Sarah Catherine Nelson

List of Publications by Year
in descending order

49 papers	5,442 citations	147801 31 h-index	197818 49 g-index
52 all docs	52 docs citations	52 times ranked	12429 citing authors

#	Article	IF	Citations
1	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
3	Whoâ€™s on third? Regulation of third-party genetic interpretation services. Genetics in Medicine, 2020, 22, 4-11.	2.4	39
4	Recipient and donor genetic variants associated with mortality after allogeneic hematopoietic cell transplantation. Blood Advances, 2020, 4, 3224-3233.	5.2	20
5	Third-Party Genetic Interpretation Tools: A Mixed-Methods Study of Consumer Motivation and Behavior. American Journal of Human Genetics, 2019, 105, 122-131.	6.2	42
6	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679
7	Genome-wide association reveals contribution of MRAS to painful temporomandibular disorder in males. Pain, 2019, 160, 579-591.	4.2	37
8	Genomic analyses in African populations identify novel risk loci for cleft palate. Human Molecular Genetics, 2019, 28, 1038-1051.	2.9	61
9	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377
10	â€œBridge to the Literatureâ€? Thirdâ€Party Genetic Interpretation Tools and the Views of Tool Developers. Journal of Genetic Counseling, 2018, 27, 770-781.	1.6	28
11	Genetic variants in sex hormone pathways and the risk of type 2 diabetes among African American, Hispanic American, and European American postmenopausal women in the US. Journal of Diabetes, 2018, 10, 524-533.	1.8	3
12	A content analysis of the views of genetics professionals on race, ancestry, and genetics. AJOB Empirical Bioethics, 2018, 9, 222-234.	1.6	22
13	APPLaUD: access for patients and participants to individual level uninterpreted genomic data. Human Genomics, 2018, 12, 7.	2.9	45
14	Genome-wide association study of familial lung cancer. Carcinogenesis, 2018, 39, 1135-1140.	2.8	42
15	Genome-wide minor histocompatibility matching as related to the risk of graft-versus-host disease. Blood, 2017, 129, 791-798.	1.4	109
16	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	21.4	114
17	Geneticists should offer data to participants. Nature, 2016, 539, 7-7.	27.8	14
18	Use of metaphors about exome and whole genome sequencing. American Journal of Medical Genetics, Part A, 2016, 170, 1127-1133.	1.2	4

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19	Improved imputation accuracy in Hispanic/Latino populations with larger and more diverse reference panels: applications in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Human Molecular Genetics, 2016, 25, 3245-3254.	2.9	23
20	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	6.2	71
21	Shared genetic susceptibility of vascular-related biomarkers with ischemic and recurrent stroke. Neurology, 2016, 86, 351-359.	1.1	33
22	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2016, 98, 165-184.	6.2	266
23	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
24	How Metaphors About the Genome Constrain CRISPR Metaphors: Separating the â€œTextâ€•From Its â€œEditorâ€• American Journal of Bioethics, 2015, 15, 60-62.	0.9	10
25	Genome-Wide Meta-Analysis of Homocysteine and Methionine Metabolism Identifies Five One Carbon Metabolism Loci and a Novel Association of ALDH1L1 with Ischemic Stroke. PLoS Genetics, 2014, 10, e1004214.	3.5	69
26	Acquired chromosomal anomalies in chronic lymphocytic leukemia patients compared with more than 50,000 quasi-normal participants. Cancer Genetics, 2014, 207, 19-30.	0.4	5
27	Imputation-Based Genomic Coverage Assessments of Current Human Genotyping Arrays. G3: Genes, Genomes, Genetics, 2013, 3, 1795-1807.	1.8	43
28	Epigenetic regulation of COL15A1 in smooth muscle cell replicative aging and atherosclerosis. Human Molecular Genetics, 2013, 22, 5107-5120.	2.9	66
29	Genome-Wide Linkage Analysis of Cardiovascular Disease Biomarkers in a Large, Multigenerational Family. PLoS ONE, 2013, 8, e71779.	2.5	12
30	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormoneâ€“Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	3.5	151
31	GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. Bioinformatics, 2012, 28, 3329-3331.	4.1	177
32	Is â€˜forwardâ€™ the same as â€˜plusâ€™?â€¦ and other adventures in SNP allele nomenclature. Trends in Genetics, 2012, 28, 361-363.	6.7	21
33	Genome-wide association Scan of dental caries in the permanent dentition. BMC Oral Health, 2012, 12, 57.	2.3	69
34	Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nature Genetics, 2012, 44, 642-650.	21.4	511
35	Genetic variants associated with the white blood cell count in 13,923 subjects in the eMERGE Network. Human Genetics, 2012, 131, 639-652.	3.8	103
36	Branched-chain amino acid levels are associated with improvement in insulin resistance with weight loss. Diabetologia, 2012, 55, 321-330.	6.3	309

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37	Polymorphic variants in tenascin-C (TNC) are associated with atherosclerosis and coronary artery disease. Human Genetics, 2011, 129, 641-654.	3.8	25
38	Genome-Wide Association Analysis of Ischemic Stroke in Young Adults. G3: Genes, Genomes, Genetics, 2011, 1, 505-514.	1.8	34
39	Genomeâ€wide linkage analysis of quantitative biomarker traits of osteoarthritis in a large, multigenerational extended family. Arthritis and Rheumatism, 2010, 62, 781-790.	6.7	20
40	Aging-related atherosclerosis is exacerbated by arterial expression of tumor necrosis factor receptor-1: evidence from mouse models and human association studies. Human Molecular Genetics, 2010, 19, 2754-2766.	2.9	32
41	Neuropeptide Y Gene Polymorphisms Confer Risk of Early-Onset Atherosclerosis. PLoS Genetics, 2009, 5, e1000318.	3.5	87
42	Genetic effects in the leukotriene biosynthesis pathway and association with atherosclerosis. Human Genetics, 2009, 125, 217-229.	3.8	51
43	A general integrative genomic feature transcription factor binding site prediction method applied to analysis of USF1 binding in cardiovascular disease. Human Genomics, 2009, 3, 221.	2.9	7
44	Genetic and functional association of FAM5C with myocardial infarction. BMC Medical Genetics, 2008, 9, 33.	2.1	31
45	ALOX5AP variants are associated with in-stent restenosis after percutaneous coronary intervention. Atherosclerosis, 2008, 201, 148-154.	0.8	22
46	Comprehensive genetic analysis of the platelet activating factor acetylhydrolase (PLA2G7) gene and cardiovascular disease in caseâ€“control and family datasets. Human Molecular Genetics, 2008, 17, 1318-1328.	2.9	66
47	Peakwide Mapping on Chromosome 3q13 Identifies the Kalirin Gene as a Novel Candidate Gene for Coronary Artery Disease. American Journal of Human Genetics, 2007, 80, 650-663.	6.2	110
48	GATA2 Is Associated with Familial Early-Onset Coronary Artery Disease. PLoS Genetics, 2006, 2, e139.	3.5	82
49	Mice Heterozygous for Atp10c, a Putative Amphipath, Represent a Novel Model of Obesity and Type 2 Diabetes. Journal of Nutrition, 2004, 134, 799-805.	2.9	79