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	DGIdb 3.0: a redesign and expansion of the drugâ€“gene interaction database. Nucleic Acids Research, 2018, 46, D1068-D1073.	14.5	686
2	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	21.4	460
3	Integration of the Drugâ€“Gene Interaction Database (DGIdb 4.0) with open crowdsource efforts. Nucleic Acids Research, 2021, 49, D1144-D1151.	14.5	439
4	DGIdb 2.0: mining clinically relevant drugâ€“gene interactions. Nucleic Acids Research, 2016, 44, D1036-D1044.	14.5	359
5	GenVisR: Genomic Visualizations in R. Bioinformatics, 2016, 32, 3012-3014.	4.1	237
6	Non-exomic and synonymous variants in ABCA4 are an important cause of Stargardt disease. Human Molecular Genetics, 2013, 22, 5136-5145.	2.9	159
7	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
8	Recurrent WNT pathway alterations are frequent in relapsed small cell lung cancer. Nature Communications, 2018, 9, 3787.	12.8	112
9	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
10	DoCM: a database of curated mutations in cancer. Nature Methods, 2016, 13, 806-807.	19.0	96
11	Exon-level expression profiling of ocular tissues. Experimental Eye Research, 2013, 111, 105-111.	2.6	94
12	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
13	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
14	A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data. Nature Genetics, 2018, 50, 1735-1743.	21.4	62
15	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
16	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
17	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
18	The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 2022, 40, 817-820.	17.5	38

#	Article	IF	Citations
19	FHIR Genomics: enabling standardization for precision medicine use cases. Npj Genomic Medicine, 2020, 5, 13.	3.8	32
20	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
21	A Simple Standard for Sharing Ontological Mappings (SSSOM). Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	23
22	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. Cell Genomics, 2021, 1, 100027.	6.5	18
23	Standard operating procedure for curation and clinical interpretation of variants in cancer. Genome Medicine, 2019, 11, 76.	8.2	16
24	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
25	Discovery of clinically relevant fusions in pediatric cancer. BMC Genomics, 2021, 22, 872.	2.8	13
26	CIViCpy: A Python Software Development and Analysis Toolkit for the CIViC Knowledgebase. JCO Clinical Cancer Informatics, 2020, 4, 245-253.	2.1	10
27	Prioritization of Retinal Disease Genes: An Integrative Approach. Human Mutation, 2013, 34, 853-859.	2.5	7
28	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
29	Creating a Variant Database for the American Society of Hematology By Consensus Variant Classification of Common Genes Associated with Hematologic Malignancies. Blood, 2020, 136, 4-5.	1.4	2
30	Sequencing and disease variation detection tools and techniques. , 2011, , .		1
31	Recommendations for future extensions to the HGNC gene fusion nomenclature. Leukemia, 2021, 35, 3611-3612.	7.2	1
32	Abstract 210: Advancing knowledgebase representation of pediatric cancer variants through ClinGen/CIViC collaboration. , 2021, , .		0
33	Abstract 208: Development of Evidence Statement curation algorithms to aid cancer variant interpretation. , 2021, , .		0
34	Abstract 449: A standard operating procedure for the curation of gene fusions. , 2021, , .		0
35	Expert Curation of Somatic FLT3 Variants By the Clingen Somatic Hematologic Cancer Taskforce (ClinGen HCT). Blood, 2021, 138, 4387-4387.	1.4	0
36	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

#	Article	IF	Citations
37	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
38	eP055: The Clinical Genome Resource (ClinGen) Somatic Cancer Clinical Domain Working Group. Genetics in Medicine, 2022, 24, S34-S35.	2.4	0