

# Scott D Gordon

## List of Publications by Year in descending order

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Version: 2024-02-01

78  
papers

24,278  
citations

57758

44  
h-index

64796

79  
g-index

84  
all docs

84  
docs citations

84  
times ranked

32567  
citing authors

#	ARTICLE	IF	CITATIONS
1	Common Genetic Variation and Age of Onset of Anorexia Nervosa. <i>Biological Psychiatry Global Open Science</i> , 2022, 2, 368-378.	2.2	10
2	Enhancing Discovery of Genetic Variants for Posttraumatic Stress Disorder Through Integration of Quantitative Phenotypes and Trauma Exposure Information. <i>Biological Psychiatry</i> , 2022, 91, 626-636.	1.3	21
3	The Australian Genetics of Depression Study: New Risk Loci and Dissecting Heterogeneity Between Subtypes. <i>Biological Psychiatry</i> , 2022, 92, 227-235.	1.3	18
4	Associations of keratinocyte cancers with snp variants in the sonic hedgehog pathway. <i>BMC Cancer</i> , 2022, 22, 490.	2.6	2
5	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. <i>Nature Genetics</i> , 2022, 54, 581-592.	21.4	142
6	Genome-wide association meta-analysis of nicotine metabolism and cigarette consumption measures in smokers of European descent. <i>Molecular Psychiatry</i> , 2021, 26, 2212-2223.	7.9	45
7	Shared genetic risk between eating disorder and substance use-related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, e12880.	2.6	28
8	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021, 5, 59-70.	12.0	79
9	A prospective cohort study of prodromal Alzheimer's disease: Prospective Imaging Study of Ageing: Genes, Brain and Behaviour (PISA). <i>NeuroImage: Clinical</i> , 2021, 29, 102527.	2.7	19
10	Associations between the <i>CADM2</i> gene, substance use, risky sexual behavior, and self-control: A phenome-wide association study. <i>Addiction Biology</i> , 2021, 26, e13015.	2.6	15
11	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. <i>Science Advances</i> , 2021, 7, .	10.3	36
12	Ethnic Identity and Genome Wide Runs of Homozygosity. <i>Behavior Genetics</i> , 2021, 51, 405-413.	2.1	1
13	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	21.4	629
14	Genetic meta-analysis of twin birth weight shows high genetic correlation with singleton birth weight. <i>Human Molecular Genetics</i> , 2021, 30, 1894-1905.	2.9	6
15	Examining the Vanishing Twin Hypothesis of Neural Tube Defects: Application of an Epigenetic Predictor for Monozygotic Twinning. <i>Twin Research and Human Genetics</i> , 2021, 24, 155-159.	0.6	1
16	Genetic association study of childhood aggression across raters, instruments, and age. <i>Translational Psychiatry</i> , 2021, 11, 413.	4.8	31
17	Polygenic Risk Scores Derived From Varying Definitions of Depression and Risk of Depression. <i>JAMA Psychiatry</i> , 2021, 78, 1152.	11.0	22
18	Continuity of Genetic Risk for Aggressive Behavior Across the Life-Course. <i>Behavior Genetics</i> , 2021, 51, 592-606.	2.1	13

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19	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	12.8	26
20	Genome-wide analysis of thyroid function in Australian adolescents highlights SERPINA7 and NCOA3. <i>European Journal of Endocrinology</i> , 2021, 185, 743-753.	3.7	5
21	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	1.3	137
22	Molecular genetic overlap between posttraumatic stress disorder and sleep phenotypes. <i>Sleep</i> , 2020, 43, .	1.1	32
23	The genetic architecture of sporadic and multiple consecutive miscarriage. <i>Nature Communications</i> , 2020, 11, 5980.	12.8	52
24	Septic Shock: A Genomewide Association Study and Polygenic Risk Score Analysis. <i>Twin Research and Human Genetics</i> , 2020, 23, 204-213.	0.6	9
25	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020, 106, 389-404.	6.2	118
26	The Association of Dyslexia and Developmental Speech and Language Disorder Candidate Genes with Reading and Language Abilities in Adults. <i>Twin Research and Human Genetics</i> , 2020, 23, 23-32.	0.6	13
27	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. <i>Nature Genetics</i> , 2020, 52, 494-504.	21.4	138
28	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	21.4	641
29	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. <i>Nature Communications</i> , 2019, 10, 4558.	12.8	363
30	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
31	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. <i>Nature Communications</i> , 2019, 10, 4857.	12.8	90
32	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
33	Combined analysis of keratinocyte cancers identifies novel genome-wide loci. <i>Human Molecular Genetics</i> , 2019, 28, 3148-3160.	2.9	46
34	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549
35	New insight into human sweet taste: a genome-wide association study of the perception and intake of sweet substances. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 1724-1737.	4.7	53
36	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	21.4	1,191

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37	Genome wide analysis for mouth ulcers identifies associations at immune regulatory loci. Nature Communications, 2019, 10, 1052.	12.8	50
38	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	21.4	1,307
39	Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. Nature Genetics, 2018, 50, 652-656.	21.4	86
40	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
41	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
42	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. Nature Neuroscience, 2018, 21, 1656-1669.	14.8	490
43	Bivariate genome-wide association analysis strengthens the role of bitter receptor clusters on chromosomes 7 and 12 in human bitter taste. BMC Genomics, 2018, 19, 678.	2.8	16
44	Common genetic variants contribute to risk of rare severe neurodevelopmental disorders. Nature, 2018, 562, 268-271.	27.8	246
45	The Anorexia Nervosa Genetics Initiative (ANGI): Overview and methods. Contemporary Clinical Trials, 2018, 74, 61-69.	1.8	73
46	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
47	Association Between Population Density and Genetic Risk for Schizophrenia. JAMA Psychiatry, 2018, 75, 901.	11.0	67
48	Accuracy of Inferred APOE Genotypes for a Range of Genotyping Arrays and Imputation Reference Panels. Journal of Alzheimer's Disease, 2018, 64, 49-54.	2.6	9
49	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
50	Genome-wide association meta-analysis of age at first cannabis use. Addiction, 2018, 113, 2073-2086.	3.3	24
51	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Biological Psychiatry, 2017, 81, 325-335.	1.3	175
52	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
53	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
54	Genome-Wide Association Shows that Pigmentation Genes Play a Role in Skin Aging. Journal of Investigative Dermatology, 2017, 137, 1887-1894.	0.7	48

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55	Genome-wide association study of borderline personality disorder reveals genetic overlap with bipolar disorder, major depression and schizophrenia. <i>Translational Psychiatry</i> , 2017, 7, e1155-e1155.	4.8	150
56	Genetic effects influencing risk for major depressive disorder in China and Europe. <i>Translational Psychiatry</i> , 2017, 7, e1074-e1074.	4.8	64
57	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. <i>Biological Psychiatry</i> , 2017, 82, 322-329.	1.3	84
58	No Genetic Overlap Between Circulating Iron Levels and Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2017, 59, 85-99.	2.6	10
59	Genome-wide compound heterozygote analysis highlights alleles associated with adult height in Europeans. <i>Human Genetics</i> , 2017, 136, 1407-1417.	3.8	19
60	Heritability and GWAS Analyses of Acne in Australian Adolescent Twins. <i>Twin Research and Human Genetics</i> , 2017, 20, 541-549.	0.6	15
61	The Association of Genetic Predisposition to Depressive Symptoms with Non-suicidal and Suicidal Self-Injuries. <i>Behavior Genetics</i> , 2017, 47, 3-10.	2.1	24
62	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. <i>PLoS ONE</i> , 2017, 12, e0171595.	2.5	77
63	Genome-wide association study of lifetime cannabis use based on a large meta-analytic sample of 32,330 subjects from the International Cannabis Consortium. <i>Translational Psychiatry</i> , 2016, 6, e769-e769.	4.8	136
64	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. <i>American Journal of Human Genetics</i> , 2016, 98, 898-908.	6.2	89
65	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	2.1	178
66	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	11.0	289
67	Genetic burden associated with varying degrees of disease severity in endometriosis. <i>Molecular Human Reproduction</i> , 2015, 21, 594-602.	2.8	30
68	Association between endometriosis and the interleukin 1A (IL1A) locus. <i>Human Reproduction</i> , 2015, 30, 239-248.	0.9	58
69	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
70	Multicohort analysis of the maternal age effect on recombination. <i>Nature Communications</i> , 2015, 6, 7846.	12.8	29
71	Genome-wide analysis implicates microRNAs and their target genes in the development of bipolar disorder. <i>Translational Psychiatry</i> , 2015, 5, e678-e678.	4.8	67
72	Genome-wide association study reveals two new risk loci for bipolar disorder. <i>Nature Communications</i> , 2014, 5, 3339.	12.8	294

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73	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
74	Genome-wide association meta-analysis identifies new endometriosis risk loci. Nature Genetics, 2012, 44, 1355-1359.	21.4	257
75	Genome-wide Association Study Identifies Genetic Variation in Neurocan as a Susceptibility Factor for Bipolar Disorder. American Journal of Human Genetics, 2011, 88, 372-381.	6.2	257
76	A 3p26-3p25 Genetic Linkage Finding for DSM-IV Major Depression in Heavy Smoking Families. American Journal of Psychiatry, 2011, 168, 848-852.	7.2	37
77	Common SNPs explain a large proportion of the heritability for human height. Nature Genetics, 2010, 42, 565-569.	21.4	3,888
78	Residual linkage: why do linkage peaks not disappear after an association study?. Human Genetics, 2007, 121, 77-82.	3.8	2