

Jennifer E. Below

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

8,206
citations

126907

33
h-index

54911

84
g-index

99
all docs

99
docs citations

99
times ranked

16473
citing authors

#	ARTICLE	IF	CITATIONS
1	Associations of carotid intima media thickness with gene expression in whole blood and genetically predicted gene expression across 48 tissues. <i>Human Molecular Genetics</i> , 2022, 31, 1171-1182.	2.9	4
2	Gut microbiome features associated with liver fibrosis in Hispanics, a population at high risk for fatty liver disease. <i>Hepatology</i> , 2022, 75, 955-967.	7.3	25
3	Population-based genetic effects for developmental stuttering. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100073.	1.7	4
4	Novel diabetes gene discovery through comprehensive characterization and integrative analysis of longitudinal gene expression changes. <i>Human Molecular Genetics</i> , 2022, 31, 3191-3205.	2.9	4
5	Test of Prosody via Syllable Emphasis (â€œTOPsyâ€): Psychometric Validation of a Brief Scalable Test of Lexical Stress Perception. <i>Frontiers in Neuroscience</i> , 2022, 16, 765945.	2.8	3
6	Polygenic risk impacts <i>PDGFRA</i> mutation penetrance in non-syndromic cleft lip and palate. <i>Human Molecular Genetics</i> , 2022, 31, 2348-2357.	2.9	7
7	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. <i>Diabetologia</i> , 2022, 65, 477-489.	6.3	15
8	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. <i>Communications Biology</i> , 2022, 5, 329.	4.4	21
9	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traitsâ€”The Hispanic/Latino Anthropometry Consortium. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100099.	1.7	3
10	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
11	Host genetic effects in pneumonia. <i>American Journal of Human Genetics</i> , 2021, 108, 194-201.	6.2	17
12	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100029.	1.7	23
13	Revisiting Some Useful Statistical Guidelines in Circulation Research in Response to a Changing Landscape. <i>Circulation Research</i> , 2021, 128, 1724-1727.	4.5	1
14	Identifying developmental stuttering and associated comorbidities in electronic health records and creating a phenome risk classifier. <i>Journal of Fluency Disorders</i> , 2021, 68, 105847.	1.7	17
15	Genome-wide association study of body fat distribution traits in Hispanics/Latinos from the HCHS/SOL. <i>Human Molecular Genetics</i> , 2021, 30, 2190-2204.	2.9	8
16	Recommendations for Statistical Reporting in Cardiovascular Medicine: A Special Report From the American Heart Association. <i>Circulation</i> , 2021, 144, e70-e91.	1.6	36
17	Pedigree reconstruction and distant pairwise relatedness estimation from genome sequence data: A demonstration in a population of rhesus macaques (<i>Macaca mulatta</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 1333-1346.	4.8	3
18	Phenome risk classification enables phenotypic imputation and gene discovery in developmental stuttering. <i>American Journal of Human Genetics</i> , 2021, 108, 2271-2283.	6.2	11

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19	Genetically regulated expression in late-onset Alzheimer's disease implicates risk genes within known and novel loci. <i>Translational Psychiatry</i> , 2021, 11, 618.	4.8	17
20	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. <i>Molecular Psychiatry</i> , 2020, 25, 1859-1875.	7.9	191
21	A diagnostic ceiling for exome sequencing in cerebellar ataxia and related neurological disorders. <i>Human Mutation</i> , 2020, 41, 487-501.	2.5	58
22	Alternative Applications of Genotyping Array Data Using Multivariant Methods. <i>Trends in Genetics</i> , 2020, 36, 857-867.	6.7	7
23	Optimizing Genetic Analyses of Serum Lipids in Longitudinal Data. <i>Circulation Research</i> , 2020, 127, 1337-1339.	4.5	0
24	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245.	27.8	282
25	Importance of Genetic Studies of Cardiometabolic Disease in Diverse Populations. <i>Circulation Research</i> , 2020, 126, 1816-1840.	4.5	19
26	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>PLoS Genetics</i> , 2020, 16, e1008684.	3.5	17
27	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. <i>Journal of Speech, Language, and Hearing Research</i> , 2020, 63, 3019-3035.	1.6	7
28	Title is missing!. , 2020, 16, e1008684.		0
29	Title is missing!. , 2020, 16, e1008684.		0
30	Title is missing!. , 2020, 16, e1008684.		0
31	Title is missing!. , 2020, 16, e1008684.		0
32	Title is missing!. , 2020, 16, e1008684.		0
33	Title is missing!. , 2020, 16, e1008684.		0
34	A Genome-Wide Association Study Identifies Blood Disorder-Related Variants Influencing Hemoglobin A1c With Implications for Glycemic Status in U.S. Hispanics/Latinos. <i>Diabetes Care</i> , 2019, 42, 1784-1791.	8.6	9
35	CWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. <i>PLoS ONE</i> , 2019, 14, e0217796.	2.5	8
36	My Cousin Also Has Atrial Fibrillation. <i>JACC: Clinical Electrophysiology</i> , 2019, 5, 501-503.	3.2	1

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37	Associations of variants in the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. <i>PLoS Genetics</i> , 2019, 15, e1007739.	3.5	28
38	GWAS and Beyond: Using Omics Approaches to Interpret SNP Associations. <i>Current Genetic Medicine Reports</i> , 2019, 7, 30-40.	1.9	4
39	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. <i>Human Molecular Genetics</i> , 2019, 28, 675-687.	2.9	41
40	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. <i>Human Molecular Genetics</i> , 2019, 28, 1212-1224.	2.9	12
41	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimer's Disease Sequencing Project. <i>Dementia and Geriatric Cognitive Disorders</i> , 2018, 45, 1-17.	1.5	22
42	Expanding the global prevalence of spinocerebellar ataxia type 42. <i>Neurology: Genetics</i> , 2018, 4, e232.	1.9	14
43	Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. <i>Genetics</i> , 2018, 209, 607-616.	2.9	8
44	Critical Evaluation of Data Requires Rigorous but Broadly Based Statistical Inference. <i>Circulation Research</i> , 2018, 122, 1049-1051.	4.5	0
45	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 379-384.	7.1	28
46	Multiethnic Meta-Analysis Identifies <i>RAI1</i> as a Possible Obstructive Sleep Apnea-related Quantitative Trait Locus in Men. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2018, 58, 391-401.	2.9	65
47	Whole-Exome Sequencing Identifies Novel Variants for Tooth Agenesis. <i>Journal of Dental Research</i> , 2018, 97, 49-59.	5.2	44
48	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	21.4	1,331
49	Complex patterns of direct and indirect association between the transcription Factor-7 like 2 gene, body mass index and type 2 diabetes diagnosis in adulthood in the Hispanic Community Health Study/Study of Latinos. <i>BMC Obesity</i> , 2018, 5, 26.	3.1	6
50	Managing Deviant Behavior in Online Communities III. , 2018, , .		4
51	Identification of likely pathogenic and known variants in <i>TSPEAR</i> , <i>LAMB3</i> , <i>BCOR</i> , and <i>WNT10A</i> in four Turkish families with tooth agenesis. <i>Human Genetics</i> , 2018, 137, 689-703.	3.8	24
52	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.6	47
53	Prevalence of spinocerebellar ataxia 36 in a US population. <i>Neurology: Genetics</i> , 2017, 3, e174.	1.9	15
54	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. <i>Scientific Reports</i> , 2017, 7, 17075.	3.3	23

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55	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
56	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. <i>Lipids in Health and Disease</i> , 2017, 16, 200.	3.0	18
57	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. <i>PLoS ONE</i> , 2017, 12, e0172880.	2.5	16
58	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. <i>Cardiovascular Diabetology</i> , 2016, 15, 86.	6.8	32
59	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
60	PADRE: Pedigree-Aware Distant-Relationship Estimation. <i>American Journal of Human Genetics</i> , 2016, 99, 154-162.	6.2	36
61	Genome-Wide Studies of Type 2 Diabetes and Lipid Traits in Hispanics. <i>Current Diabetes Reports</i> , 2016, 16, 41.	4.2	10
62	Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects and tissue-specific enrichment of eQTLs. <i>Scientific Reports</i> , 2016, 6, 19429.	3.3	63
63	The population genomics of rhesus macaques (<i>Macaca mulatta</i>) based on whole-genome sequences. <i>Genome Research</i> , 2016, 26, 1651-1662.	5.5	101
64	Variants in angiotensin-converting enzyme 2 (<i>ANGPT2</i>) contribute to variation in nocturnal oxyhaemoglobin saturation level. <i>Human Molecular Genetics</i> , 2016, 25, ddw324.	2.9	21
65	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. <i>BMC Proceedings</i> , 2016, 10, 71-77.	1.6	17
66	Ataxia-Pancytopenia Syndrome Is Caused by Missense Mutations in <i>SAMD9L</i> . <i>American Journal of Human Genetics</i> , 2016, 98, 1146-1158.	6.2	136
67	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 886-897.	5.6	107
68	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016, 25, 2070-2081.	2.9	21
69	PRIMUS: improving pedigree reconstruction using mitochondrial and Y haplotypes. <i>Bioinformatics</i> , 2016, 32, 596-598.	4.1	11
70	Secondary findings and carrier test frequencies in a large multiethnic sample. <i>Genome Medicine</i> , 2015, 7, 54.	8.2	47
71	Genome-Wide Association Study of <i>Staphylococcus aureus</i> Carriage in a Community-Based Sample of Mexican-Americans in Starr County, Texas. <i>PLoS ONE</i> , 2015, 10, e0142130.	2.5	17
72	Genetic Variants Associated With Quantitative Glucose Homeostasis Traits Translate to Type 2 Diabetes in Mexican Americans: The GUARDIAN (Genetics Underlying Diabetes in Hispanics) Consortium. <i>Diabetes</i> , 2015, 64, 1853-1866.	0.6	77

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73	<i>TCIRG1</i> -Associated Congenital Neutropenia. <i>Human Mutation</i> , 2014, 35, 824-827.	2.5	35
74	Rare variants in <i>PPARG</i> with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13127-13132.	7.1	152
75	PRIMUS: Rapid Reconstruction of Pedigrees from Genome-wide Estimates of Identity by Descent. <i>American Journal of Human Genetics</i> , 2014, 95, 553-564.	6.2	129
76	Cross-Tissue and Tissue-Specific eQTLs: Partitioning the Heritability of a Complex Trait. <i>American Journal of Human Genetics</i> , 2014, 95, 521-534.	6.2	82
77	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
78	Mutations in <i>ECEL1</i> Cause Distal Arthrogyrosis Type 5D. <i>American Journal of Human Genetics</i> , 2013, 92, 150-156.	6.2	71
79	Whole-Genome Analysis Reveals that Mutations in Inositol Polyphosphate Phosphatase-like 1 Cause Opsismodysplasia. <i>American Journal of Human Genetics</i> , 2013, 92, 137-143.	6.2	53
80	Utilizing Graph Theory to Select the Largest Set of Unrelated Individuals for Genetic Analysis. <i>Genetic Epidemiology</i> , 2013, 37, 136-141.	1.3	47
81	Correlation of rare coding variants in the gene encoding human glucokinase regulatory protein with phenotypic, cellular, and kinetic outcomes. <i>Journal of Clinical Investigation</i> , 2012, 122, 205-217.	8.2	41
82	Genome-wide association study of type 2 diabetes in a sample from Mexico City and a meta-analysis of a Mexican-American sample from Starr County, Texas. <i>Diabetologia</i> , 2011, 54, 2038-2046.	6.3	114
83	Genome-wide association and meta-analysis in populations from Starr County, Texas, and Mexico City identify type 2 diabetes susceptibility loci and enrichment for expression quantitative trait loci in top signals. <i>Diabetologia</i> , 2011, 54, 2047-2055.	6.3	106
84	Germline <i>BAP1</i> mutations predispose to malignant mesothelioma. <i>Nature Genetics</i> , 2011, 43, 1022-1025.	21.4	924
85	Genome-wide meta-analysis for severe diabetic retinopathy. <i>Human Molecular Genetics</i> , 2011, 20, 2472-2481.	2.9	141
86	Factors that Impact Susceptibility to Fiber-Induced Health Effects. <i>Journal of Toxicology and Environmental Health - Part B: Critical Reviews</i> , 2011, 14, 246-266.	6.5	19
87	Spoiling the Whole Bunch: Quality Control Aimed at Preserving the Integrity of High-Throughput Genotyping. <i>American Journal of Human Genetics</i> , 2010, 87, 123-128.	6.2	48
88	A Genome-Wide Association Study Identifies a Novel Major Locus for Glycemic Control in Type 1 Diabetes, as Measured by Both A1C and Glucose. <i>Diabetes</i> , 2010, 59, 539-549.	0.6	103
89	Obesity and hyperinsulinemia in a family with pancreatic agenesis and MODY caused by the <i>IPF1</i> mutation Pro63fsX60. <i>Translational Research</i> , 2010, 156, 7-14.	5.0	39
90	T2051 Genetic Analysis of Base Excision Repair Genes in African-Americans and Caucasians with Colorectal Cancer. <i>Gastroenterology</i> , 2008, 134, A-608-A-609.	1.3	0

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91	Identification of Type 2 Diabetes Genes in Mexican Americans Through Genome-Wide Association Studies. <i>Diabetes</i> , 2007, 56, 3033-3044.	0.6	125
92	Insulin gene mutations as a cause of permanent neonatal diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15040-15044.	7.1	494