Alex H Wagner

List of Publications by Year
in descending order

38 papers	3,495 citations	361413 20 h-index	454955 30 g-index
50 all docs	50 docs citations	50 times ranked	8501 citing authors

#	Article	IF	Citations
1	Artificial intelligence and pathology: From principles to practice and future applications in histomorphology and molecular profiling. Seminars in Cancer Biology, 2022, 84, 129-143.	9.6	41
2	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
3	eP063: Genetic variants associated with childhood cancers: Curation initiatives of the ClinGen Somatic Cancer Pediatric Taskforce. Genetics in Medicine, 2022, 24, S41-S42.	2.4	0
4	eP055: The Clinical Genome Resource (ClinGen) Somatic Cancer Clinical Domain Working Group. Genetics in Medicine, 2022, 24, S34-S35.	2.4	0
5	A Simple Standard for Sharing Ontological Mappings (SSSOM). Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	23
6	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
7	The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 2022, 40, 817-820.	17.5	38
8	Integration of the Drugâ€“Gene Interaction Database (DGIdb 4.0) with open crowdsource efforts. Nucleic Acids Research, 2021, 49, D1144-D1151.	14.5	439
9	Abstract 210: Advancing knowledgebase representation of pediatric cancer variants through ClinGen/CIViC collaboration. , 2021, , .		0
10	Abstract 208: Development of Evidence Statement curation algorithms to aid cancer variant interpretation. , 2021, , .		0
11	Abstract 449: A standard operating procedure for the curation of gene fusions. , 2021, , .		0
12	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
13	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. Cell Genomics, 2021, 1, 100027.	6.5	18
14	Expert Curation of Somatic FLT3 Variants By the Clingen Somatic Hematologic Cancer Taskforce (ClinGen HCT). Blood, 2021, 138, 4387-4387.	1.4	0
15	Recommendations for future extensions to the HGNC gene fusion nomenclature. Leukemia, 2021, 35, 3611-3612.	7.2	1
16	Discovery of clinically relevant fusions in pediatric cancer. BMC Genomics, 2021, 22, 872.	2.8	13
17	Collaborative, Multidisciplinary Evaluation of Cancer Variants Through Virtual Molecular Tumor Boards Informs Local Clinical Practices. JCO Clinical Cancer Informatics, 2020, 4, 602-613.	2.1	26
18	FHIR Genomics: enabling standardization for precision medicine use cases. Npj Genomic Medicine, 2020, 5, 13.	3.8	32

#	Article	IF	Citations
19	CIViCpy: A Python Software Development and Analysis Toolkit for the CIViC Knowledgebase. JCO Clinical Cancer Informatics, 2020, 4, 245-253.	2.1	10
20	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
21	Creating a Variant Database for the American Society of Hematalogy By Consensus Variant Classification of Common Genes Associated with Hematologic Malignancies. Blood, 2020, 136, 4-5.	1.4	2
22	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
23	Standard operating procedure for curation and clinical interpretation of variants in cancer. Genome Medicine, 2019, 11, 76.	8.2	16
24	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
25	DGIdb 3.0: a redesign and expansion of the drugâ€“gene interaction database. Nucleic Acids Research, 2018, 46, D1068-D1073.	14.5	686
26	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. Nature Genetics, 2018, 50, 1735-1743.	21.4	62
27	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
28	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. Nature Communications, 2018, 9, 3787.	12.8	112
29	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	21.4	460
30	DGIdb 2.0: mining clinically relevant drugâ€“gene interactions. Nucleic Acids Research, 2016, 44, D1036-D1044.	14.5	359
31	DoCM: a database of curated mutations in cancer. Nature Methods, 2016, 13, 806-807.	19.0	96
32	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. Experimental Hematology, 2016, 44, 603-613.	0.4	44
33	GenVisR: Genomic Visualizations in R. Bioinformatics, 2016, 32, 3012-3014.	4.1	237
34	Transcriptomic analysis across nasal, temporal, and macular regions of human neural retina and RPE/choroid by RNA-Seq. Experimental Eye Research, 2014, 129, 93-106.	2.6	122
35	Prioritization of Retinal Disease Genes: An Integrative Approach. Human Mutation, 2013, 34, 853-859.	2.5	7
36	Exon-level expression profiling of ocular tissues. Experimental Eye Research, 2013, 111, 105-111.	2.6	94

#	Article	IF	Citations
37	Non-exomic and synonymous variants in ABCA4 are an important cause of Stargardt disease. Human Molecular Genetics, 2013, 22, 5136-5145.	2.9	159
38	Sequencing and disease variation detection tools and techniques. , 2011, , .		1