Kristian Cibulskis

List of Publications by Year
in descending order

64 papers	98,395 citations	22548 61 h-index	124990 64 g-index
66 all docs	66 docs citations	66 times ranked	134876 citing authors

#	Article	IF	Citations
1	The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data. Genome Research, 2010, 20, 1297-1303.	2.4	21,358
2	A framework for variation discovery and genotyping using next-generation DNA sequencing data. Nature Genetics, 2011, 43, 491-498.	9.4	10,018
3	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
4	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	13.7	4,761
5	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
6	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. Nature Biotechnology, 2013, 31, 213-219.	9.4	3,934
7	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	13.7	2,694
8	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
9	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	13.5	2,562
10	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	13.5	2,435
11	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
12	A Landscape of Driver Mutations in Melanoma. Cell, 2012, 150, 251-263.	13.5	2,247
13	The Mutational Landscape of Head and Neck Squamous Cell Carcinoma. Science, 2011, 333, 1157-1160.	6.0	2,225
14	Absolute quantification of somatic DNA alterations in human cancer. Nature Biotechnology, 2012, 30, 413-421.	9.4	1,710
15	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	13.5	1,710
16	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. Cell, 2012, 150, 1107-1120.	13.5	1,591
17	Exome sequencing identifies recurrent SPOP, FOXA1 and MED12 mutations in prostate cancer. Nature Genetics, 2012, 44, 685-689.	9.4	1,300
18	Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472.	13.7	1,288

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19	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. Cell, 2013, 152, 714-726.	13.5	1,202
20	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. Nature Genetics, 2012, 44, 1104-1110.	9.4	1,186
21	The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220.	13.7	1,107
22	Sequence analysis of mutations and translocations across breast cancer subtypes. Nature, 2012, 486, 405-409.	13.7	1,107
23	Punctuated Evolution of Prostate Cancer Genomes. Cell, 2013, 153, 666-677.	13.5	1,107
24	SF3B1and Other Novel Cancer Genes in Chronic Lymphocytic Leukemia. New England Journal of Medicine, 2011, 365, 2497-2506.	13.9	1,021
25	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	9.4	990
26	Mutations driving CLL and their evolution in progression and relapse. Nature, 2015, 526, 525-530.	13.7	868
27	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. Cancer Cell, 2014, 25, 91-101.	7.7	847
28	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. Cancer Discovery, 2015, 5, 1164-1177.	7.7	821
29	The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. Cancer Discovery, 2014, 4, 94-109.	7.7	782
30	Landscape of genomic alterations in cervical carcinomas. Nature, 2014, 506, 371-375.	13.7	708
31	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. Nature, 2012, 488, 106-110.	13.7	675
32	Melanoma genome sequencing reveals frequent PREX2 mutations. Nature, 2012, 485, 502-506.	13.7	671
33	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. Nature Genetics, 2013, 45, 478-486.	9.4	671
34	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. Nature Genetics, 2010, 42, 715-721.	9.4	642
35	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	7.7	642
36	Exome Sequencing,ANGPTL3Mutations, and Familial Combined Hypolipidemia. New England Journal of Medicine, 2010, 363, 2220-2227.	13.9	640

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37	Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. Nature Biotechnology, 2015, 33, 1152-1158.	9.4	573
38	A scalable, fully automated process for construction of sequence-ready human exome targeted capture libraries. Genome Biology, 2011, 12, R1.	13.9	547
39	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. Nature Medicine, 2014, 20, 682-688.	15.2	508
40	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	9.4	495
41	MAP Kinase Pathway Alterations in BRAF-Mutant Melanoma Patients with Acquired Resistance to Combined RAF/MEK Inhibition. Cancer Discovery, 2014, 4, 61-68.	7.7	419
42	The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.	7.7	415
43	RNF43 is frequently mutated in colorectal and endometrial cancers. Nature Genetics, 2014, 46, 1264-1266.	9.4	388
44	A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. Journal of Clinical Investigation, 2012, 122, 2983-2988.	3.9	347
45	Drug-sensitiveFGFR2mutations in endometrial carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8713-8717.	3.3	329
46	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	7.7	309
47	Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. Blood, 2014, 124, 453-462.	0.6	286
48	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. Nature Communications, 2016, 7, 11589.	5.8	285
49	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. Nature Genetics, 2013, 45, 1483-1486.	9.4	275
50	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. Nature Genetics, 2011, 43, 964-968.	9.4	270
51	Genetic Mapping and Exome Sequencing Identify Variants Associated with Five Novel Diseases. PLoS ONE, 2012, 7, e28936.	1.1	254
52	Integrative analysis of the melanoma transcriptome. Genome Research, 2010, 20, 413-427.	2.4	248
53	Genetic and Clonal Dissection of Murine Small Cell Lung Carcinoma Progression by Genome Sequencing. Cell, 2014, 156, 1298-1311.	13.5	241
54	Temporal Dissection of Tumorigenesis in Primary Cancers. Cancer Discovery, 2011, 1, 137-143.	7.7	240

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55	ContEst: estimating cross-contamination of human samples in next-generation sequencing data. Bioinformatics, 2011, 27, 2601-2602.	1.8	235
56	Integrative and Comparative Genomic Analysis of Lung Squamous Cell Carcinomas in East Asian Patients. Journal of Clinical Oncology, 2014, 32, 121-128.	0.8	176
57	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	13.9	173
58	Transcript expression-aware annotation improves rare variant interpretation. Nature, 2020, 581, 452-458.	13.7	142
59	Evaluating drug targets through human loss-of-function genetic variation. Nature, 2020, 581, 459-464.	13.7	115
60	A homozygous missense mutation inHERC2associated with global developmental delay and autism spectrum disorder. Human Mutation, 2012, 33, 1639-1646.	1.1	90
61	Sporadic hemangioblastomas are characterized by cryptic VHL inactivation. Acta Neuropathologica Communications, 2014, 2, 167.	2.4	65
62	Targeted Exon Sequencing by Inâ€Solution Hybrid Selection. Current Protocols in Human Genetics, 2010, 66, Unit 18.4.	3.5	40
63	Systematic genomic and translational efficiency studies of uveal melanoma. PLoS ONE, 2017, 12, e0178189.	1.1	34
64	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.	7.9	24