Anjali K Henders

List of Publications by Year
in descending order

123	21,572	19608 61	16127 124
papers	citations	h-index	g-index

134	134	134	33111
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Common SNPs explain a large proportion of the heritability for human height. Nature Genetics, 2010, 42, 565-569.	9.4	3,888
2	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
3	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
4	A mega-analysis of genome-wide association studies for major depressive disorder. Molecular Psychiatry, 2013, 18, 497-511.	4.1	1,002
5	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	3.8	928
6	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808
7	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
8	Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. Molecular Psychiatry, 2012, 17, 36-48.	4.1	405
9	Genome-wide association study identifies susceptibility loci for open angle glaucoma at TMCO1 and CDKN2B-AS1. Nature Genetics, 2011, 43, 574-578.	9.4	381
10	Meta-analysis of telomere length in 19â€‰713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	1.4	380
11	Meta-analysis of genome-wide association studies of anxiety disorders. Molecular Psychiatry, 2016, 21, 1391-1399.	4.1	373
12	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.	1.5	331
13	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	6.0	289
14	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. Nature Genetics, 2011, 43, 51-54.	9.4	261
15	Genome-wide association meta-analysis identifies new endometriosis risk loci. Nature Genetics, 2012, 44, 1355-1359.	9.4	257
16	Contribution of genetic variation to transgenerational inheritance of DNA methylation. Genome Biology, 2014, 15, R73.	13.9	231
17	Common Variants in the Trichohyalin Gene Are Associated with Straight Hair in Europeans. American Journal of Human Genetics, 2009, 85, 750-755.	2.6	230
18	Common variants in TMPRSS6 are associated with iron status and erythrocyte volume. Nature Genetics, 2009, 41, 1173-1175.	9.4	226

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19	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.	9.4	223
20	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	9.4	209
21	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	3.6	191
22	A Quantitative-Trait Genome-Wide Association Study of Alcoholism Risk in the Community: Findings and Implications. Biological Psychiatry, 2011, 70, 513-518.	0.7	184
23	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	5.8	178
24	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	1.4	178
25	Autism-related dietary preferences mediate autism-gut microbiome associations. Cell, 2021, 184, 5916-5931.e17.	13.5	172
26	Genetic predisposition to schizophrenia associated with increased use of cannabis. Molecular Psychiatry, 2014, 19, 1201-1204.	4.1	168
27	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	1.6	157
28	Variants in TF and HFE Explain â¹¼40% of Genetic Variation in Serum-Transferrin Levels. American Journal of Human Genetics, 2009, 84, 60-65.	2.6	155
29	Genetic and environmental exposures constrain epigenetic drift over the human life course. Genome Research, 2014, 24, 1725-1733.	2.4	152
30	A genome-wide association study of Cloninger's temperament scales: Implications for the evolutionary genetics of personality. Biological Psychology, 2010, 85, 306-317.	1.1	150
31	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	9.4	140
32	Genome-wide association study of lifetime cannabis use based on a large meta-analytic sample of 32â€‰330 subjects from the International Cannabis Consortium. Translational Psychiatry, 2016, 6, e769-e769.	2.4	136
33	Genome-wide association identifies ATOH7 as a major gene determining human optic disc size. Human Molecular Genetics, 2010, 19, 2716-2724.	1.4	133
34	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. Human Genetics, 2015, 134, 823-835.	1.8	133
35	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, 4278-4285.	1.4	125
36	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116

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37	Association of Polymorphisms in the Hepatocyte Growth Factor Gene Promoter with Keratoconus. , 2011, 52, 8514.		114
38	Evidence of CNIH3 involvement in opioid dependence. Molecular Psychiatry, 2016, 21, 608-614.	4.1	109
39	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	107
40	Association between ORMDL3, IL1RL1 and a deletion on chromosome 17q21 with asthma risk in Australia. European Journal of Human Genetics, 2011, 19, 458-464.	1.4	105
41	Inference of the Genetic Architecture Underlying BMI and Height with the Use of 20,240 Sibling Pairs. American Journal of Human Genetics, 2013, 93, 865-875.	2.6	104
42	A genomeâ€wide association study of sleep habits and insomnia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 439-451.	1.1	104
43	Telomere length in circulating leukocytes is associated with lung function and disease. European Respiratory Journal, 2014, 43, 983-992.	3.1	103
44	Highly cost-efficient genome-wide association studies using DNA pools and dense SNP arrays. Nucleic Acids Research, 2008, 36, e35-e35.	6.5	95
45	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. Nature Communications, 2017, 8, 611.	5.8	93
46	Monozygotic twins affected with major depressive disorder have greater variance in methylation than their unaffected co-twin. Translational Psychiatry, 2013, 3, e269-e269.	2.4	89
47	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.	0.7	87
48	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
49	Analysis of DNA methylation associates the cystineâ€“glutamate antiporter SLC7A11 with risk of Parkinsonâ€™s disease. Nature Communications, 2020, 11, 1238.	5.8	85
50	Attention Deficit Hyperactivity Disorder in Australian Adults: Prevalence, Persistence, Conduct Problems and Disadvantage. PLoS ONE, 2012, 7, e47404.	1.1	84
51	The Brisbane Systems Genetics Study: Genetical Genomics Meets Complex Trait Genetics. PLoS ONE, 2012, 7, e35430.	1.1	83
52	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.	2.6	80
53	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, 519-525.	2.6	79
54	Congruence of Additive and Non-Additive Effects on Gene Expression Estimated from Pedigree and SNP Data. PLoS Genetics, 2013, 9, e1003502.	1.5	79

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55	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
56	Genetic control of gene expression in whole blood and lymphoblastoid cell lines is largely independent. Genome Research, 2012, 22, 456-466.	2.4	75
57	Cannabinoid Receptor Genotype Moderation of the Effects of Childhood Physical Abuse on Anhedonia and Depression. Archives of General Psychiatry, 2012, 69, 732-40.	13.8	75
58	Sequence Variants in Three Loci Influence Monocyte Counts and Erythrocyte Volume. American Journal of Human Genetics, 2009, 85, 745-749.	2.6	73
59	Association ofOPRD1polymorphisms with heroin dependence in a large case-control series. Addiction Biology, 2014, 19, 111-121.	1.4	70
60	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	1.4	68
61	ANKK1, TTC12, and NCAM1 Polymorphisms and Heroin Dependence. JAMA Psychiatry, 2013, 70, 325.	6.0	66
62	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.	1.1	65
63	Applying polygenic risk scores to postpartum depression. Archives of Women's Mental Health, 2014, 17, 519-528.	1.2	62
64	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	1.6	62
65	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	1.3	62
66	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	4.1	59
67	Association between endometriosis and the interleukin 1A (IL1A) locus. Human Reproduction, 2015, 30, 239-248.	0.4	58
68	Genome-Wide Association Study of Height and Body Mass Index in Australian Twin Families. Twin Research and Human Genetics, 2010, 13, 179-193.	0.3	56
69	Significant evidence of one or more susceptibility loci for endometriosis with near-Mendelian inheritance on chromosome 7p13â€“15. Human Reproduction, 2007, 22, 717-728.	0.4	54
70	Overlap of expression Quantitative Trait Loci (eQTL) in human brain and blood. BMC Medical Genomics, 2014, 7, 31.	0.7	53
71	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, 559-572.	1.2	51
72	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50

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73	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. Genome Biology, 2021, 22, 90.	3.8	49
74	Genome-Wide Association Shows thatÂPigmentation Genes Play a Role in SkinÂAging. Journal of Investigative Dermatology, 2017, 137, 1887-1894.	0.3	48
75	Seasonal Effects on Gene Expression. PLoS ONE, 2015, 10, e0126995.	1.1	48
76	A case of true hermaphroditism reveals an unusual mechanism of twinning. Human Genetics, 2007, 121, 179-185.	1.8	46
77	Rapid inexpensive genome-wide association using pooled whole blood. Genome Research, 2009, 19, 2075-2080.	2.4	45
78	GWAS of butyrylcholinesterase activity identifies four novel loci, independent effects within BCHE and secondary associations with metabolic risk factors. Human Molecular Genetics, 2011, 20, 4504-4514.	1.4	45
79	Genetic loci for Epstein-Barr virus nuclear antigen-1 are associated with risk of multiple sclerosis. Multiple Sclerosis Journal, 2016, 22, 1655-1664.	1.4	44
80	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanolâ€Response Behaviors in Model Organisms. Alcoholism: Clinical and Experimental Research, 2017, 41, 911-928.	1.4	43
81	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	5.8	38
82	A 3p26-3p25 Genetic Linkage Finding for DSM-IV Major Depression in Heavy Smoking Families. American Journal of Psychiatry, 2011, 168, 848-852.	4.0	37
83	The association between childhood maltreatment, psychopathology, and adult sexual victimization in men and women: results from three independent samples. Psychological Medicine, 2016, 46, 563-573.	2.7	37
84	High-density fine-mapping of a chromosome 10q26 linkage peak suggests association between endometriosis and variants close to CYP2C19. Fertility and Sterility, 2011, 95, 2236-2240.	0.5	36
85	Parental separation and early substance involvement: Results from children of alcoholic and cannabis dependent twins. Drug and Alcohol Dependence, 2014, 134, 78-84.	1.6	36
86	A simple and fast twoâ€locus quality control test to detect false positives due to batch effects in genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 854-862.	0.6	33
87	The genetic regulation of transcription in human endometrial tissue. Human Reproduction, 2017, 32, 893-904.	0.4	32
88	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, 1159-1166.	1.1	31
89	A genome wide linkage scan for dizygotic twinning in 525 families of mothers of dizygotic twins. Human Reproduction, 2010, 25, 1569-1580.	0.4	31
90	Genetic burden associated with varying degrees of disease severity in endometriosis. Molecular Human Reproduction, 2015, 21, 594-602.	1.3	30

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91	Loci affecting gamma-glutamyl transferase in adults and adolescents show age Ã— SNP interaction and cardiometabolic disease associations. Human Molecular Genetics, 2012, 21, 446-455.	1.4	26
92	The Brisbane Longitudinal Twin Study: Pathways to Cannabis Use, Abuse, and Dependence Projectâ€"Current Status, Preliminary Results, and Future Directions. Twin Research and Human Genetics, 2013, 16, 21-33.	0.3	26
93	Serum cholesterol and variant in cholesterol-related gene CETP predict white matter microstructure. Neurobiology of Aging, 2014, 35, 2504-2513.	1.5	26
94	Genome-wide Association Meta-analysis of Childhood and Adolescent Internalizing Symptoms. Journal of the American Academy of Child and Adolescent Psychiatry, 2022, 61, 934-945.	0.3	26
95	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. Npj Genomic Medicine, 2020, 5, 10.	1.7	25
96	Variation in BMPR1B, TGFRB1 and BMPR2 and Control of Dizygotic Twinning. Twin Research and Human Genetics, 2011, 14, 408-416.	0.3	24
97	Genetic and Nongenetic Variation Revealed for the Principal Components of Human Gene Expression. Genetics, 2013, 195, 1117-1128.	1.2	23
98	Heritability of Transforming Growth Factor-Î²1 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.	0.3	22
99	LPAR1andITGA4regulate peripheral blood monocyte counts. Human Mutation, 2011, 32, 873-876.	1.1	20
100	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.	1.0	20
101	Genetic linkage findings for DSMâ€IV nicotine withdrawal in two populations. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 950-959.	1.1	19
102	Common Genetic Variants Influence Whorls inÂFingerprint Patterns. Journal of Investigative Dermatology, 2016, 136, 859-862.	0.3	19
103	Identification of tag haplotypes for 5HTTLPR for different genome-wide SNP platforms. Molecular Psychiatry, 2011, 16, 1073-1075.	4.1	18
104	PPD ACT: an app-based genetic study of postpartum depression. Translational Psychiatry, 2018, 8, 260.	2.4	18
105	Evaluation of multiple displacement amplification in a 5 cM STR genome-wide scan. Nucleic Acids Research, 2005, 33, e119-e119.	6.5	17
106	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.	0.3	17
107	Phantom epistasis between unlinked loci. Nature, 2021, 596, E1-E3.	13.7	16
108	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.	0.4	16

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109	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, 187-193.	1.6	12
110	Hemani et al. reply. Nature, 2014, 514, E5-E6.	13.7	12
111	<scp>PTSD</scp> risk associated with a functional <scp>DRD2</scp> polymorphism in heroinâ€dependent cases and controls is limited to amphetamineâ€dependent individuals. Addiction Biology, 2014, 19, 700-707.	1.4	11
112	Contrast Effects and Sex Influence Maternal and Self-Report Dimensional Measures of Attention-Deficit Hyperactivity Disorder. Behavior Genetics, 2015, 45, 35-50.	1.4	11
113	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. Molecular Autism, 2021, 12, 12.	2.6	11
114	Shared genetic control of expression and methylation in peripheral blood. BMC Genomics, 2016, 17, 278.	1.2	10
115	Investigating the relationship between iron and depression. Journal of Psychiatric Research, 2017, 94, 148-155.	1.5	10
116	Accuracy of Inferred APOE Genotypes for a Range of Genotyping Arrays and Imputation Reference Panels. Journal of Alzheimer's Disease, 2018, 64, 49-54.	1.2	9
117	GWAS of DNA Methylation Variation Within Imprinting Control Regions Suggests Parent-of-Origin Association. Twin Research and Human Genetics, 2013, 16, 767-781.	0.3	8
118	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, 680-685.	0.3	6
119	Evidence for mitochondrial genetic control of autosomal gene expression. Human Molecular Genetics, 2016, 25, ddw347.	1.4	6
120	Schizophrenia polygenic risk scores in youth mental health: preliminary associations with diagnosis, clinical stage and functioning. BJPsych Open, 2021, 7, e58.	0.3	4
121	Identifying candidate gene effects by restricting search space in a multivariate genetic analysis of white matter microstructure. , 2014, , .		1
122	Genome-Wide Association Study Identifies a Locus at 7p15.2 Associated With Endometriosis. Obstetrical and Gynecological Survey, 2011, 66, 214-216.	0.2	0
123	Nick Martin and the Genetics of Depression: Sample Size, Sample Size, Sample Size. Twin Research and Human Genetics, 2020, 23, 109-111.	0.3	0