Oliver A Hampton

List of Publications by Year
in descending order

27	1,453	759233 12	752698 20
papers	citations	h-index	g-index

28	28	28	3182
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Racial and ethnic differences in clonal hematopoiesis, tumor markers, and outcomes of patients with multiple myeloma. Blood Advances, 2022, 6, 3767-3778.	5.2	13
2	Metabolic Changes Are Associated with Melphalan Resistance in Multiple Myeloma. Journal of Proteome Research, 2021, 20, 3134-3149.	3.7	11
3	Racial and Ethnic Differences in Clonal Hematopoiesis, Tumor Markers, and Clinical Outcomes of Patients with Multiple Myeloma. Blood, 2021, 138, 402-402.	1.4	0
4	Plasma cell dependence on histone/protein deacetylase 11 reveals a therapeutic target in multiple myeloma. JCI Insight, 2021, 6, .	5.0	8
5	Acid Ceramidase (ASAH1) Mediates Intrinsic and Intercellular Transfer of Proteasome Inhibitor Resistance in Multiple Myeloma. Blood, 2021, 138, 1206-1206.	1.4	1
6	NF-Îºb and STAT3 co-operation enhances high glucose induced aggressiveness of cholangiocarcinoma cells. Life Sciences, 2020, 262, 118548.	4.3	9
7	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. PLoS ONE, 2020, 15, e0244558.	2.5	10
8	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. , 2020, 15, e0244558.		0
9	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. , 2020, 15, e0244558.		0
10	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. , 2020, 15, e0244558.		0
11	DACH1 mutation frequency in endometrial cancer is associated with high tumor mutation burden. , 2020, 15, e0244558.		0
12	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. Nature Genetics, 2017, 49, 1487-1494.	21.4	255
13	Therapy-related Acute Leukemia With Mixed Phenotype and Novel t(1:6)(q25;p23) After Treatment for High-risk Neuroblastoma. Journal of Pediatric Hematology/Oncology, 2017, 39, e486-e488.	0.6	2
14	Genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. Hepatology, 2017, 65, 104-121.	7.3	192
15	Non-malignant respiratory epithelial cells preferentially proliferate from resected non-small cell lung cancer specimens cultured under conditionally reprogrammed conditions. Oncotarget, 2017, 8, 11114-11126.	1.8	22
16	Activating MAPK1 (ERK2) mutation in an aggressive case of disseminated juvenile xanthogranuloma. Oncotarget, 2017, 8, 46065-46070.	1.8	24
17	Novel patient-derived xenograft and cell line models for therapeutic testing of pediatric liver cancer. Journal of Hepatology, 2016, 65, 325-333.	3.7	56
18	Significance of TP53 Mutation in Wilms Tumors with Diffuse Anaplasia: A Report from the Children's Oncology Group. Clinical Cancer Research, 2016, 22, 5582-5591.	7.0	82

#	Article	IF	Citations
19	Genomic Profiling of Pediatric Acute Myeloid Leukemia Reveals a Changing Mutational Landscape from Disease Diagnosis to Relapse. Cancer Research, 2016, 76, 2197-2205.	0.9	133
20	Integrated Genomic Analysis of Down Syndrome Acute Lymphoblastic Leukemia Reveals Recurrent Cancer Gene Alterations and Evidence of Frequent Subclonal Driver Events. Blood, 2016, 128, 4083-4083.	1.4	0
21	Initial testing (stage 1) of the PARP inhibitor BMN 673 by the pediatric preclinical testing program: PALB2 mutation predicts exceptional in vivo response to BMN 673. Pediatric Blood and Cancer, 2015, 62, 91-98.	1.5	65
22	Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. Cancer Cell, 2015, 27, 286-297.	16.8	244
23	Comparison Of Mutational Profiles Of Diagnosis and Relapsed Pediatric B-Acute Lymphoblastic Leukemia: A Report From The COG ALL Target Project. Blood, 2013, 122, 824-824.	1.4	4
24	Identification of Novel Somatic Mutations, Regions of Recurrent Loss of Heterozygosity (LOH) and Significant Clonal Evolution From Diagnosis to Relapse in Childhood AML Determined by Exome Capture Sequencing â€“ an NCI/COG Target AML Study. Blood, 2012, 120, 123-123.	1.4	2
25	Long-range massively parallel mate pair sequencing detects distinct mutations and similar patterns of structural mutability in two breast cancer cell lines. Cancer Genetics, 2011, 204, 447-457.	0.4	16
26	ReadDepth: A Parallel R Package for Detecting Copy Number Alterations from Short Sequencing Reads. PLoS ONE, 2011, 6, e16327.	2.5	193
27	A sequence-level map of chromosomal breakpoints in the MCF-7 breast cancer cell line yields insights into the evolution of a cancer genome. Genome Research, 2009, 19, 167-177.	5.5	111