Andrew J Walley

List of Publications by Year in Descending Order

67 papers	8,492 citations	39 h-index	71 g-index
71 ext. papers	9,383 ext. citations	13 avg, IF	4.91 L-index

#	Paper	IF	Citations
67	Genetics of Severe Obesity. *Current Diabetes Reports*, **2018**, 18, 85	5.6	42
66	Integrative genomics of microglia implicates DLG4 (PSD95) in the white matter development of preterm infants. *Nature Communications*, **2017**, 8, 428	17.4	47
65	Possible relationship between common genetic variation and white matter development in a pilot study of preterm infants. *Brain and Behavior*, **2016**, 6, e00434	3.4	21
64	Systematic review and metaanalysis of genetic association studies of urinary symptoms and prolapse in women. *American Journal of Obstetrics and Gynecology*, **2015**, 212, 199.e1-24	6.4	55
63	Truncating Homozygous Mutation of Carboxypeptidase E (CPE) in a Morbidly Obese Female with Type 2 Diabetes Mellitus, Intellectual Disability and Hypogonadotrophic Hypogonadism. *PLoS ONE*, **2015**, 10, e0131417	3.7	46
62	Systematic review and meta-analysis of candidate gene association studies of lower urinary tract symptoms in men. *European Urology*, **2014**, 66, 752-68	10.2	21
61	Low copy number of the salivary amylase gene predisposes to obesity. *Nature Genetics*, **2014**, 46, 492-7	36.3	177
60	Common genetic variants and risk of brain injury after preterm birth. *Pediatrics*, **2014**, 133, e1655-63	7.4	32
59	The DNA methylomes of serous borderline tumors reveal subgroups with malignant- or benign-like profiles. *American Journal of Pathology*, **2013**, 182, 668-77	5.8	11
58	116 CANDIDATE GENE ASSOCIATION STUDIES OF URINARY SYMPTOMS AND PELVIC ORGAN PROLAPSE IN WOMEN: A SYSTEMATIC REVIEW AND META-ANALYSIS. *Journal of Urology*, **2013**, 189,	2.5	1
57	1733 CANDIDATE GENE ASSOCIATION STUDIES OF LOWER URINARY TRACT SYMPTOMS IN MEN: A SYSTEMATIC REVIEW AND META-ANALYSIS. *Journal of Urology*, **2013**, 189,	2.5	1
56	Aberrant DNA methylation at genes associated with a stem cell-like phenotype in cholangiocarcinoma tumors. *Cancer Prevention Research*, **2013**, 6, 1348-55	3.2	20
55	Adipose tissue resting energy expenditure and expression of genes involved in mitochondrial function are higher in women than in men. *Journal of Clinical Endocrinology and Metabolism*, **2013**, 98, E370-8	5.6	68
54	Integration of clinical data with a genome-scale metabolic model of the human adipocyte. *Molecular Systems Biology*, **2013**, 9, 649	12.2	167
53	ITIH-5 expression in human adipose tissue is increased in obesity. *Obesity*, **2012**, 20, 708-14	8	21
52	Candidate DNA methylation drivers of acquired cisplatin resistance in ovarian cancer identified by methylome and expression profiling. *Oncogene*, **2012**, 31, 4567-76	9.2	192
51	Association of sirtuin 1 (SIRT1) gene SNPs and transcript expression levels with severe obesity. *Obesity*, **2012**, 20, 178-85	8	63

50	Differential coexpression analysis of obesity-associated networks in human subcutaneous adipose tissue. *International Journal of Obesity*, **2012**, 36, 137-47	5.5	35
49	Low-frequency variants in HMGA1 are not associated with type 2 diabetes risk. *Diabetes*, **2012**, 61, 524-30	8.9	13
48	Novel association approach for variable number tandem repeats (VNTRs) identifies DOCK5 as a susceptibility gene for severe obesity. *Human Molecular Genetics*, **2012**, 21, 3727-38	5.6	29
47	A genome-wide association study identifies rs2000999 as a strong genetic determinant of circulating haptoglobin levels. *PLoS ONE*, **2012**, 7, e32327	3.7	27
46	Lack of association of CD36 SNPs with early onset obesity: a meta-analysis in 9,973 European subjects. *Obesity*, **2011**, 19, 833-9	8	17
45	Expression of the selenoprotein S (SELS) gene in subcutaneous adipose tissue and SELS genotype are associated with metabolic risk factors. *Metabolism: Clinical and Experimental*, **2011**, 60, 114-20	12.7	49
44	famCNV: copy number variant association for quantitative traits in families. *Bioinformatics*, **2011**, 27, 1873-5	7.2	9
43	The Contribution of Heredity to Clinical Obesity. *Growth Hormone*, **2011**, 25-52		2
42	A new highly penetrant form of obesity due to deletions on chromosome 16p11.2. *Nature*, **2010**, 463, 671-5	50.4	403
41	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527
40	Common NFKBIL2 polymorphisms and susceptibility to pneumococcal disease: a genetic association study. *Critical Care*, **2010**, 14, R227	10.8	17
39	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
38	CISH and susceptibility to infectious diseases. *New England Journal of Medicine*, **2010**, 362, 2092-101	59.2	103
37	Tenomodulin is highly expressed in adipose tissue, increased in obesity, and down-regulated during diet-induced weight loss. *Journal of Clinical Endocrinology and Metabolism*, **2009**, 94, 3987-94	5.6	42
36	The role of ghrelin and ghrelin-receptor gene variants and promoter activity in type 2 diabetes. *European Journal of Endocrinology*, **2009**, 161, 307-15	6.5	28
35	A variant near MTNR1B is associated with increased fasting plasma glucose levels and type 2 diabetes risk. *Nature Genetics*, **2009**, 41, 89-94	36.3	466
34	Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. *Nature Genetics*, **2009**, 41, 157-9	36.3	521
33	The genetic contribution to non-syndromic human obesity. *Nature Reviews Genetics*, **2009**, 10, 431-42	30.1	294

32	A rare variant in the visfatin gene (NAMPT/PBEF1) is associated with protection from obesity. *Obesity*, **2009**, 17, 1549-53	8	52
31	ALK7 expression is specific for adipose tissue, reduced in obesity and correlates to factors implicated in metabolic disease. *Biochemical and Biophysical Research Communications*, **2009**, 382, 309-14	3.4	50
30	Regulation of carboxylesterase 1 (CES1) in human adipose tissue. *Biochemical and Biophysical Research Communications*, **2009**, 383, 63-7	3.4	47
29	Common nonsynonymous variants in PCSK1 confer risk of obesity. *Nature Genetics*, **2008**, 40, 943-5	36.3	242
28	A Mal functional variant is associated with protection against invasive pneumococcal disease, bacteremia, malaria and tuberculosis. *Nature Genetics*, **2007**, 39, 523-8	36.3	364
27	No contribution of angiotensin-converting enzyme (ACE) gene variants to severe obesity: a model for comprehensive case/control and quantitative cladistic analysis of ACE in human diseases. *European Journal of Human Genetics*, **2007**, 15, 320-7	5.3	9
26	Positive replication and linkage disequilibrium mapping of the chromosome 21q22.1 malaria susceptibility locus. *Genes and Immunity*, **2007**, 8, 570-6	4.4	22
25	Leptin receptor genotype at Gln223Arg is associated with body composition, BMD, and vertebral fracture in postmenopausal Danish women. *Journal of Bone and Mineral Research*, **2007**, 22, 544-50	6.3	40
24	Single nucleotide polymorphisms in the neuropeptide Y2 receptor (NPY2R) gene and association with severe obesity in French white subjects. *Diabetologia*, **2007**, 50, 574-84	10.3	27
23	IkappaB genetic polymorphisms and invasive pneumococcal disease. *American Journal of Respiratory and Critical Care Medicine*, **2007**, 176, 181-7	10.2	66
22	Genetics of obesity and the prediction of risk for health. *Human Molecular Genetics*, **2006**, 15 Spec No 2, R124-30	5.6	125
21	Bardet-Biedl syndrome gene variants are associated with both childhood and adult common obesity in French Caucasians. *Diabetes*, **2006**, 55, 2876-82	0.9	68
20	ACDC/adiponectin and PPAR-gamma gene polymorphisms: implications for features of obesity. *Obesity*, **2005**, 13, 2113-21		46
19	Variants of ENPP1 are associated with childhood and adult obesity and increase the risk of glucose intolerance and type 2 diabetes. *Nature Genetics*, **2005**, 37, 863-7	36.3	260
18	The genetics of human obesity. *Nature Reviews Genetics*, **2005**, 6, 221-34	30.1	462
17	Association of melanin-concentrating hormone receptor 1 5Upolymorphism with early-onset extreme obesity. *Diabetes*, **2005**, 54, 3049-55	0.9	27
16	Common apolipoprotein E polymorphisms and risk of clinical malaria in the Gambia. *Journal of Medical Genetics*, **2004**, 41, 21-4	5.8	14
15	Interleukin-1 gene cluster polymorphisms and susceptibility to clinical malaria in a Gambian case-control study. *European Journal of Human Genetics*, **2004**, 12, 132-8	5.3	53

14	Interferon-alpha receptor-1 (IFNAR1) variants are associated with protection against cerebral malaria in the Gambia. *Genes and Immunity*, **2003**, 4, 275-82	4.4	72
13	ASSOCIATION OF FcRECEPTOR IIa (CD32) POLYMORPHISM WITH SEVERE MALARIA IN WEST AFRICA. *American Journal of Tropical Medicine and Hygiene*, **2003**, 69, 565-568	3.2	72
12	Association of Fcgamma receptor IIa (CD32) polymorphism with severe malaria in West Africa. *American Journal of Tropical Medicine and Hygiene*, **2003**, 69, 565-8	3.2	38
11	Haptoglobin genotypes are not associated with resistance to severe malaria in The Gambia. *Transactions of the Royal Society of Tropical Medicine and Hygiene*, **2002**, 96, 327-8	2	31
10	Genetic linkage of childhood atopic dermatitis to psoriasis susceptibility loci. *Nature Genetics*, **2001**, 27, 372-3	36.3	303
9	Gene polymorphism in Netherton and common atopic disease. *Nature Genetics*, **2001**, 29, 175-8	36.3	327
8	Linkage and allelic association of chromosome 5 cytokine cluster genetic markers with atopy and asthma associated traits. *Genomics*, **2001**, 72, 15-20	4.3	56
7	Delta 32 deletion of CCR5 gene and association with asthma or atopy. *Lancet, The*, **2000**, 356, 1491-2	40	43
6	Indication of linkage of serum IgE levels to the interleukin-4 gene and exclusion of the contribution of the (-590 C to T) interleukin-4 promoter polymorphism to IgE variation. *Genetic Epidemiology*, **1999**, 16, 84-94	2.6	30
5	Investigation of an interleukin-4 promoter polymorphism for associations with asthma and atopy. *Journal of Medical Genetics*, **1996**, 33, 689-92	5.8	159
4	Three unrelated Gaucherâ disease patients with three novel point mutations in the glucocerebrosidase gene (P266R, D315H and A318D). *British Journal of Haematology*, **1995**, 91, 330-2	4.5	10
3	A novel point mutation (D380A) and a rare deletion (1255del55) in the glucocerebrosidase gene causing Gaucherâ disease. *Human Molecular Genetics*, **1993**, 2, 1737-8	5.6	24
2	Gaucherâ disease in the United Kingdom: screening non-Jewish patients for the two common mutations. *Journal of Medical Genetics*, **1993**, 30, 280-3	5.8	19
1	Susceptibility to infectious diseases277-301		