Jennifer Elizabeth Below

List of Publications by Year
in descending order

51 papers	5,537 citations	218677 26 h-index	243625 44 g-index
51 all docs	51 docs citations	51 times ranked	12920 citing authors

#	Article	IF	Citations
1	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
2	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
3	Germline BAP1 mutations predispose to malignant mesothelioma. Nature Genetics, 2011, 43, 1022-1025.	21.4	924
4	Insulin gene mutations as a cause of permanent neonatal diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15040-15044.	7.1	494
5	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	27.8	282
6	Genome-wide meta-analysis for severe diabetic retinopathy. Human Molecular Genetics, 2011, 20, 2472-2481.	2.9	141
7	Ataxia-Pancytopenia Syndrome Is Caused by Missense Mutations in SAMD9L. American Journal of Human Genetics, 2016, 98, 1146-1158.	6.2	136
8	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
9	Identification of Type 2 Diabetes Genes in Mexican Americans Through Genome-Wide Association Studies. Diabetes, 2007, 56, 3033-3044.	0.6	125
10	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 886-897.	5.6	107
11	A Genome-Wide Association Study Identifies a Novel Major Locus for Glycemic Control in Type 1 Diabetes, as Measured by Both A1C and Glucose. Diabetes, 2010, 59, 539-549.	0.6	103
12	The population genomics of rhesus macaques (Macaca mulatta) based on whole-genome sequences. Genome Research, 2016, 26, 1651-1662.	5.5	101
13	Cross-Tissue and Tissue-Specific eQTLs: Partitioning the Heritability of a Complex Trait. American Journal of Human Genetics, 2014, 95, 521-534.	6.2	82
14	Genetic Variants Associated With Quantitative Glucose Homeostasis Traits Translate to Type 2 Diabetes in Mexican Americans: The GUARDIAN (Genetics Underlying Diabetes in Hispanics) Consortium. Diabetes, 2015, 64, 1853-1866.	0.6	77
15	Mutations in ECEL1 Cause Distal Arthrogryposis Type 5D. American Journal of Human Genetics, 2013, 92, 150-156.	6.2	71
16	Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apneaâ€“related Quantitative Trait Locus in Men. American Journal of Respiratory Cell and Molecular Biology, 2018, 58, 391-401.	2.9	65
17	Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects and tissue-specific enrichment of eQTLs. Scientific Reports, 2016, 6, 19429.	3.3	63
18	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

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19	Spoiling the Whole Bunch: Quality Control Aimed at Preserving the Integrity of High-Throughput Genotyping. American Journal of Human Genetics, 2010, 87, 123-128.	6.2	48
20	Utilizing Graph Theory to Select the Largest Set of Unrelated Individuals for Genetic Analysis. Genetic Epidemiology, 2013, 37, 136-141.	1.3	47
21	Secondary findings and carrier test frequencies in a large multiethnic sample. Genome Medicine, 2015, 7, 54.	8.2	47
22	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
23	Correlation of rare coding variants in the gene encoding human glucokinase regulatory protein with phenotypic, cellular, and kinetic outcomes. Journal of Clinical Investigation, 2012, 122, 205-217.	8.2	41
24	Obesity and hyperinsulinemia in a family with pancreatic agenesis and MODY caused by the IPF1 mutation Pro63fsX60. Translational Research, 2010, 156, 7-14.	5.0	39
25	PADRE: Pedigree-Aware Distant-Relationship Estimation. American Journal of Human Genetics, 2016, 99, 154-162.	6.2	36
26	TCIRG1-Associated Congenital Neutropenia. Human Mutation, 2014, 35, 824-827.	2.5	35
27	Beyond type 2 diabetes, obesity and hypertension: an axis including sleep apnea, left ventricular hypertrophy, endothelial dysfunction, and aortic stiffness among Mexican Americans in Starr County, Texas. Cardiovascular Diabetology, 2016, 15, 86.	6.8	32
28	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
29	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	7.1	28
30	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. Scientific Reports, 2017, 7, 17075.	3.3	23
31	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimerâ€™s Disease Sequencing Project. Dementia and Geriatric Cognitive Disorders, 2018, 45, 1-17.	1.5	22
32	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	2.9	21
33	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
34	Factors that Impact Susceptibility to Fiber-Induced Health Effects. Journal of Toxicology and Environmental Health - Part B: Critical Reviews, 2011, 14, 246-266.	6.5	19
35	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. Lipids in Health and Disease, 2017, 16, 200.	3.0	18
36	Genome-Wide Association Study of Staphylococcus aureus Carriage in a Community-Based Sample of Mexican-Americans in Starr County, Texas. PLoS ONE, 2015, 10, e0142130.	2.5	17

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37	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.6	17
38	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. PLoS Genetics, 2020, 16, e1008684.	3.5	17
39	Admixture mapping in two Mexican samples identifies significant associations of locus ancestry with triglyceride levels in the BUD13/ZNF259/APOA5 region and fine mapping points to rs964184 as the main driver of the association signal. PLoS ONE, 2017, 12, e0172880.	2.5	16
40	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	6.3	15
41	PRIMUS: improving pedigree reconstruction using mitochondrial and Y haplotypes. Bioinformatics, 2016, 32, 596-598.	4.1	11
42	Genome-Wide Studies of Type 2 Diabetes and Lipid Traits in Hispanics. Current Diabetes Reports, 2016, 16, 41.	4.2	10
43	Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. Genetics, 2018, 209, 607-616.	2.9	8
44	Automated Phenotyping Tool for Identifying Developmental Language Disorder Cases in Health Systems Data (APT-DLD): A New Research Algorithm for Deployment in Large-Scale Electronic Health Record Systems. Journal of Speech, Language, and Hearing Research, 2020, 63, 3019-3035.	1.6	7
45	Tissueâ€specific genetically regulated expression in lateâ€onset Alzheimerâ€™s disease implicates risk genes within known and 30 novel loci. Alzheimer's and Dementia, 2020, 16, e039475.	0.8	0
46	Title is missing!. , 2020, 16, e1008684.		0
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