Nicole L Washington

List of Publications by Citations

34 papers	3,782 citations	22 h-index	36 g-index
36 ext. papers	4,884 ext. citations	15.9 avg, IF	4.16 L-index

#	Paper	IF	Citations
34	Identification of functional elements and regulatory circuits by Drosophila modENCODE. *Science*, **2010**, 330, 1787-97	33.3	892
33	Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project. *Science*, **2010**, 330, 1775-87	33.3	744
32	The Matchmaker Exchange: a platform for rare disease gene discovery. *Human Mutation*, **2015**, 36, 915-21	4.7	280
31	Improved exome prioritization of disease genes through cross-species phenotype comparison. *Genome Research*, **2014**, 24, 340-8	9.7	219
30	Linking human diseases to animal models using ontology-based phenotype annotation. *PLoS Biology*, **2009**, 7, e1000247	9.7	209
29	Next-generation diagnostics and disease-gene discovery with the Exomiser. *Nature Protocols*, **2015**, 10, 2004-15	18.8	159
28	The Human Phenotype Ontology: Semantic Unification of Common and Rare Disease. *American Journal of Human Genetics*, **2015**, 97, 111-24	11	147
27	A Whole-Genome Analysis Framework for Effective Identification of Pathogenic Regulatory Variants in Mendelian Disease. *American Journal of Human Genetics*, **2016**, 99, 595-606	11	136
26	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. *Cell*, **2021**, 184, 2587-2594.e7	38.2	132
25	FER-1 regulates Ca2+ -mediated membrane fusion during C. elegans spermatogenesis. *Journal of Cell Science*, **2006**, 119, 2552-62	5.3	110
24	Deletions of chromosomal regulatory boundaries are associated with congenital disease. *Genome Biology*, **2014**, 15, 423	18.3	108
23	modMine: flexible access to modENCODE data. *Nucleic Acids Research*, **2012**, 40, D1082-8	20.1	104
22	PhenomeCentral: a portal for phenotypic and genotypic matchmaking of patients with rare genetic diseases. *Human Mutation*, **2015**, 36, 931-40	4.7	91
21	Computational evaluation of exome sequence data using human and model organism phenotypes improves diagnostic efficiency. *Genetics in Medicine*, **2016**, 18, 608-17	8.1	69
20	Long-term COVID-19 symptoms in a large unselected population		53
19	Genome-wide rare variant analysis for thousands of phenotypes in over 70,000 exomes from two cohorts. *Nature Communications*, **2020**, 11, 542	17.4	47
18	Population genetic screening efficiently identifies carriers of autosomal dominant diseases. *Nature Medicine*, **2020**, 26, 1235-1239	50.5	47

17	Genomic epidemiology identifies emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States **2021**,		44
16	Navigating the Phenotype Frontier: The Monarch Initiative. *Genetics*, **2016**, 203, 1491-5	4	40
15	Use of model organism and disease databases to support matchmaking for human disease gene discovery. *Human Mutation*, **2015**, 36, 979-84	4.7	30
14	The modENCODE Data Coordination Center: lessons in harvesting comprehensive experimental details. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar023	5	27
13	SARS-CoV-2 variant Delta rapidly displaced variant Alpha in the United States and led to higher viral loads		27
12	S gene dropout patterns in SARS-CoV-2 tests suggest spread of the H69del/V70del mutation in the US		15
11	Genetic counseling, 2030: An on-demand service tailored to the needs of a price conscious, genetically literate, and busy world. *Journal of Genetic Counseling*, **2019**, 28, 456-465	2.5	9
10	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. *Nature Metabolism*, **2020**, 2, 1126-1134	14.6	9
9	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	18	6
8	Population Health Genetic Screening for Tier 1 Inherited Diseases in Northern Nevada: 90% of At-Risk Carriers are Missed		5
7	Evidence for SARS-CoV-2 Delta and Omicron co-infections and recombination		5
6	Revealing variants in SARS-CoV-2 interaction domain of ACE2 and loss of function intolerance through analysis of >200,000 exomes		4
5	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. *PLoS ONE*, **2021**, 16, e0255402	3.7	3
4	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility		1
3	HLA-A*03:01 is associated with increased risk of fever, chills, and more severe reaction to Pfizer-BioNTech COVID-19 vaccination		1
2	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	8.1	1
1	Comprehensive Allele Genotyping in Critical Pharmacogenes Reduces Residual Clinical Risk in Diverse Populations. *Clinical Pharmacology and Therapeutics*, **2021**, 110, 759-767	6.1	0