Andrew J Schork

List of Publications by Year
in descending order

50 papers	8,139 citations	185998 28 h-index	182168 51 g-index
62 all docs	62 docs citations	62 times ranked	15466 citing authors

#	Article	IF	Citations
1	A comprehensive map of genetic relationships among diagnostic categories based on 48.6 million relative pairs from the Danish genealogy. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
2	Indirect paths from genetics to education. Nature Genetics, 2022, 54, 372-373.	9.4	5
3	Genetic factors underlying the bidirectional relationship between autoimmune and mental disorders â€“ Findings from a Danish population-based study. Brain, Behavior, and Immunity, 2021, 91, 10-23.	2.0	8
4	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	2.4	24
5	Associations between patterns in comorbid diagnostic trajectories of individuals with schizophrenia and etiological factors. Nature Communications, 2021, 12, 6617.	5.8	9
6	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	4.1	49
7	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	6.0	54
8	A large population-based investigation into the genetics of susceptibility to gastrointestinal infections and the link between gastrointestinal infections and mental illness. Human Genetics, 2020, 139, 593-604.	1.8	14
9	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
10	Association between Mental Disorders and Subsequent Medical Conditions. New England Journal of Medicine, 2020, 382, 1721-1731.	13.9	258
11	A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment. Nature Neuroscience, 2019, 22, 353-361.	7.1	173
12	Genetic correlations of polygenic disease traits: from theory to practice. Nature Reviews Genetics, 2019, 20, 567-581.	7.7	236
13	Human Disease Variation in the Light of Population Genomics. Cell, 2019, 177, 115-131.	13.5	75
14	A new common functional coding variant at the DDC gene change renal enzyme activity and modify renal dopamine function. Scientific Reports, 2019, 9, 5055.	1.6	6
15	Exploring Comorbidity Within Mental Disorders Among a Danish National Population. JAMA Psychiatry, 2019, 76, 259.	6.0	374
16	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
17	Novel Loci Associated With Attention-Deficit/Hyperactivity Disorder Are Revealed by Leveraging Polygenic Overlap With Educational Attainment. Journal of the American Academy of Child and Adolescent Psychiatry, 2018, 57, 86-95.	0.3	30
18	Identification of shared genetic variants between schizophrenia and lung cancer. Scientific Reports, 2018, 8, 674.	1.6	33

#	Article	IF	Citations
19	Spatial fine-mapping for gene-by-environment effects identifies risk hot spots for schizophrenia. Nature Communications, 2018, 9, 5296.	5.8	17
20	Enrichment of genetic markers of recent human evolution in educational and cognitive traits. Scientific Reports, 2018, 8, 12585.	1.6	9
21	Genetic risks and clinical rewards. Nature Genetics, 2018, 50, 1210-1211.	9.4	23
22	Williams Syndrome neuroanatomical score associates with GTF2IRD1 in large-scale magnetic resonance imaging cohorts: a proof of concept for multivariate endophenotypes. Translational Psychiatry, 2018, 8, 114.	2.4	6
23	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250
24	Subcortical brain volume differences in participants with attention deficit hyperactivity disorder in children and adults: a cross-sectional mega-analysis. Lancet Psychiatry,the, 2017, 4, 310-319.	3.7	565
25	Genome-wide analyses for personality traits identify six genomic loci and show correlations with psychiatric disorders. Nature Genetics, 2017, 49, 152-156.	9.4	350
26	Williams syndrome-specific neuroanatomical profile and its associations with behavioral features. NeuroImage: Clinical, 2017, 15, 343-347.	1.4	33
27	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
28	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	1.6	16
29	Leveraging genome characteristics to improve gene discovery for putamen subcortical brain structure. Scientific Reports, 2017, 7, 15736.	1.6	15
30	Modeling prior information of common genetic variants improves gene discovery for neuroticism. Human Molecular Genetics, 2017, 26, 4530-4539.	1.4	10
31	Probing the Association between Early Evolutionary Markers and Schizophrenia. PLoS ONE, 2017, 12, e0169227.	1.1	17
32	Genetic assessment of age-associated Alzheimer disease risk: Development and validation of a polygenic hazard score. PLoS Medicine, 2017, 14, e1002258.	3.9	311
33	Leveraging Genomic Annotations and Pleiotropic Enrichment for Improved Replication Rates in Schizophrenia GWAS. PLoS Genetics, 2016, 12, e1005803.	1.5	34
34	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213
35	New statistical approaches exploit the polygenic architecture of schizophreniaâ€"implications for the underlying neurobiology. Current Opinion in Neurobiology, 2016, 36, 89-98.	2.0	53
36	Genetic Markers of Human Evolution Are Enriched in Schizophrenia. Biological Psychiatry, 2016, 80, 284-292.	0.7	92

#	Article	IF	Citations
37	Conservation of Distinct Genetically-Mediated Human Cortical Pattern. PLoS Genetics, 2016, 12, e1006143.	1.5	15
38	An Empirical Bayes Mixture Model for Effect Size Distributions in Genome-Wide Association Studies. PLoS Genetics, 2015, 11, e1005717.	1.5	22
39	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	13.7	772
40	Modeling the 3D Geometry of the Cortical Surface with Genetic Ancestry. Current Biology, 2015, 25, 1988-1992.	1.8	34
41	Large-scale genomics unveil polygenic architecture of human cortical surface area. Nature Communications, 2015, 6, 7549.	5.8	30
42	Polygenic Overlap Between C-Reactive Protein, Plasma Lipids, and Alzheimer Disease. Circulation, 2015, 131, 2061-2069.	1.6	145
43	Heritability of Biomarkers of Oxidized Lipoproteins. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1704-1711.	1.1	44
44	Shared common variants in prostate cancer and blood lipids. International Journal of Epidemiology, 2014, 43, 1205-1214.	0.9	45
45	Human Heart Rate. Journal of the American College of Cardiology, 2014, 63, 358-368.	1.2	11
46	Covariate-modulated local false discovery rate for genome-wide association studies. Bioinformatics, 2014, 30, 2098-2104.	1.8	46
47	Genetic Implication of a Novel Thiamine Transporter in Human Hypertension. Journal of the American College of Cardiology, 2014, 63, 1542-1555.	1.2	36
48	Improved Detection of Common Variants Associated with Schizophrenia by Leveraging Pleiotropy with Cardiovascular-Disease Risk Factors. American Journal of Human Genetics, 2013, 92, 197-209.	2.6	422
49	All SNPs Are Not Created Equal: Genome-Wide Association Studies Reveal a Consistent Pattern of Enrichment among Functionally Annotated SNPs. PLoS Genetics, 2013, 9, e1003449.	1.5	268
50	Improved Detection of Common Variants Associated with Schizophrenia and Bipolar Disorder Using Pleiotropy-Informed Conditional False Discovery Rate. PLoS Genetics, 2013, 9, e1003455.	1.5	298