamous cell carcinomas in East Asian patients. *Journal of Clinical Oncology*, **2014**, 32, 121-8	2.2	140
9	Calling Somatic SNVs and Indels with Mutect2		83
8	A homozygous missense mutation in HERC2 associated with global developmental delay and autism spectrum disorder. *Human Mutation*, **2012**, 33, 1639-46	4.7	69
7	Transcript expression-aware annotation improves rare variant interpretation. *Nature*, **2020**, 581, 452-458	50.4	55
6	Evaluating drug targets through human loss-of-function genetic variation. *Nature*, **2020**, 581, 459-464	50.4	53
5	Sporadic hemangioblastomas are characterized by cryptic VHL inactivation. *Acta Neuropathologica Communications*, **2014**, 2, 167	7.3	45
4	Targeted exon sequencing by in-solution hybrid selection. *Current Protocols in Human Genetics*, **2010**, Chapter 18, Unit 18.4	3.2	37
3	Colon cancer-derived oncogenic EGFR G724S mutant identified by whole genome sequence analysis is dependent on asymmetric dimerization and sensitive to cetuximab. *Molecular Cancer*, **2014**, 13, 141	42.1	22
2	Systematic genomic and translational efficiency studies of uveal melanoma. *PLoS ONE*, **2017**, 12, e0178189	3.7	21
1	FireCloud, a scalable cloud-based platform for collaborative genome analysis: Strategies for reducing and controlling costs		21