

Kristian Cibulskis

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

98,395
citations

19608

61
h-index

110170

64
g-index

66
all docs

66
docs citations

66
times ranked

124346
citing authors

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

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19	Evolution and Impact of Subclonal Mutations in Chronic Lymphocytic Leukemia. <i>Cell</i> , 2013, 152, 714-726.	13.5	1,202
20	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , 2012, 44, 1104-1110.	9.4	1,186
21	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011, 470, 214-220.	13.7	1,107
22	Sequence analysis of mutations and translocations across breast cancer subtypes. <i>Nature</i> , 2012, 486, 405-409.	13.7	1,107
23	Punctuated Evolution of Prostate Cancer Genomes. <i>Cell</i> , 2013, 153, 666-677.	13.5	1,107
24	<i>SF3B1</i> and Other Novel Cancer Genes in Chronic Lymphocytic Leukemia. <i>New England Journal of Medicine</i> , 2011, 365, 2497-2506.	13.9	1,021
25	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284.	9.4	990
26	Mutations driving CLL and their evolution in progression and relapse. <i>Nature</i> , 2015, 526, 525-530.	13.7	868
27	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. <i>Cancer Cell</i> , 2014, 25, 91-101.	7.7	847
28	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015, 5, 1164-1177.	7.7	821
29	The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. <i>Cancer Discovery</i> , 2014, 4, 94-109.	7.7	782
30	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , 2014, 506, 371-375.	13.7	708
31	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. <i>Nature</i> , 2012, 488, 106-110.	13.7	675
32	Melanoma genome sequencing reveals frequent PREX2 mutations. <i>Nature</i> , 2012, 485, 502-506.	13.7	671
33	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. <i>Nature Genetics</i> , 2013, 45, 478-486.	9.4	671
34	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. <i>Nature Genetics</i> , 2010, 42, 715-721.	9.4	642
35	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
36	Exome Sequencing, <i>ANGPTL3</i> Mutations, and Familial Combined Hypolipidemia. <i>New England Journal of Medicine</i> , 2010, 363, 2220-2227.	13.9	640

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37	Comprehensive analysis of cancer-associated somatic mutations in class I HLA genes. <i>Nature Biotechnology</i> , 2015, 33, 1152-1158.	9.4	573
38	A scalable, fully automated process for construction of sequence-ready human exome targeted capture libraries. <i>Genome Biology</i> , 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. <i>Nature Medicine</i> , 2014, 20, 682-688.	15.2	508
40	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014, 32, 479-484.	9.4	495
41	MAP Kinase Pathway Alterations in <i>BRAF</i> -Mutant Melanoma Patients with Acquired Resistance to Combined RAF/MEK Inhibition. <i>Cancer Discovery</i> , 2014, 4, 61-68.	7.7	419
42	The Genomic Landscape of Pediatric Ewing Sarcoma. <i>Cancer Discovery</i> , 2014, 4, 1326-1341.	7.7	415
43	RNF43 is frequently mutated in colorectal and endometrial cancers. <i>Nature Genetics</i> , 2014, 46, 1264-1266.	9.4	388
44	A remarkably simple genome underlies highly malignant pediatric rhabdoid cancers. <i>Journal of Clinical Investigation</i> , 2012, 122, 2983-2988.	3.9	347
45	Drug-sensitive <i>FGFR2</i> mutations in endometrial carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8713-8717.	3.3	329
46	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
47	Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. <i>Blood</i> , 2014, 124, 453-462.	0.6	286
48	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. <i>Nature Communications</i> , 2016, 7, 11589.	5.8	285
49	Somatic mutation of <i>CDKN1B</i> in small intestine neuroendocrine tumors. <i>Nature Genetics</i> , 2013, 45, 1483-1486.	9.4	275
50	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent <i>VTI1A</i> - <i>TCF7L2</i> fusion. <i>Nature Genetics</i> , 2011, 43, 964-968.	9.4	270
51	Genetic Mapping and Exome Sequencing Identify Variants Associated with Five Novel Diseases. <i>PLoS ONE</i> , 2012, 7, e28936.	1.1	254
52	Integrative analysis of the melanoma transcriptome. <i>Genome Research</i> , 2010, 20, 413-427.	2.4	248
53	Genetic and Clonal Dissection of Murine Small Cell Lung Carcinoma Progression by Genome Sequencing. <i>Cell</i> , 2014, 156, 1298-1311.	13.5	241
54	Temporal Dissection of Tumorigenesis in Primary Cancers. <i>Cancer Discovery</i> , 2011, 1, 137-143.	7.7	240

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55	ContEst: estimating cross-contamination of human samples in next-generation sequencing data. <i>Bioinformatics</i> , 2011, 27, 2601-2602.	1.8	235
56	Integrative and Comparative Genomic Analysis of Lung Squamous Cell Carcinomas in East Asian Patients. <i>Journal of Clinical Oncology</i> , 2014, 32, 121-128.	0.8	176
57	The functional spectrum of low-frequency coding variation. <i>Genome Biology</i> , 2011, 12, R84.	13.9	173
58	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , 2020, 581, 452-458.	13.7	142
59	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020, 581, 459-464.	13.7	115
60	A homozygous missense mutation in <i>HERC2</i> associated with global developmental delay and autism spectrum disorder. <i>Human Mutation</i> , 2012, 33, 1639-1646.	1.1	90
61	Sporadic hemangioblastomas are characterized by cryptic VHL inactivation. <i>Acta Neuropathologica Communications</i> , 2014, 2, 167.	2.4	65
62	Targeted Exon Sequencing by In-solution Hybrid Selection. <i>Current Protocols in Human Genetics</i> , 2010, 66, Unit 18.4.	3.5	40
63	Systematic genomic and translational efficiency studies of uveal melanoma. <i>PLoS ONE</i> , 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. <i>Molecular Cancer</i> , 2014, 13, 141.	7.9	24