Arpad M Danos

List of Publications by Year
in descending order

15	678	1307594 7	1281871 11
papers	citations	h-index	g-index

19	19	19	1844
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Standards for the classification of pathogenicity of somatic variants in cancer (oncogenicity): Joint recommendations of Clinical Genome Resource (ClinGen), Cancer Genomics Consortium (CGC), and Variant Interpretation for Cancer Consortium (VICC). Genetics in Medicine, 2022, 24, 986-998.	2.4	55
2	Standardized evidence-based approach for assessment of oncogenic and clinical significance of NTRK fusions. Cancer Genetics, 2022, 264-265, 50-59.	0.4	5
3	Large scale genotypeâ€•and phenotypeâ€driven machine learning in Von Hippelâ€Lindau disease. Human Mutation, 2022, 43, 1268-1285.	2.5	6
4	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
5	Abstract 449: A standard operating procedure for the curation of gene fusions. , 2021, , .		0
6	Expert Curation of Somatic FLT3 Variants By the Clingen Somatic Hematologic Cancer Taskforce (ClinGen HCT). Blood, 2021, 138, 4387-4387.	1.4	0
7	CIViCpy: A Python Software Development and Analysis Toolkit for the CIViC Knowledgebase. JCO Clinical Cancer Informatics, 2020, 4, 245-253.	2.1	10
8	Expert Curation of Somatic Variants in Hematological Malignancies By the Clingen Somatic Hematological Cancer Taskforce (ClinGen HCT). Blood, 2020, 136, 23-23.	1.4	0
9	Open-Sourced CIViC Annotation Pipeline to Identify and Annotate Clinically Relevant Variants Using Single-Molecule Molecular Inversion Probes. JCO Clinical Cancer Informatics, 2019, 3, 1-12.	2.1	6
10	Standard operating procedure for curation and clinical interpretation of variants in cancer. Genome Medicine, 2019, 11, 76.	8.2	16
11	Text-mining clinically relevant cancer biomarkers for curation into the CIViC database. Genome Medicine, 2019, 11, 78.	8.2	35
12	Standard operating procedure for somatic variant refinement of sequencing data with paired tumor andÂnormal samples. Genetics in Medicine, 2019, 21, 972-981.	2.4	67
13	Adapting crowdsourced clinical cancer curation in CIViC to the ClinGen minimum variant level data communityâ€driven standards. Human Mutation, 2018, 39, 1721-1732.	2.5	15
14	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	21.4	460
15	Deleterious Germline Mutations in Telomere Maintenance Genes Identified in a Subset of Patients with Myelodysplastic Syndrome and Idiopathic Pulmonary Fibrosis. Blood, 2016, 128, 4306-4306.	1.4	0