

# John F Peden

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

23,425  
citations

117625

34  
h-index

315739

38  
g-index

38  
all docs

38  
docs citations

38  
times ranked

30143  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
2	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	21.4	1,982
3	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	27.8	1,855
4	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
5	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 25-33.	21.4	1,439
6	Genetic Variants Associated with Lp(a) Lipoprotein Level and Coronary Disease. <i>New England Journal of Medicine</i> , 2009, 361, 2518-2528.	27.0	1,233
7	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	21.4	1,104
8	Complete Genome Sequence of <i>Neisseria meningitidis</i> Serogroup B Strain MC58. <i>Science</i> , 2000, 287, 1809-1815.	12.6	1,083
9	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
10	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	21.4	762
11	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	21.4	746
12	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	21.4	675
13	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	21.4	578
14	Genetic Loci Associated With C-Reactive Protein Levels and Risk of Coronary Heart Disease. <i>JAMA - Journal of the American Medical Association</i> , 2009, 302, 37.	7.4	544
15	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	21.4	501
16	Susceptibility to coronary artery disease and diabetes is encoded by distinct, tightly linked SNPs in the ANRIL locus on chromosome 9p. <i>Human Molecular Genetics</i> , 2008, 17, 806-814.	2.9	472
17	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. <i>PLoS Genetics</i> , 2009, 5, e1000508.	3.5	453
18	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	21.4	403

#	ARTICLE	IF	CITATIONS
19	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.6	387
20	Variation in the strength of selected codon usage bias among bacteria. <i>Nucleic Acids Research</i> , 2005, 33, 1141-1153.	14.5	348
21	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. <i>Diabetes</i> , 2011, 60, 2624-2634.	0.6	335
22	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. <i>Circulation</i> , 2010, 121, 1382-1392.	1.6	311
23	Codon usage: mutational bias, translational selection, or both?. <i>Biochemical Society Transactions</i> , 1993, 21, 835-841.	3.4	280
24	Repeat-associated phase variable genes in the complete genome sequence of <i>Neisseria meningitidis</i> strain MC58. <i>Molecular Microbiology</i> , 2000, 37, 207-215.	2.5	231
25	Simple sequence repeats in the <i>Helicobacter pylori</i> genome. <i>Molecular Microbiology</i> , 1998, 27, 1091-1098.	2.5	203
26	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	2.9	168
27	Blood Pressure Loci Identified with a Gene-Centric Array. <i>American Journal of Human Genetics</i> , 2011, 89, 688-700.	6.2	159
28	Apolipoprotein(a) Genetic Sequence Variants Associated With Systemic Atherosclerosis and Coronary Atherosclerotic Burden But Not With Venous Thromboembolism. <i>Journal of the American College of Cardiology</i> , 2012, 60, 722-729.	2.8	149
29	Thirty-five common variants for coronary artery disease: the fruits of much collaborative labour. <i>Human Molecular Genetics</i> , 2011, 20, R198-R205.	2.9	135
30	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. <i>American Journal of Human Genetics</i> , 2011, 88, 6-18.	6.2	122
31	Genome-Wide Mapping of Susceptibility to Coronary Artery Disease Identifies a Novel Replicated Locus on Chromosome 17. <i>PLoS Genetics</i> , 2006, 2, e72.	3.5	69
32	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	2.5	64
33	Systematic base composition variation around the genome of <i>Mycoplasma genitalium</i> , but not <i>Mycoplasma pneumoniae</i> . <i>Molecular Microbiology</i> , 1997, 25, 1177-1179.	2.5	51
34	Monosomy for the most telomeric, gene-rich region of the short arm of human chromosome 16 causes minimal phenotypic effects. <i>European Journal of Human Genetics</i> , 2001, 9, 217-225.	2.8	47
35	Absence in <i>Helicobacter pylori</i> of an uptake sequence for enhancing uptake of homospesific DNA during transformation. <i>Microbiology (United Kingdom)</i> , 1999, 145, 3523-3528.	1.8	28
36	Inter-species horizontal transfer resulting in core-genome and niche-adaptive variation within <i>Helicobacter pylori</i> . <i>BMC Genomics</i> , 2005, 6, 9.	2.8	27