John F Peden

List of Publications by Year
in descending order

36	23,425	117625	315739
papers	citations	34 h-index	38 g-index

38	38	38	30143
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
3	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
4	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
5	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
6	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
7	Apolipoprotein(a) Genetic Sequence Variants Associated With Systemic Atherosclerosis and Coronary Atherosclerotic Burden But Not With Venous Thromboembolism. Journal of the American College of Cardiology, 2012, 60, 722-729.	2.8	149
8	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
9	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
10	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
11	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.6	335
12	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122
13	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
14	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
15	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
16	Thirty-five common variants for coronary artery disease: the fruits of much collaborative labour. Human Molecular Genetics, 2011, 20, R198-R205.	2.9	135
17	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
18	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836

#	Article	IF	Citations
19	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. Circulation, 2010, 121, 1382-1392.	1.6	311
20	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
21	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
22	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
23	Genetic Loci Associated With C-Reactive Protein Levels and Risk of Coronary Heart Disease. JAMA - Journal of the American Medical Association, 2009, 302, 37.	7.4	544
24	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	21.4	1,104
25	Genetic Variants Associated with Lp(a) Lipoprotein Level and Coronary Disease. New England Journal of Medicine, 2009, 361, 2518-2528.	27.0	1,233
26	Susceptibility to coronary artery disease and diabetes is encoded by distinct, tightly linked SNPs in the ANRIL locus on chromosome 9p. Human Molecular Genetics, 2008, 17, 806-814.	2.9	472
27	Genome-Wide Mapping of Susceptibility to Coronary Artery Disease Identifies a Novel Replicated Locus on Chromosome 17. PLoS Genetics, 2006, 2, e72.	3.5	69
28	Inter-species horizontal transfer resulting in core-genome and niche-adaptive variation within Helicobacter pylori. BMC Genomics, 2005, 6, 9.	2.8	27
29	Variation in the strength of selected codon usage bias among bacteria. Nucleic Acids Research, 2005, 33, 1141-1153.	14.5	348
30	Monosomy for the most telomeric, gene-rich region of the short arm of human chromosome 16 causes minimal phenotypic effects. European Journal of Human Genetics, 2001, 9, 217-225.	2.8	47
31	Repeat-associated phase variable genes in the complete genome sequence of Neisseria meningitidis strain MC58. Molecular Microbiology, 2000, 37, 207-215.	2.5	231
32	Complete Genome Sequence of Neisseria meningitidis Serogroup B Strain MC58. Science, 2000, 287, 1809-1815.	12.6	1,083
33	Absence in Helicobacter pylori of an uptake sequence for enhancing uptake of homospecific DNA during transformation. Microbiology (United Kingdom), 1999, 145, 3523-3528.	1.8	28
34	Simple sequence repeats in the Helicobacter pylori genome. Molecular Microbiology, 1998, 27, 1091-1098.	2.5	203
35	Systematic base composition variation around the genome of Mycoplasma genitalium , but not Mycoplasma pneumoniae. Molecular Microbiology, 1997, 25, 1177-1179.	2.5	51
36	Codon usage: mutational bias, translational selection, or both?. Biochemical Society Transactions, 1993, 21, 835-841.	3.4	280