Deborah A Nickerson

List of Publications by Year
in descending order

53	22,589	172457	175258
papers	citations	29 h-index	52 g-index

64	64	64	44629
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	2.9	9
2	Diagnostic Accuracy of an At-Home, Rapid Self-test for Influenza: Prospective Comparative Accuracy Study. JMIR Public Health and Surveillance, 2022, 8, e28268.	2.6	5
3	CYP2C8, CYP2C9, and CYP2C19 Characterization Using Next-Generation Sequencing and Haplotype Analysis. Journal of Molecular Diagnostics, 2022, 24, 337-350.	2.8	23
4	Exome sequencing identifies genetic variants in anophthalmia and microphthalmia. American Journal of Medical Genetics, Part A, 2022, 188, 2376-2388.	1.2	2
5	Diversity of variant alleles encoding <scp>Kidd, Duffy, and Kell</scp> antigens in individuals with sickle cell disease using whole genome sequencing data from the <scp>NHLBI TOPMed Program</scp>. Transfusion, 2021, 61, 603-616.	1.6	7
6	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
7	Further delineation of van den Endeâ€Gupta syndrome: Genetic heterogeneity and overlap with congenital heart defects and skeletal malformations syndrome. American Journal of Medical Genetics, Part A, 2021, 185, 2136-2149.	1.2	5
8	Germline SAMD9L truncation variants trigger global translational repression. Journal of Experimental Medicine, 2021, 218, .	8.5	20
9	Comparable Specimen Collection from Both Ends of At-Home Midturbinate Swabs. Journal of Clinical Microbiology, 2021, 59, .	3.9	2
10	Evaluating Specimen Quality and Results from a Community-Wide, Home-Based Respiratory Surveillance Study. Journal of Clinical Microbiology, 2021, 59, .	3.9	17
11	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
12	Pharmacogenomics of Nicotine Metabolism: Novel CYP2A6 and CYP2B6 Genetic Variation Patterns in Alaska Native and American Indian Populations. Nicotine and Tobacco Research, 2020, 22, 910-918.	2.6	14
13	Interrogation of <scp>CYP</scp>2D6 Structural Variant Alleles Improves the Correlation Between <scp>CYP</scp>2D6 Genotype and <scp>CYP</scp>2D6â€Mediated Metabolic Activity. Clinical and Translational Science, 2020, 13, 147-156.	3.1	42
14	The Seattle Flu Study: a multiarm community-based prospective study protocol for assessing influenza prevalence, transmission and genomic epidemiology. BMJ Open, 2020, 10, e037295.	1.9	25
15	Mutations in MYLPF Cause a Novel Segmental Amyoplasia that Manifests as Distal Arthrogryposis. American Journal of Human Genetics, 2020, 107, 293-310.	6.2	21
16	Cryptic transmission of SARS-CoV-2 in Washington state. Science, 2020, 370, 571-575.	12.6	217
17	Multiplexed Functional Assessment of Genetic Variants in CARD11. American Journal of Human Genetics, 2020, 107, 1029-1043.	6.2	38
18	Whole-Genome Sequencing Identifies Novel Functional Loci Associated with Lung Function in Puerto Rican Youth. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 962-972.	5.6	11

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19	Early Detection of Covid-19 through a Citywide Pandemic Surveillance Platform. New England Journal of Medicine, 2020, 383, 185-187.	27.0	97
20	Stargazer: a software tool for calling star alleles from next-generation sequencing data using CYP2D6 as a model. Genetics in Medicine, 2019, 21, 361-372.	2.4	86
21	Genomic characterization of the RH locus detects complex and novel structural variation in multi-ethnic cohorts. Genetics in Medicine, 2019, 21, 477-486.	2.4	24
22	Mendelian Gene Discovery: Fast and Furious with No End in Sight. American Journal of Human Genetics, 2019, 105, 448-455.	6.2	166
23	Calling Star Alleles With Stargazer in 28 Pharmacogenes With Whole Genome Sequences. Clinical Pharmacology and Therapeutics, 2019, 106, 1328-1337.	4.7	57
24	GGC Repeat Expansion and Exon 1 Methylation of XYLT1 Is a Common Pathogenic Variant in Baratela-Scott Syndrome. American Journal of Human Genetics, 2019, 104, 35-44.	6.2	81
25	Hepatic Abundance and Activity of Androgen- and Drug-Metabolizing Enzyme UGT2B17 Are Associated with Genotype, Age, and Sex. Drug Metabolism and Disposition, 2018, 46, 888-896.	3.3	42
26	Multigenic Disease and Bilineal Inheritance in Dilated Cardiomyopathy Is Illustrated in Nonsegregating LMNA Pedigrees. Circulation Genomic and Precision Medicine, 2018, 11, e002038.	3.6	20
27	Genetic and Nongenetic Factors Associated with Protein Abundance of Flavin-Containing Monooxygenase 3 in Human Liver. Journal of Pharmacology and Experimental Therapeutics, 2017, 363, 265-274.	2.5	43
28	Influence of common and rare genetic variation on warfarin dose among Africanâ€“Americans and Europeanâ€“Americans using the exome array. Pharmacogenomics, 2017, 18, 1059-1073.	1.3	12
29	PADRE: Pedigree-Aware Distant-Relationship Estimation. American Journal of Human Genetics, 2016, 99, 154-162.	6.2	36
30	Analysis of exome sequencing data sets reveals structural variation in the coding region of ABO in individuals of African ancestry. Transfusion, 2016, 56, 2744-2749.	1.6	5
31	PGRNseq. Pharmacogenetics and Genomics, 2016, 26, 161-168.	1.5	93
32	Raceâ€Specific Influence of <scp>CYP</scp>4F2 on Dose and Risk of Hemorrhage Among Warfarin Users. Pharmacotherapy, 2016, 36, 263-272.	2.6	22
33	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
34	Maternal Modifiers and Parent-of-Origin Bias of the Autism-Associated 16p11.2 CNV. American Journal of Human Genetics, 2016, 98, 45-57.	6.2	55
35	PRIMUS: improving pedigree reconstruction using mitochondrial and Y haplotypes. Bioinformatics, 2016, 32, 596-598.	4.1	11
36	The Genetic Basis of Mendelian Phenotypes: Discoveries, Challenges, and Opportunities. American Journal of Human Genetics, 2015, 97, 199-215.	6.2	574

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37	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
38	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. Human Molecular Genetics, 2014, 23, 6607-6615.	2.9	14
39	RNF213 Rare Variants in an Ethnically Diverse Population With Moyamoya Disease. Stroke, 2014, 45, 3200-3207.	2.0	129
40	TCIRG1-Associated Congenital Neutropenia. Human Mutation, 2014, 35, 824-827.	2.5	35
41	Opsismodysplasia resulting from an insertion mutation in the SH2 domain, which destabilizes INPPL1. American Journal of Medical Genetics, Part A, 2014, 164, 2407-2411.	1.2	10
42	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
43	PRIMUS: Rapid Reconstruction of Pedigrees from Genome-wide Estimates of Identity by Descent. American Journal of Human Genetics, 2014, 95, 553-564.	6.2	129
44	Mutations in ECEL1 Cause Distal Arthrogryposis Type 5D. American Journal of Human Genetics, 2013, 92, 150-156.	6.2	71
45	Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. Nature, 2013, 493, 216-220.	27.8	898
46	Whole-Genome Analysis Reveals that Mutations in Inositol Polyphosphate Phosphatase-like 1 Cause Opsismodysplasia. American Journal of Human Genetics, 2013, 92, 137-143.	6.2	53
47	Utilizing Graph Theory to Select the Largest Set of Unrelated Individuals for Genetic Analysis. Genetic Epidemiology, 2013, 37, 136-141.	1.3	47
48	Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. Blood, 2013, 122, 590-597.	1.4	70
49	Copy number variation detection and genotyping from exome sequence data. Genome Research, 2012, 22, 1525-1532.	5.5	550
50	Optimal Unified Approach for Rare-Variant Association Testing with Application to Small-Sample Case-Control Whole-Exome Sequencing Studies. American Journal of Human Genetics, 2012, 91, 224-237.	6.2	880
51	De novo rates and selection of large copy number variation. Genome Research, 2010, 20, 1469-1481.	5.5	264
52	Genetic Ancestry in Lung-Function Predictions. New England Journal of Medicine, 2010, 363, 321-330.	27.0	230
53	Targeted capture and massively parallel sequencing of 12 human exomes. Nature, 2009, 461, 272-276.	27.8	1,801