Nicole L Washington

List of Publications by Year
in descending order

26 papers	5,565 citations	304368 22 h-index	552369 26 g-index
36 all docs	36 docs citations	36 times ranked	11072 citing authors

#	Article	IF	Citations
1	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
2	Integrative Analysis of the Caenorhabditis elegans Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
3	The Matchmaker Exchange: A Platform for Rare Disease Gene Discovery. Human Mutation, 2015, 36, 915-921.	1.1	390
4	Improved exome prioritization of disease genes through cross-species phenotype comparison. Genome Research, 2014, 24, 340-348.	2.4	300
5	Next-generation diagnostics and disease-gene discovery with the Exomiser. Nature Protocols, 2015, 10, 2004-2015.	5.5	296
6	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. Cell, 2021, 184, 2587-2594.e7.	13.5	285
7	Linking Human Diseases to Animal Models Using Ontology-Based Phenotype Annotation. PLoS Biology, 2009, 7, e1000247.	2.6	247
8	A Whole-Genome Analysis Framework for Effective Identification of Pathogenic Regulatory Variants in Mendelian Disease. American Journal of Human Genetics, 2016, 99, 595-606.	2.6	223
9	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. American Journal of Human Genetics, 2015, 97, 111-124.	2.6	203
10	Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. Nature, 2022, 609, 101-108.	13.7	200
11	Deletions of chromosomal regulatory boundaries are associated with congenital disease. Genome Biology, 2014, 15, 423.	3.8	144
12	FER-1 regulates Ca2+-mediated membrane fusion during C. elegans spermatogenesis. Journal of Cell Science, 2006, 119, 2552-2562.	1.2	126
13	modMine: flexible access to modENCODE data. Nucleic Acids Research, 2012, 40, D1082-D1088.	6.5	126
14	Population genetic screening efficiently identifies carriers of autosomal dominant diseases. Nature Medicine, 2020, 26, 1235-1239.	15.2	121
15	PhenomeCentral: A Portal for Phenotypic and Genotypic Matchmaking of Patients with Rare Genetic Diseases. Human Mutation, 2015, 36, 931-940.	1.1	107
16	Genome-wide rare variant analysis for thousands of phenotypes in over 70,000 exomes from two cohorts. Nature Communications, 2020, 11, 542.	5.8	101
17	Computational evaluation of exome sequence data using human and model organism phenotypes improves diagnostic efficiency. Genetics in Medicine, 2016, 18, 608-617.	1.1	85
18	Navigating the Phenotype Frontier: The Monarch Initiative. Genetics, 2016, 203, 1491-1495.	1.2	65

#	Article	IF	Citations
19	SARS-CoV-2 variant Delta rapidly displaced variant Alpha in the United States and led to higher viral loads. Cell Reports Medicine, 2022, 3, 100564.	3.3	61
20	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. Nature Metabolism, 2020, 2, 1126-1134.	5.1	43
21	Use of Model Organism and Disease Databases to Support Matchmaking for Human Disease Gene Discovery. Human Mutation, 2015, 36, 979-984.	1.1	36
22	The modENCODE Data Coordination Center: lessons in harvesting comprehensive experimental details. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar023.	1.4	32
23	Genetic counseling, 2030: An onâ€demand service tailored to the needs of a price conscious, genetically literate, and busy world. Journal of Genetic Counseling, 2019, 28, 456-465.	0.9	14
24	Positive predictive value highlights four novel candidates for actionable genetic screening from analysis of 220,000 clinicogenomic records. Genetics in Medicine, 2021, 23, 2300-2308.	1.1	13
25	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. PLoS ONE, 2021, 16, e0255402.	1.1	6
26	Comprehensive Allele Genotyping in Critical Pharmacogenes Reduces Residual Clinical Risk in Diverse Populations. Clinical Pharmacology and Therapeutics, 2021, 110, 759-767.	2.3	4