Anjali K Henders

List of Publications by Citations

127 papers	16,164 citations	55 h-index	127 g-index
134 ext. papers	19,549 ext. citations	11.4 avg, IF	5.28 L-index

#	Paper	IF	Citations
127	Common SNPs explain a large proportion of the heritability for human height. *Nature Genetics*, **2010**, 42, 565-9	36.3	2935
126	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics*, **2013**, 45, 984-94	36.3	1628
125	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
124	A mega-analysis of genome-wide association studies for major depressive disorder. *Molecular Psychiatry*, **2013**, 18, 497-511	15.1	853
123	DNA methylation age of blood predicts all-cause mortality in later life. *Genome Biology*, **2015**, 16, 25	18.3	670
122	Identification of seven loci affecting mean telomere length and their association with disease. *Nature Genetics*, **2013**, 45, 422-7, 427e1-2	36.3	624
121	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335
120	Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. *Molecular Psychiatry*, **2012**, 17, 36-48	15.1	335
119	Genome-wide association study identifies susceptibility loci for open angle glaucoma at TMCO1 and CDKN2B-AS1. *Nature Genetics*, **2011**, 43, 574-8	36.3	329
118	Meta-analysis of telomere length in 19,713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. *European Journal of Human Genetics*, **2013**, 21, 1163-8	5.3	291
117	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. *Nature Genetics*, **2011**, 43, 51-4	36.3	227
116	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. *JAMA Psychiatry*, **2015**, 72, 642-50	14.5	222
115	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
114	Genome-wide association meta-analysis identifies new endometriosis risk loci. *Nature Genetics*, **2012**, 44, 1355-9	36.3	214
113	Meta-analysis of genome-wide association studies of anxiety disorders. *Molecular Psychiatry*, **2016**, 21, 1391-9	15.1	213
112	Common variants in the trichohyalin gene are associated with straight hair in Europeans. *American Journal of Human Genetics*, **2009**, 85, 750-5	11	200
111	Common variants in TMPRSS6 are associated with iron status and erythrocyte volume. *Nature Genetics*, **2009**, 41, 1173-5	36.3	189

110	Common sequence variants on 20q11.22 confer melanoma susceptibility. *Nature Genetics*, **2008**, 40, 838-40	36.3	188
109	Contribution of genetic variation to transgenerational inheritance of DNA methylation. *Genome Biology*, **2014**, 15, R73	18.3	179
108	A quantitative-trait genome-wide association study of alcoholism risk in the community: findings and implications. *Biological Psychiatry*, **2011**, 70, 513-8	7.9	157
107	Detection and replication of epistasis influencing transcription in humans. *Nature*, **2014**, 508, 249-53	50.4	149
106	Genetic predisposition to schizophrenia associated with increased use of cannabis. *Molecular Psychiatry*, **2014**, 19, 1201-4	15.1	136
105	Variants in TF and HFE explain approximately 40% of genetic variation in serum-transferrin levels. *American Journal of Human Genetics*, **2009**, 84, 60-5	11	131
104	A genome-wide association study of Cloninger's temperament scales: implications for the evolutionary genetics of personality. *Biological Psychology*, **2010**, 85, 306-17	3.2	128
103	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. *Nature Communications*, **2015**, 6, 7208	17.4	126
102	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. *Nature Genetics*, **2011**, 43, 1114-8	36.3	126
101	Genetic and environmental exposures constrain epigenetic drift over the human life course. *Genome Research*, **2014**, 24, 1725-33	9.7	123
100	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. *Behavior Genetics*, **2016**, 46, 170-82	3.2	122
99	Genome-wide association identifies ATOH7 as a major gene determining human optic disc size. *Human Molecular Genetics*, **2010**, 19, 2716-24	5.6	118
98	The perception of quinine taste intensity is associated with common genetic variants in a bitter receptor cluster on chromosome 12. *Human Molecular Genetics*, **2010**, 19, 4278-85	5.6	105
97	Genome-wide association study of lifetime cannabis use based on a large meta-analytic sample of 32 330 subjects from the International Cannabis Consortium. *Translational Psychiatry*, **2016**, 6, e769	8.6	102
96	Association of polymorphisms in the hepatocyte growth factor gene promoter with keratoconus **2011**, 52, 8514-9		101
95	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. *Human Genetics*, **2015**, 134, 823-35	6.3	97
94	Association between ORMDL3, IL1RL1 and a deletion on chromosome 17q21 with asthma risk in Australia. *European Journal of Human Genetics*, **2011**, 19, 458-64	5.3	92
93	Highly cost-efficient genome-wide association studies using DNA pools and dense SNP arrays. *Nucleic Acids Research*, **2008**, 36, e35	20.1	87

92	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. *American Journal of Human Genetics*, **2015**, 97, 75-85	11	85
91	Telomere length in circulating leukocytes is associated with lung function and disease. *European Respiratory Journal*, **2014**, 43, 983-92	13.6	83
90	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. *Genome Medicine*, **2019**, 11, 54	14.4	81
89	A genome-wide association study of sleep habits and insomnia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2013**, 162B, 439-51	3.5	81
88	Inference of the genetic architecture underlying BMI and height with the use of 20,240 sibling pairs. *American Journal of Human Genetics*, **2013**, 93, 865-75	11	80
87	Monozygotic twins affected with major depressive disorder have greater variance in methylation than their unaffected co-twin. *Translational Psychiatry*, **2013**, 3, e269	8.6	78
86	Identification of 55,000 Replicated DNA Methylation QTL. *Scientific Reports*, **2018**, 8, 17605	4.9	78
85	Evidence of CNIH3 involvement in opioid dependence. *Molecular Psychiatry*, **2016**, 21, 608-14	15.1	74
84	A variant in LIN28B is associated with 2D:4D finger-length ratio, a putative retrospective biomarker of prenatal testosterone exposure. *American Journal of Human Genetics*, **2010**, 86, 519-25	11	74
83	The Brisbane Systems Genetics Study: genetical genomics meets complex trait genetics. *PLoS ONE*, **2012**, 7, e35430	3.7	73
82	Cannabinoid receptor genotype moderation of the effects of childhood physical abuse on anhedonia and depression. *Archives of General Psychiatry*, **2012**, 69, 732-40		71
81	Quantitative trait loci for CD4:CD8 lymphocyte ratio are associated with risk of type 1 diabetes and HIV-1 immune control. *American Journal of Human Genetics*, **2010**, 86, 88-92	11	71
80	Genetic variants in LPL, OASL and TOMM40/APOE-C1-C2-C4 genes are associated with multiple cardiovascular-related traits. *BMC Medical Genetics*, **2011**, 12, 123	2.1	68
79	Sequence variants in three loci influence monocyte counts and erythrocyte volume. *American Journal of Human Genetics*, **2009**, 85, 745-9	11	67
78	Genetic control of gene expression in whole blood and lymphoblastoid cell lines is largely independent. *Genome Research*, **2012**, 22, 456-66	9.7	67
77	Attention deficit hyperactivity disorder in Australian adults: prevalence, persistence, conduct problems and disadvantage. *PLoS ONE*, **2012**, 7, e47404	3.7	67
76	Congruence of additive and non-additive effects on gene expression estimated from pedigree and SNP data. *PLoS Genetics*, **2013**, 9, e1003502	6	64
75	Impact of the genome on the epigenome is manifested in DNA methylation patterns of imprinted regions in monozygotic and dizygotic twins. *PLoS ONE*, **2011**, 6, e25590	3.7	61

74	Association of OPRD1 polymorphisms with heroin dependence in a large case-control series. *Addiction Biology*, **2014**, 19, 111-21	4.6	59
73	Five endometrial cancer risk loci identified through genome-wide association analysis. *Nature Genetics*, **2016**, 48, 667-674	36.3	56
72	Genome-wide association study of height and body mass index in Australian twin families. *Twin Research and Human Genetics*, **2010**, 13, 179-93	2.2	51
71	Association between endometriosis and the interleukin 1A (IL1A) locus. *Human Reproduction*, **2015**, 30, 239-48	5.7	49
70	Applying polygenic risk scores to postpartum depression. *Archives of Womens Mental Health*, **2014**, 17, 519-28	5	49
69	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. *Human Molecular Genetics*, **2015**, 24, 5955-64	5.6	48
68	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. *Biological Psychiatry*, **2018**, 84, 138-147	7.9	48
67	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. *Nature Communications*, **2018**, 9, 4774	17.4	47
66	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. *Human Molecular Genetics*, **2015**, 24, 1478-92	5.6	46
65	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. *Nature Communications*, **2017**, 8, 611	17.4	45
64	ANKK1, TTC12, and NCAM1 polymorphisms and heroin dependence: importance of considering drug exposure. *JAMA Psychiatry*, **2013**, 70, 325-33	14.5	45
63	Significant evidence of one or more susceptibility loci for endometriosis with near-Mendelian inheritance on chromosome 7p13-15. *Human Reproduction*, **2007**, 22, 717-28	5.7	42
62	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. *Endocrine-Related Cancer*, **2016**, 23, 77-91	5.7	41
61	Overlap of expression quantitative trait loci (eQTL) in human brain and blood. *BMC Medical Genomics*, **2014**, 7, 31	3.7	41
60	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. *Cancer Medicine*, **2018**, 7, 1978-1987	4.8	40
59	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. *Molecular Psychiatry*, **2015**, 20, 735-43	15.1	39
58	A case of true hermaphroditism reveals an unusual mechanism of twinning. *Human Genetics*, **2007**, 121, 179-85	6.3	39
57	First all-in-one diagnostic tool for DNA intelligence: genome-wide inference of biogeographic ancestry, appearance, relatedness, and sex with the Identitas v1 Forensic Chip. *International Journal of Legal Medicine*, **2013**, 127, 559-72	3.1	38

56	Genetic loci for Epstein-Barr virus nuclear antigen-1 are associated with risk of multiple sclerosis. *Multiple Sclerosis Journal*, **2016**, 22, 1655-1664	5	37
55	GWAS of butyrylcholinesterase activity identifies four novel loci, independent effects within BCHE and secondary associations with metabolic risk factors. *Human Molecular Genetics*, **2011**, 20, 4504-14	5.6	35
54	Rapid inexpensive genome-wide association using pooled whole blood. *Genome Research*, **2009**, 19, 2075-80	9.7	35
53	Parental separation and early substance involvement: results from children of alcoholic and cannabis dependent twins. *Drug and Alcohol Dependence*, **2014**, 134, 78-84	4.9	33
52	A 3p26-3p25 genetic linkage finding for DSM-IV major depression in heavy smoking families. *American Journal of Psychiatry*, **2011**, 168, 848-52	11.9	33
51	Comprehensive analysis of tagging sequence variants in DTNBP1 shows no association with schizophrenia or with its composite neurocognitive endophenotypes. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 1159-66	3.5	31
50	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanol-Response Behaviors in Model Organisms. *Alcoholism: Clinical and Experimental Research*, **2017**, 41, 911-928	3.7	30
49	Genome-Wide Association Shows that Pigmentation Genes Play a Role in Skin Aging. *Journal of Investigative Dermatology*, **2017**, 137, 1887-1894	4.3	30
48	High-density fine-mapping of a chromosome 10q26 linkage peak suggests association between endometriosis and variants close to CYP2C19. *Fertility and Sterility*, **2011**, 95, 2236-40	4.8	30
47	A simple and fast two-locus quality control test to detect false positives due to batch effects in genome-wide association studies. *Genetic Epidemiology*, **2010**, 34, 854-62	2.6	30
46	Autism-related dietary preferences mediate autism-gut microbiome associations. *Cell*, **2021**, 184, 5916-5931.e17	36.1	30
45	The association between childhood maltreatment, psychopathology, and adult sexual victimization in men and women: results from three independent samples. *Psychological Medicine*, **2016**, 46, 563-73	6.9	29
44	The genetic regulation of transcription in human endometrial tissue. *Human Reproduction*, **2017**, 32, 893-904	5.7	27
43	A genome wide linkage scan for dizygotic twinning in 525 families of mothers of dizygotic twins. *Human Reproduction*, **2010**, 25, 1569-80	5.7	27
42	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. *Nature Communications*, **2020**, 11, 1238	17.4	25
41	The Brisbane Longitudinal Twin Study: Pathways to Cannabis Use, Abuse, and Dependence project-current status, preliminary results, and future directions. *Twin Research and Human Genetics* , **2013**, 16, 21-33	2.2	25
40	Seasonal effects on gene expression. *PLoS ONE*, **2015**, 10, e0126995	3.7	24
39	Loci affecting gamma-glutamyl transferase in adults and adolescents show age SNP interaction and cardiometabolic disease associations. *Human Molecular Genetics*, **2012**, 21, 446-55	5.6	23

38	Genetic burden associated with varying degrees of disease severity in endometriosis. *Molecular Human Reproduction*, **2015**, 21, 594-602	4.4	22
37	Variation in BMPR1B, TGFRB1 and BMPR2 and control of dizygotic twinning. *Twin Research and Human Genetics*, **2011**, 14, 408-16	2.2	19
36	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. *Nature Genetics*, **2021**, 53, 1636-1648	36.3	19
35	Serum cholesterol and variant in cholesterol-related gene CETP predict white matter microstructure. *Neurobiology of Aging*, **2014**, 35, 2504-2513	5.6	18
34	Low Birth Weight in MZ Twins Discordant for Birth Weight is Associated with Shorter Telomere Length and lower IQ, but not Anxiety/Depression in Later Life. *Twin Research and Human Genetics*, **2015**, 18, 198-209	2.2	17
33	Identification of tag haplotypes for 5HTTLPR for different genome-wide SNP platforms. *Molecular Psychiatry*, **2011**, 16, 1073-5	15.1	17
32	LPAR1 and ITGA4 regulate peripheral blood monocyte counts. *Human Mutation*, **2011**, 32, 873-6	4.7	17
31	Genetic linkage findings for DSM-IV nicotine withdrawal in two populations. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2009**, 150B, 950-9	3.5	17
30	Evaluation of multiple displacement amplification in a 5 cM STR genome-wide scan. *Nucleic Acids Research*, **2005**, 33, e119	20.1	17
29	Heritability of Transforming Growth Factor-β and Tumor Necrosis Factor-Receptor Type 1 Expression and Vitamin D Levels in Healthy Adolescent Twins. *Twin Research and Human Genetics*, **2015**, 18, 28-35	2.2	16
28	Genetic and nongenetic variation revealed for the principal components of human gene expression. *Genetics*, **2013**, 195, 1117-28	4	16
27	The variance shared across forms of childhood trauma is strongly associated with liability for psychiatric and substance use disorders. *Brain and Behavior*, **2016**, 6, e00432	3.4	16
26	Fine mapping of variants associated with endometriosis in the WNT4 region on chromosome 1p36. *International Journal of Molecular Epidemiology and Genetics*, **2013**, 4, 193-206	0.9	15
25	Common Genetic Variants Influence Whorls in Fingerprint Patterns. *Journal of Investigative Dermatology*, **2016**, 136, 859-862	4.3	14
24	Identification of 55,000 Replicated DNA Methylation QTL		14
23	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. *Npj Genomic Medicine*, **2020**, 5, 10	6.2	11
22	Examining the association of NRXN3 SNPs with borderline personality disorder phenotypes in heroin dependent cases and socio-economically disadvantaged controls. *Drug and Alcohol Dependence*, **2013**, 128, 187-93	4.9	11
21	Contrast effects and sex influence maternal and self-report dimensional measures of attention-deficit hyperactivity disorder. *Behavior Genetics*, **2015**, 45, 35-50	3.2	10

20	Shared genetic control of expression and methylation in peripheral blood. *BMC Genomics*, **2016**, 17, 278	4.5	10
19	PPD ACT: an app-based genetic study of postpartum depression. *Translational Psychiatry*, **2018**, 8, 260	8.6	10
18	PTSD risk associated with a functional DRD2 polymorphism in heroin-dependent cases and controls is limited to amphetamine-dependent individuals. *Addiction Biology*, **2014**, 19, 700-7	4.6	9
17	Hemani et al. reply. *Nature*, **2014**, 514, E5-6	50.4	8
16	GWAS of DNA methylation variation within imprinting control regions suggests parent-of-origin association. *Twin Research and Human Genetics*, **2013**, 16, 767-81	2.2	8
15	Sharing a Placenta is Associated With a Greater Similarity in DNA Methylation in Monochorionic Versus Dichorionic Twin Pars in Blood at Age 14. *Twin Research and Human Genetics*, **2015**, 18, 680-5	2.2	6
14	Improved prediction of chronological age from DNA methylation limits it as a biomarker of ageing		6
13	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. *Genome Biology*, **2021**, 22, 90	18.3	6
12	Accuracy of Inferred APOE Genotypes for a Range of Genotyping Arrays and Imputation Reference Panels. *Journal of Alzheimer's Disease*, **2018**, 64, 49-54	4.3	5
11	Evidence for mitochondrial genetic control of autosomal gene expression. *Human Molecular Genetics*, **2016**, 25, 5332-5338	5.6	4
10	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. *Molecular Autism*, **2021**, 12, 12	6.5	4
9	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS.. *Science Translational Medicine*, **2022**, 14, eabj0264	17.5	4
8	Investigating the relationship between iron and depression. *Journal of Psychiatric Research*, **2017**, 94, 148-155	5.2	3
7	A genome-wide association study of total child psychiatric problems scores		2
6	Genome-wide Association Meta-analysis of Childhood and Adolescent Internalizing Symptoms.. *Journal of the American Academy of Child and Adolescent Psychiatry*, **2022**,	7.2	2
5	Identifying candidate gene effects by restricting search space in a multivariate genetic analysis of white matter microstructure **2014**,		1
4	Genome-wide study of DNA methylation in Amyotrophic Lateral Sclerosis identifies differentially methylated loci and implicates metabolic, inflammatory and cholesterol pathways		1
3	Schizophrenia polygenic risk scores in youth mental health: preliminary associations with diagnosis, clinical stage and functioning. *BJPsych Open*, **2021**, 7, e58	5	1

2	Phantom epistasis between unlinked loci. *Nature*, **2021**, 596, E1-E3	50.4	1
1	Nick Martin and the Genetics of Depression: Sample Size, Sample Size, Sample Size. *Twin Research and Human Genetics*, **2020**, 23, 109-111	2.2	