Matthew D Ducar

List of Publications by Year
in descending order

38 papers	6,477 citations	172457 29 h-index	315739 38 g-index
39 all docs	39 docs citations	39 times ranked	11638 citing authors

#	Article	IF	Citations
1	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nature Medicine, 2018, 24, 679-690.	30.7	1,224
2	Genomic sequencing of meningiomas identifies oncogenic SMO and AKT1 mutations. Nature Genetics, 2013, 45, 285-289.	21.4	532
3	High-Throughput Detection of Actionable Genomic Alterations in Clinical Tumor Samples by Targeted, Massively Parallel Sequencing. Cancer Discovery, 2012, 2, 82-93.	9.4	484
4	Integration of gene mutations in risk prognostication for patients receiving first-line immunochemotherapy for follicular lymphoma: a retrospective analysis of a prospective clinical trial and validation in a population-based registry. Lancet Oncology, The, 2015, 16, 1111-1122.	10.7	483
5	Targetable genetic features of primary testicular and primary central nervous system lymphomas. Blood, 2016, 127, 869-881.	1.4	429
6	Validation of OncoPanel: A Targeted Next-Generation Sequencing Assay for the Detection of Somatic Variants in Cancer. Archives of Pathology and Laboratory Medicine, 2017, 141, 751-758.	2.5	350
7	Institutional implementation of clinical tumor profiling on an unselected cancer population. JCI Insight, 2016, 1, e87062.	5.0	340
8	Genomic Heterogeneity as a Barrier to Precision Medicine in Gastroesophageal Adenocarcinoma. Cancer Discovery, 2018, 8, 37-48.	9.4	248
9	MYB-QKI rearrangements in angiocentric glioma drive tumorigenicity through a tripartite mechanism. Nature Genetics, 2016, 48, 273-282.	21.4	214
10	Genomic analysis of diffuse pediatric low-grade gliomas identifies recurrent oncogenic truncating rearrangements in the transcription factor MYBL1. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8188-8193.	7.1	188
11	Novel Peptide Inhibitors of Angiotensin-converting Enzyme 2. Journal of Biological Chemistry, 2003, 278, 15532-15540.	3.4	185
12	MAP2K1 and MAP3K1 mutations in langerhans cell histiocytosis. Genes Chromosomes and Cancer, 2015, 54, 361-368.	2.8	167
13	Somatic activating ARAF mutations in Langerhans cell histiocytosis. Blood, 2014, 123, 3152-3155.	1.4	161
14	BreaKmer: detection of structural variation in targeted massively parallel sequencing data using kmers. Nucleic Acids Research, 2015, 43, e19-e19.	14.5	161
15	Association of Alterations in Main Driver Genes With Outcomes of Patients With Resected Pancreatic Ductal Adenocarcinoma. JAMA Oncology, 2018, 4, e173420.	7.1	155
16	The impact of tumor profiling approaches and genomic data strategies for cancer precision medicine. Genome Medicine, 2016, 8, 79.	8.2	151
17	Germline cancer susceptibility gene variants, somatic second hits, and survival outcomes in patients with resected pancreatic cancer. Genetics in Medicine, 2019, 21, 213-223.	2.4	151
18	Genomic analyses of flow-sorted Hodgkin Reed-Sternberg cells reveal complementary mechanisms of immune evasion. Blood Advances, 2019, 3, 4065-4080.	5.2	99

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19	Landscape of Genomic Alterations in Pituitary Adenomas. Clinical Cancer Research, 2017, 23, 1841-1851.	7.0	94
20	Comparison of Prevalence and Types of Mutations in Lung Cancers Among Black and White Populations. JAMA Oncology, 2017, 3, 801.	7.1	78
21	Prospective Enterprise-Level Molecular Genotyping of a Cohort of Cancer Patients. Journal of Molecular Diagnostics, 2014, 16, 660-672.	2.8	70
22	Diffuse large B-cell lymphoma patient-derived xenograft models capture the molecular and biological heterogeneity of the disease. Blood, 2016, 127, 2203-2213.	1.4	68
23	Clinical targeted exome-based sequencing in combination with genome-wide copy number profiling: precision medicine analysis of 203 pediatric brain tumors. Neuro-Oncology, 2017, 19, now294.	1.2	54
24	Recurrent genetic HLA loss in AML relapsed after matched unrelated allogeneic hematopoietic cell transplantation. Blood Advances, 2019, 3, 2199-2204.	5.2	52
25	Nextâ€generation sequencing of cytologic preparations: An analysis of quality metrics. Cancer Cytopathology, 2017, 125, 786-794.	2.4	51
26	OncoTree: A Cancer Classification System for Precision Oncology. JCO Clinical Cancer Informatics, 2021, 5, 221-230.	2.1	51
27	Hedgehog pathway mutations drive oncogenic transformation in high-risk T-cell acute lymphoblastic leukemia. Leukemia, 2018, 32, 2126-2137.	7.2	48
28	Genomic aberrations in cervical adenocarcinomas in Hong Kong Chinese women. International Journal of Cancer, 2015, 137, 776-783.	5.1	39
29	Correlation Between Surrogate End Points and Overall Survival in a Multi-institutional Clinicogenomic Cohort of Patients With Nonâ€“Small Cell Lung or Colorectal Cancer. JAMA Network Open, 2021, 4, e2117547.	5.9	20
30	Molecular Characterization and Therapeutic Targeting of Colorectal Cancers Harboring Receptor Tyrosine Kinase Fusions. Clinical Cancer Research, 2021, 27, 1695-1705.	7.0	19
31	Somatic mutations in CDH1 and CTNNB1 in primary carcinomas at 13 anatomic sites. Oncotarget, 2017, 8, 85680-85691.	1.8	16
32	Clinical and mutational spectrum of highly differentiated, paired box 3:forkhead box protein o1 fusionâ€“negative rhabdomyosarcoma: A report from the Children's Oncology Group. Cancer, 2018, 124, 1973-1981.	4.1	14
33	Insulin-Like Growth Factor-1 Receptor Expression and Disease Recurrence and Survival in Patients with Resected Pancreatic Ductal Adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1586-1595.	2.5	8
34	ViroPanel. Journal of Molecular Diagnostics, 2020, 22, 476-487.	2.8	6
35	Diffuse Large B-Cell Lymphoma Patient-Derived Xenograft Models Capture Molecular and Biologic Heterogeneity and Inform Therapy. Blood, 2015, 126, 817-817.	1.4	5
36	Dissection of PIK3CA Aberration for Cervical Adenocarcinoma Outcomes. Cancers, 2021, 13, 3218.	3.7	2

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37	Comprehensive Genomic Analysis of Flow-Sorted Hodgkin Reed Sternberg Cells Reveals Additional Genetic Bases of Immune Evasion. Blood, 2018, 132, 1559-1559.	1.4	2
38	Recurrent Genetic HLA Loss in Acute Myeloid Leukemia Relapsed after Matched Unrelated Allogeneic Hematopoietic Cell Transplant. Blood, 2018, 132, 817-817.	1.4	0