Jennifer Wessel

List of Publications by Year
in descending order

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Version: 2024-02-01

49 papers	3,751 citations	201385 27 h-index	189595 50 g-index
57 all docs	57 docs citations	57 times ranked	9077 citing authors

#	Article	IF	Citations
1	Common Disease-Common Variant. , 2020, , 506-507.		0
2	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	2.6	44
3	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
4	The Continuing Evolution of Precision Health in Type 2 Diabetes: Achievements and Challenges. Current Diabetes Reports, 2019, 19, 16.	1.7	2
5	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
6	Maternal lipid profile differs by gestational diabetes physiologic subtype. Metabolism: Clinical and Experimental, 2019, 91, 39-42.	1.5	35
7	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
8	Type 2 Diabetes Genetic Risk Scores Are Associated With Increased Type 2 Diabetes Risk Among African Americans by Cardiometabolic Status. Clinical Medicine Insights: Endocrinology and Diabetes, 2018, 11, 117955141774894.	1.0	9
9	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
10	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
11	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
12	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	3.0	39
13	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
14	Clinical characteristics and 12-month outcomes of patients with valvular and non-valvular atrial fibrillation in Kenya. PLoS ONE, 2017, 12, e0185204.	1.1	13
15	Factors Motivating Individuals to Consider Genetic Testing for Type 2 Diabetes Risk Prediction. PLoS ONE, 2016, 11, e0147071.	1.1	7
16	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	5.8	100
17	Do Genes Determine Our Health?. Circulation: Cardiovascular Genetics, 2016, 9, 2-3.	5.1	2
18	A null mutation in ANGPTL8 does not associate with either plasma glucose or type 2 diabetes in humans. BMC Endocrine Disorders, 2016, 16, 7.	0.9	9

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19	Genetic mutations in African patients with atrial fibrillation: Rationale and design of the Study of Genetics of Atrial Fibrillation in an African Population (SIGNAL). American Heart Journal, 2015, 170, 455-464.e5.	1.2	5
20	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	173
21	Genetic Testing and Type 2 Diabetes Risk Awareness. The Diabetes Educator, 2014, 40, 427-433.	2.6	4
22	Genome-wide meta-analyses of smoking behaviors in African Americans. Translational Psychiatry, 2012, 2, e119-e119.	2.4	94
23	Varenicline for smoking cessation: nausea severity and variation in nicotinic receptor genes. Pharmacogenomics Journal, 2012, 12, 349-358.	0.9	34
24	Naturally Occurring Variations in the Human Cholinesterase Genes: Heritability and Association with Cardiovascular and Metabolic Traits. Journal of Pharmacology and Experimental Therapeutics, 2011, 338, 125-133.	1.3	22
25	Environmental and Genetic Contributions to Indicators of Oral Malodor in Twins. Twin Research and Human Genetics, 2011, 14, 568-572.	0.3	1
26	Human Tyrosine Hydroxylase Natural Allelic Variation: Influence on Autonomic Function and Hypertension. Cellular and Molecular Neurobiology, 2010, 30, 1391-1394.	1.7	16
27	Presymptomatic Risk Assessment for Chronic Non-Communicable Diseases. PLoS ONE, 2010, 5, e14338.	1.1	15
28	Resequencing of Nicotinic Acetylcholine Receptor Genes and Association of Common and Rare Variants with the FagerstrÃ¶m Test for Nicotine Dependence. Neuropsychopharmacology, 2010, 35, 2392-2402.	2.8	62
29	Nicotine Withdrawal Sensitivity, Linkage to chr6q26, and Association ofOPRM1SNPs in the SMOking in FAMilies (SMOFAM) Sample. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3399-3406.	1.1	17
30	Natural Variation within the Neuronal Nicotinic Acetylcholine Receptor Cluster on Human Chromosome 15q24: Influence on Heritable Autonomic Traits in Twin Pairs. Journal of Pharmacology and Experimental Therapeutics, 2009, 331, 419-428.	1.3	8
31	CACNA1CGene Polymorphisms, Cardiovascular Disease Outcomes, and Treatment Response. Circulation: Cardiovascular Genetics, 2009, 2, 362-370.	5.1	58
32	Evidence for a heritable unidimensional symptom factor underlying obsessionality. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 676-685.	1.1	11
33	Adrenergic Polymorphism and the Human Stress Response. Annals of the New York Academy of Sciences, 2008, 1148, 282-296.	1.8	18
34	DNA Sequenceâ€Based Phenotypic Association Analysis. Advances in Genetics, 2008, 60, 195-217.	0.8	17
35	Renal Albumin Excretion. Hypertension, 2007, 49, 1015-1031.	1.3	50
36	An ancestral variant of Secretogranin II confers regulation by PHOX2 transcription factors and association with hypertension. Human Molecular Genetics, 2007, 16, 1752-1764.	1.4	29

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37	C-reactive protein, an â€˜intermediate phenotypeâ€™ for inflammation: human twin studies reveal heritability, association with blood pressure and the metabolic syndrome, and the influence of common polymorphism at catecholaminergic/Î²2-adrenergic pathway loci. Journal of Hypertension, 2007, 25, 329-343.	0.3	88
38	Single nucleotide polymorphism discovery and haplotype analysis of Ca2+-dependent K+ channel beta-1 subunit. Pharmacogenetics and Genomics, 2007, 17, 267-275.	0.7	5
39	Accommodating pathway information in expression quantitative trait locus analysis. Genomics, 2007, 90, 132-142.	1.3	15
40	Tyrosine Hydroxylase, the Rate-Limiting Enzyme in Catecholamine Biosynthesis. Circulation, 2007, 116, 993-1006.	1.6	89
41	Heritability and clinical features of multigenerational families with obsessive-compulsive disorder and hoarding. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 174-182.	1.1	55
42	Powerful designs for genetic association studies that consider twins and sibling pairs with discordant genotypes. Genetic Epidemiology, 2007, 31, 789-796.	0.6	11
43	Discovery of common human genetic variants of GTP cyclohydrolase 1 (GCH1) governing nitric oxide, autonomic activity, and cardiovascular risk. Journal of Clinical Investigation, 2007, 117, 2658-2671.	3.9	87
44	Generalized Genomic Distanceâ€“Based Regression Methodology for Multilocus Association Analysis. American Journal of Human Genetics, 2006, 79, 792-806.	2.6	157
45	Rho Kinase Polymorphism Influences Blood Pressure and Systemic Vascular Resistance in Human Twins. Hypertension, 2006, 47, 937-947.	1.3	70
46	A comprehensive literature review of haplotyping software and methods for use with unrelated individuals. Human Genomics, 2005, 2, 39.	1.4	72
47	Functional allelic heterogeneity and pleiotropy of a repeat polymorphism in tyrosine hydroxylase: prediction of catecholamines and response to stress in twins. Physiological Genomics, 2004, 19, 277-291.	1.0	80
48	Replication of the association between the thrombospondin-4 A387P polymorphism and myocardial infarction. American Heart Journal, 2004, 147, 905-909.	1.2	54
49	Genetic Testing for Type 2 Diabetes in High-Risk Children: the Case for Primordial Prevention. Research Ideas and Outcomes, 0, 3, e20695.	1.0	3