Robert Karlsson

List of Publications by Year
in descending order

61 papers	10,900 citations	94269 37 h-index	110170 64 g-index
68 all docs	68 docs citations	68 times ranked	17830 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
2	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
3	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893
4	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
5	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
6	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	9.4	536
7	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
8	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	9.4	432
9	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	9.4	426
10	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
11	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
12	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
13	RICOPILI: Rapid Imputation for COnsortias PIpeLIne. Bioinformatics, 2020, 36, 930-933.	1.8	201
14	Genetic Architectures of Childhood- and Adult-Onset Asthma Are Partly Distinct. American Journal of Human Genetics, 2019, 104, 665-684.	2.6	183
15	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
16	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
17	SweGen: a whole-genome data resource of genetic variability in a cross-section of the Swedish population. European Journal of Human Genetics, 2017, 25, 1253-1260.	1.4	148
18	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. Journal of Allergy and Clinical Immunology, 2019, 143, 2062-2074.	1.5	147

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19	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	5.8	140
20	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
21	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. Nature Genetics, 2017, 49, 1133-1140.	9.4	120
22	Gene regulatory mechanisms underpinning prostate cancer susceptibility. Nature Genetics, 2016, 48, 387-397.	9.4	119
23	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	2.6	118
24	A Population-based Assessment of Germline HOXB13 G84E Mutation and Prostate Cancer Risk. European Urology, 2014, 65, 169-176.	0.9	116
25	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
26	Telomere Length Shortening and Alzheimer Diseaseâ€"A Mendelian Randomization Study. JAMA Neurology, 2015, 72, 1202.	4.5	107
27	Meta-analysis of five genome-wide association studies identifies multiple new loci associated with testicular germ cell tumor. Nature Genetics, 2017, 49, 1141-1147.	9.4	105
28	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
29	The contribution of common genetic risk variants for ADHD to a general factor of childhood psychopathology. Molecular Psychiatry, 2020, 25, 1809-1821.	4.1	105
30	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
31	Exploring the Causal Pathway From Telomere Length to Coronary Heart Disease. Circulation Research, 2017, 121, 214-219.	2.0	74
32	Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins. Epigenetics, 2018, 13, 975-987.	1.3	65
33	The risk of prostate cancer for men on aspirin, statin or antidiabetic medications. European Journal of Cancer, 2015, 51, 725-733.	1.3	61
34	Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. Nature Communications, 2020, 11, 1842.	5.8	56
35	Two new loci and gene sets related to sex determination and cancer progression are associated with susceptibility to testicular germ cell tumor. Human Molecular Genetics, 2015, 24, 4138-4146.	1.4	49
36	Eleven loci with new reproducible genetic associations with allergic disease risk. Journal of Allergy and Clinical Immunology, 2019, 143, 691-699.	1.5	49

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37	Dominant Genetic Variation and Missing Heritability for Human Complex Traits: Insights from Twin versus Genome-wide Common SNP Models. American Journal of Human Genetics, 2015, 97, 708-714.	2.6	45
38	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. Genome Medicine, 2020, 12, 105.	3.6	41
39	Comparison of Genetic Liability for Sleep Traits Among Individuals With Bipolar Disorder I or II and Control Participants. JAMA Psychiatry, 2020, 77, 303.	6.0	32
40	Genome-wide association study of patients with a severe major depressive episode treated with electroconvulsive therapy. Molecular Psychiatry, 2021, 26, 2429-2439.	4.1	32
41	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	1.1	27
42	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. PLoS Genetics, 2020, 16, e1008725.	1.5	27
43	Identification of 22 susceptibility loci associated with testicular germ cell tumors. Nature Communications, 2021, 12, 4487.	5.8	27
44	Investigation of six testicular germ cell tumor susceptibility genes suggests a parent-of-origin effect in SPRY4. Human Molecular Genetics, 2013, 22, 3373-3380.	1.4	26
45	Genetics of response to cognitive behavior therapy in adults with major depression: a preliminary report. Molecular Psychiatry, 2019, 24, 484-490.	4.1	26
46	Identification of two novel mammographic density loci at 6Q25.1. Breast Cancer Research, 2015, 17, 75.	2.2	24
47	Elevated expression of a minor isoform of ANK3 is a risk factor for bipolar disorder. Translational Psychiatry, 2018, 8, 210.	2.4	24
48	Copy number variation and neuropsychiatric problems in females and males in the general population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 341-350.	1.1	23
49	Comprehensive longitudinal study of epigenetic mutations in aging. Clinical Epigenetics, 2019, 11, 187.	1.8	21
50	Common genetic variation and novel loci associated with volumetric mammographic density. Breast Cancer Research, 2018, 20, 30.	2.2	18
51	Childhood Adoption and Mental Health in Adulthood: The Role of Gene-Environment Correlations and Interactions in the UK Biobank. Biological Psychiatry, 2020, 87, 708-716.	0.7	18
52	A comprehensive evaluation of the role of genetic variation in follicular lymphoma survival. BMC Medical Genetics, 2014, 15, 113.	2.1	17
53	Rare variant analysis in eczema identifies exonic variants in DUSP1, NOTCH4 and SLC9A4. Nature Communications, 2021, 12, 6618.	5.8	17
54	Genetic variation in 117 myelination-related genes in schizophrenia: Replication of association to lipid biosynthesis genes. Scientific Reports, 2018, 8, 6915.	1.6	10

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55	Genetic Variants in the 9p21.3 Locus Associated with Glioma Risk in Children, Adolescents, and Young Adults: A Caseâ€“Control Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1252-1258.	1.1	10
56	A genome-wide association study of IgM antibody against phosphorylcholine: shared genetics and phenotypic relationship to chronic lymphocytic leukemia. Human Molecular Genetics, 2018, 27, 1809-1818.	1.4	6
57	Association Study between Polymorphisms in DNA Methylationâ€“Related Genes and Testicular Germ Cell Tumor Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1769-1779.	1.1	4
58	A significant risk locus on 19q13 for bipolar disorder identified using a combined genome-wide linkage and copy number variation analysis. BioData Mining, 2015, 8, 42.	2.2	2
59	Association of Etiological Factors for Hypomanic Symptoms, Bipolar Disorder, and Other Severe Mental Illnesses. JAMA Psychiatry, 2022, 79, 143.	6.0	2
60	Genetic and Environmental Contributions to the Covariation Between Cardiometabolic Traits. Journal of the American Heart Association, 2018, 7, .	1.6	1
61	P017â€…Differences in genetic risk for insomnia, hypersomnia and chronotype in bipolar disorder subtypes. , 2019, , .		0