Cyriac Kandoth

List of Publications by Year
in descending order

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85	54,360	31976	91884
papers	citations	53 h-index	69 g-index

89	89	89	63290
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome Nexus: A Comprehensive Resource for the Annotation and Interpretation of Genomic Variants in Cancer. JCO Clinical Cancer Informatics, 2022, 6, e2100144.	2.1	4
2	Recurrent Mutations in Cyclin D3 Confer Clinical Resistance to FLT3 Inhibitors in Acute Myeloid Leukemia. Clinical Cancer Research, 2021, 27, 4003-4011.	7.0	7
3	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27
4	Coaltered Ras/B-raf and TP53 Is Associated with Extremes of Survivorship and Distinct Patterns of Metastasis in Patients with Metastatic Colorectal Cancer. Clinical Cancer Research, 2020, 26, 1077-1085.	7.0	62
5	GNAQ Mutations in Diffuse and Solitary Choroidal Hemangiomas. Ophthalmology, 2019, 126, 759-763.	5.2	26
6	Regional differences in gallbladder cancer pathogenesis: Insights from a multiâ€institutional comparison of tumor mutations. Cancer, 2019, 125, 575-585.	4.1	34
7	Abstract 1672: Clinical validation of a genomics-based classifier to predict tissue of origin from targeted tumor sequencing. , 2019, , .		0
8	Abstract 2482: A portable bioinformatics pipeline for the FDA authorized IMPACT DNAseq assay. , 2019, , .		0
9	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
10	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
11	Tumor Evolution and Drug Response in Patient-Derived Organoid Models of Bladder Cancer. Cell, 2018, 173, 515-528.e17.	28.9	540
12	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
13	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
14	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
15	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
16	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
17	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
18	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407

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19	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	6.4	205
20	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
21	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	6.4	83
22	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
23	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
24	Accelerating Discovery of Functional Mutant Alleles in Cancer. Cancer Discovery, 2018, 8, 174-183.	9.4	275
25	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
26	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
27	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
28	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
29	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
30	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.	6.2	134
31	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. Cancer Cell, 2018, 34, 427-438.e6.	16.8	633
32	Genetic and epigenetic evolution as a contributor to WT1-mutant leukemogenesis. Blood, 2018, 132, 1265-1278.	1.4	39
33	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
34	Integrative omics analyses broaden treatment targets in human cancer. Genome Medicine, 2018, 10, 60.	8.2	17
35	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas. , 2018, , .		9
36	Abstract 926: Multi-Center Mutation Calling in Multiple Cancers: The MC3 Project. , 2018, , .		3

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37	Abstract PR16: Multiplatform analysis of paired primary and recurrent well- and dedifferentiated liposarcoma samples defines copy number alterations as dominant drivers of initiation and progression. , 2018, , .		0
38	Clonal evolution of uveal melanoma metastases.. Journal of Clinical Oncology, 2018, 36, e21534-e21534.	1.6	0
39	Abstract 5351: Retrospective analysis of cancer exomes with Roslin, a portable and reproducible workflow infrastructure. , 2018, , .		0
40	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
41	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
42	Extraordinary survivorship after colorectal liver metastasis resection to identify a distinct molecular profile associated with survival in an independent cohort of 965 patients.. Journal of Clinical Oncology, 2017, 35, 3581-3581.	1.6	0
43	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. Nature Biotechnology, 2016, 34, 155-163.	17.5	634
44	Abstract B14: Molecular characterization of mucinous ovarian carcinoma.. , 2016, , .		0
45	Abstract 4509: Clinical genomic profiling of 1000 metastatic breast cancer patients: actionable targets, novel alterations, and clinical correlations. , 2016, , .		0
46	Abstract 4366: Identifying novel recurrent mutations reveals candidate actionable mutations. , 2016, , .		0
47	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
48	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
49	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	12.8	243
50	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
51	Abstract S2-04: Comprehensive molecular characterization of invasive lobular breast tumors. , 2015, , .		10
52	Recurrent Mutations in CCND3 Confer Clinical Resistance to FLT3 Inhibitors. Blood, 2015, 126, 677-677.	1.4	4
53	Transcriptomic Responses of the Heart and Brain to Anoxia in the Western Painted Turtle. PLoS ONE, 2015, 10, e0131669.	2.5	29
54	INTEGRATIVE GENOME-WIDE ANALYSIS OF THE DETERMINANTS OF RNA SPLICING IN KIDNEY RENAL CLEAR CELL CARCINOMA. , 2014, , .		3

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55	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	12.8	253
56	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
57	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. Genome Biology, 2013, 14, R28.	9.6	276
58	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. Nature Communications, 2013, 4, 2730.	12.8	104
59	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	27.8	3,695
60	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
61	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. Nature Genetics, 2013, 45, 602-612.	21.4	704
62	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
63	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
64	Clonal diversity of recurrently mutated genes in myelodysplastic syndromes. Leukemia, 2013, 27, 1275-1282.	7.2	260
65	Comprehensive identification of mutational cancer driver genes across 12 tumor types. Scientific Reports, 2013, 3, 2650.	3.3	437
66	Somatic neurofibromatosis type 1 (NF1) inactivation characterizes NF1-associated pilocytic astrocytoma. Genome Research, 2013, 23, 431-439.	5.5	99
67	Enabling transparent and collaborative computational analysis of 12 tumor types within The Cancer Genome Atlas. Nature Genetics, 2013, 45, 1121-1126.	21.4	102
68	RNAâ€seq reveals a robust transcriptomic response during anoxia in the Western painted turtle. FASEB Journal, 2013, 27, 937.21.	0.5	0
69	Abstract LB-239: Mutational and clonal analyses across TCGA cancer types using the MuSiC suite of tools.. , 2013, , .		0
70	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. Bioinformatics, 2012, 28, 1923-1924.	4.1	54
71	MuSiC: Identifying mutational significance in cancer genomes. Genome Research, 2012, 22, 1589-1598.	5.5	586
72	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	27.8	922

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73	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
74	Abstract LB-423: Whole genome comparisons of pre- and post- aromatase inhibitor treatment in estrogen receptor positive breast cancer. , 2012, , .		0
75	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	27.8	6,541
76	Recurrent DNMT3A mutations in patients with myelodysplastic syndromes. Leukemia, 2011, 25, 1153-1158.	7.2	483
77	PathScan: a tool for discerning mutational significance in groups of putative cancer genes. Bioinformatics, 2011, 27, 1595-1602.	4.1	87
78	Complete Sequencing and Comparison of 12 Normal Karyotype M1 AML Genomes with 12 t(15;17) Positive M3-APL Genomes. Blood, 2011, 118, 404-404.	1.4	1
79	A framework for automated enrichment of functionally significant inverted repeats in whole genomes. BMC Bioinformatics, 2010, 11, S20.	2.6	5
80	DNMT3AMutations in Acute Myeloid Leukemia. New England Journal of Medicine, 2010, 363, 2424-2433.	27.0	1,777
81	Protein Secondary Structure Prediction Using RT-RICO: A Rule-Based Approach. Open Bioinformatics Journal, 2010, 4, 17-30.	1.0	4
82	Mutations In the DNA Methyltransferase Gene DNMT3A Are Highly Recurrent In Patients with Intermediate Risk Acute Myeloid Leukemia, and Predict Poor Outcomes. Blood, 2010, 116, 99-99.	1.4	9
83	Angular Mobility Assisted Coverage in Directional Sensor Networks. , 2009, , .		15
84	Validation of an NSP-based (negative selection pattern) gene family identification strategy. BMC Bioinformatics, 2008, 9, S2.	2.6	5
85	Automation of an NSP-Based (Negative Selection Pattern) Gene Family Identification Strategy. , 0, , 319-326.		0