Jennifer E. Below

List of Publications by Year
in descending order

92 papers	8,206 citations	126708 33 h-index	54797 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. Human Molecular Genetics, 2022, 31, 1171-1182.	1.4	4
2	Gut microbiome features associated with liver fibrosis in Hispanics, a population at high risk for fatty liver disease. Hepatology, 2022, 75, 955-967.	3.6	25
3	Population-based genetic effects for developmental stuttering. Human Genetics and Genomics Advances, 2022, 3, 100073.	1.0	4
4	Novel diabetes gene discovery through comprehensive characterization and integrative analysis of longitudinal gene expression changes. Human Molecular Genetics, 2022, 31, 3191-3205.	1.4	4
5	Test of Prosody via Syllable Emphasis (â€œTOPsyâ€): Psychometric Validation of a Brief Scalable Test of Lexical Stress Perception. Frontiers in Neuroscience, 2022, 16, 765945.	1.4	3
6	Polygenic risk impactsPDGFRAmutation penetrance in non-syndromic cleft lip and palate. Human Molecular Genetics, 2022, 31, 2348-2357.	1.4	7
7	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	2.9	15
8	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. Communications Biology, 2022, 5, 329.	2.0	21
9	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traitsâ€”The Hispanic/Latino Anthropometry Consortium. Human Genetics and Genomics Advances, 2022, 3, 100099.	1.0	3
10	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
11	Host genetic effects in pneumonia. American Journal of Human Genetics, 2021, 108, 194-201.	2.6	17
12	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.0	23
13	Revisiting Some Useful Statistical Guidelines in Circulation Research in Response to a Changing Landscape. Circulation Research, 2021, 128, 1724-1727.	2.0	1
14	Identifying developmental stuttering and associated comorbidities in electronic health records and creating a phenome risk classifier. Journal of Fluency Disorders, 2021, 68, 105847.	0.7	17
15	Genome-wide association study of body fat distribution traits in Hispanics/Latinos from the HCHS/SOL. Human Molecular Genetics, 2021, 30, 2190-2204.	1.4	8
16	Recommendations for Statistical Reporting in Cardiovascular Medicine: A Special Report From the American Heart Association. Circulation, 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 (Macaca mulatta). Molecular Ecology Resources, 2021, 21, 1333-1346.	2.2	3
18	Phenome risk classification enables phenotypic imputation and gene discovery in developmental stuttering. American Journal of Human Genetics, 2021, 108, 2271-2283.	2.6	11

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19	Genetically regulated expression in late-onset Alzheimerâ€™s disease implicates risk genes within known and novel loci. Translational Psychiatry, 2021, 11, 618.	2.4	17
20	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	4.1	191
21	A diagnostic ceiling for exome sequencing in cerebellar ataxia and related neurological disorders. Human Mutation, 2020, 41, 487-501.	1.1	58
22	Alternative Applications of Genotyping Array Data Using Multivariant Methods. Trends in Genetics, 2020, 36, 857-867.	2.9	7
23	Optimizing Genetic Analyses of Serum Lipids in Longitudinal Data. Circulation Research, 2020, 127, 1337-1339.	2.0	0
24	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	13.7	282
25	Importance of Genetic Studies of Cardiometabolic Disease in Diverse Populations. Circulation Research, 2020, 126, 1816-1840.	2.0	19
26	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.	1.5	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. Journal of Speech, Language, and Hearing Research, 2020, 63, 3019-3035.	0.7	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 Disorderâ€“Related Variants Influencing Hemoglobin A1c With Implications for Glycemic Status in U.S. Hispanics/Latinos. Diabetes Care, 2019, 42, 1784-1791.	4.3	9
35	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. PLoS ONE, 2019, 14, e0217796.	1.1	8
36	My Cousin Also Has Atrial Fibrillation. JACC: Clinical Electrophysiology, 2019, 5, 501-503.	1.3	1

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37	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	1.5	28
38	GWAS and Beyond: Using Omics Approaches to Interpret SNP Associations. Current Genetic Medicine Reports, 2019, 7, 30-40.	1.9	4
39	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	1.4	41
40	Functionally oriented analysis of cardiometabolic traits in a trans-ethnic sample. Human Molecular Genetics, 2019, 28, 1212-1224.	1.4	12
41	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.	0.7	22
42	Expanding the global prevalence of spinocerebellar ataxia type 42. Neurology: Genetics, 2018, 4, e232.	0.9	14
43	Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. Genetics, 2018, 209, 607-616.	1.2	8
44	Critical Evaluation of Data Requires Rigorous but Broadly Based Statistical Inference. Circulation Research, 2018, 122, 1049-1051.	2.0	0
45	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.	3.3	28
46	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.	1.4	65
47	Whole-Exome Sequencing Identifies Novel Variants for Tooth Agenesis. Journal of Dental Research, 2018, 97, 49-59.	2.5	44
48	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	9.4	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. BMC Obesity, 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 TSPEAR, LAMB3, BCOR, and WNT10A in four Turkish families with tooth agenesis. Human Genetics, 2018, 137, 689-703.	1.8	24
52	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.	0.3	47
53	Prevalence of spinocerebellar ataxia 36 in a US population. Neurology: Genetics, 2017, 3, e174.	0.9	15
54	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. Scientific Reports, 2017, 7, 17075.	1.6	23

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55	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
56	Genetic architecture of lipid traits in the Hispanic community health study/study of Latinos. Lipids in Health and Disease, 2017, 16, 200.	1.2	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. PLoS ONE, 2017, 12, e0172880.	1.1	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. Cardiovascular Diabetology, 2016, 15, 86.	2.7	32
59	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
60	PADRE: Pedigree-Aware Distant-Relationship Estimation. American Journal of Human Genetics, 2016, 99, 154-162.	2.6	36
61	Genome-Wide Studies of Type 2 Diabetes and Lipid Traits in Hispanics. Current Diabetes Reports, 2016, 16, 41.	1.7	10
62	Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects and tissue-specific enrichment of eQTLs. Scientific Reports, 2016, 6, 19429.	1.6	63
63	The population genomics of rhesus macaques (Macaca mulatta) based on whole-genome sequences. Genome Research, 2016, 26, 1651-1662.	2.4	101
64	Variants in angiopoietin-2 (ANGPT2) contribute to variation in nocturnal oxyhaemoglobin saturation level. Human Molecular Genetics, 2016, 25, ddw324.	1.4	21
65	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.8	17
66	Ataxia-Pancytopenia Syndrome Is Caused by Missense Mutations in SAMD9L. American Journal of Human Genetics, 2016, 98, 1146-1158.	2.6	136
67	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 886-897.	2.5	107
68	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	1.4	21
69	PRIMUS: improving pedigree reconstruction using mitochondrial and Y haplotypes. Bioinformatics, 2016, 32, 596-598.	1.8	11
70	Secondary findings and carrier test frequencies in a large multiethnic sample. Genome Medicine, 2015, 7, 54.	3.6	47
71	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.	1.1	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. Diabetes, 2015, 64, 1853-1866.	0.3	77

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73	TCIRG1-Associated Congenital Neutropenia. Human Mutation, 2014, 35, 824-827.	1.1	35
74	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13127-13132.	3.3	152
75	PRIMUS: Rapid Reconstruction of Pedigrees from Genome-wide Estimates of Identity by Descent. American Journal of Human Genetics, 2014, 95, 553-564.	2.6	129
76	Cross-Tissue and Tissue-Specific eQTLs: Partitioning the Heritability of a Complex Trait. American Journal of Human Genetics, 2014, 95, 521-534.	2.6	82
77	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
78	Mutations in ECEL1 Cause Distal Arthrogryposis Type 5D. American Journal of Human Genetics, 2013, 92, 150-156.	2.6	71
79	Whole-Genome Analysis Reveals that Mutations in Inositol Polyphosphate Phosphatase-like 1 Cause Opsismodysplasia. American Journal of Human Genetics, 2013, 92, 137-143.	2.6	53
80	Utilizing Graph Theory to Select the Largest Set of Unrelated Individuals for Genetic Analysis. Genetic Epidemiology, 2013, 37, 136-141.	0.6	47
81	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.	3.9	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. Diabetologia, 2011, 54, 2038-2046.	2.9	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. Diabetologia, 2011, 54, 2047-2055.	2.9	106
84	Germline BAP1 mutations predispose to malignant mesothelioma. Nature Genetics, 2011, 43, 1022-1025.	9.4	924
85	Genome-wide meta-analysis for severe diabetic retinopathy. Human Molecular Genetics, 2011, 20, 2472-2481.	1.4	141
86	Factors that Impact Susceptibility to Fiber-Induced Health Effects. Journal of Toxicology and Environmental Health - Part B: Critical Reviews, 2011, 14, 246-266.	2.9	19
87	Spoiling the Whole Bunch: Quality Control Aimed at Preserving the Integrity of High-Throughput Genotyping. American Journal of Human Genetics, 2010, 87, 123-128.	2.6	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. Diabetes, 2010, 59, 539-549.	0.3	103
89	Obesity and hyperinsulinemia in a family with pancreatic agenesis and MODY caused by the IPF1 mutation Pro63fsX60. Translational Research, 2010, 156, 7-14.	2.2	39
90	T2051 Genetic Analysis of Base Excision Repair Genes in African-Americans and Caucasians with Colorectal Cancer. Gastroenterology, 2008, 134, A-608-A-609.	0.6	0

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91	Identification of Type 2 Diabetes Genes in Mexican Americans Through Genome-Wide Association Studies. Diabetes, 2007, 56, 3033-3044.	0.3	125
92	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.	3.3	494