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	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	6.3	15
2	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
3	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	27.8	282
4	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
5	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
6	Title is missing!. , 2020, 16, e1008684.		0
7	Title is missing!. , 2020, 16, e1008684.		0
8	Title is missing!. , 2020, 16, e1008684.		0
9	Title is missing!. , 2020, 16, e1008684.		0
10	Title is missing!. , 2020, 16, e1008684.		0
11	Title is missing!. , 2020, 16, e1008684.		0
12	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
13	Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. Genetics, 2018, 209, 607-616.	2.9	8
14	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
15	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
16	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
17	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
18	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31

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19	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
20	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
21	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
22	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
23	PADRE: Pedigree-Aware Distant-Relationship Estimation. American Journal of Human Genetics, 2016, 99, 154-162.	6.2	36
24	Genome-Wide Studies of Type 2 Diabetes and Lipid Traits in Hispanics. Current Diabetes Reports, 2016, 16, 41.	4.2	10
25	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
26	The population genomics of rhesus macaques (Macaca mulatta) based on whole-genome sequences. Genome Research, 2016, 26, 1651-1662.	5.5	101
27	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	2.9	21
28	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.6	17
29	Ataxia-Pancytopenia Syndrome Is Caused by Missense Mutations in SAMD9L. American Journal of Human Genetics, 2016, 98, 1146-1158.	6.2	136
30	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
31	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
32	PRIMUS: improving pedigree reconstruction using mitochondrial and Y haplotypes. Bioinformatics, 2016, 32, 596-598.	4.1	11
33	Secondary findings and carrier test frequencies in a large multiethnic sample. Genome Medicine, 2015, 7, 54.	8.2	47
34	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
35	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
36	TCIRG1-Associated Congenital Neutropenia. Human Mutation, 2014, 35, 824-827.	2.5	35

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37	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
38	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
39	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
40	Mutations in ECEL1 Cause Distal Arthrogryposis Type 5D. American Journal of Human Genetics, 2013, 92, 150-156.	6.2	71
41	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
42	Utilizing Graph Theory to Select the Largest Set of Unrelated Individuals for Genetic Analysis. Genetic Epidemiology, 2013, 37, 136-141.	1.3	47
43	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
44	Germline BAP1 mutations predispose to malignant mesothelioma. Nature Genetics, 2011, 43, 1022-1025.	21.4	924
45	Genome-wide meta-analysis for severe diabetic retinopathy. Human Molecular Genetics, 2011, 20, 2472-2481.	2.9	141
46	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
47	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
48	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
49	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
50	Identification of Type 2 Diabetes Genes in Mexican Americans Through Genome-Wide Association Studies. Diabetes, 2007, 56, 3033-3044.	0.6	125
51	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