

# Karolina A Aberg

## List of Publications by Year in descending order

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Version: 2024-02-01

70  
papers

3,350  
citations

159585

30  
h-index

155660

55  
g-index

76  
all docs

76  
docs citations

76  
times ranked

5848  
citing authors

#	ARTICLE	IF	CITATIONS
1	Association of Childhood Trauma Exposure With Adult Psychiatric Disorders and Functional Outcomes. <i>JAMA Network Open</i> , 2018, 1, e184493.	5.9	285
2	Methylome-Wide Association Study of Schizophrenia. <i>JAMA Psychiatry</i> , 2014, 71, 255.	11.0	210
3	Human QKI, a potential regulator of mRNA expression of human oligodendrocyte-related genes involved in schizophrenia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7482-7487.	7.1	193
4	Epigenetic Aging in Major Depressive Disorder. <i>American Journal of Psychiatry</i> , 2018, 175, 774-782.	7.2	172
5	A methylome-wide study of aging using massively parallel sequencing of the methyl-CpG-enriched genomic fraction from blood in over 700 subjects. <i>Human Molecular Genetics</i> , 2014, 23, 1175-1185.	2.9	147
6	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. <i>Molecular Psychiatry</i> , 2011, 16, 76-85.	7.9	141
7	Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. <i>Molecular Psychiatry</i> , 2011, 16, 321-332.	7.9	141
8	A Comprehensive Family-Based Replication Study of Schizophrenia Genes. <i>JAMA Psychiatry</i> , 2013, 70, 573.	11.0	138
9	Genomewide Association Study of Movement-Related Adverse Antipsychotic Effects. <i>Biological Psychiatry</i> , 2010, 67, 279-282.	1.3	122
10	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. <i>Genome Biology</i> , 2015, 16, 291.	8.8	112
11	Genome-Wide Pharmacogenomic Study of Neurocognition As an Indicator of Antipsychotic Treatment Response in Schizophrenia. <i>Neuropsychopharmacology</i> , 2011, 36, 616-626.	5.4	103
12	Human QKI, a new candidate gene for schizophrenia involved in myelination. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2006, 141B, 84-90.	1.7	95
13	MBD-seq as a cost-effective approach for methylome-wide association studies: demonstration in 1500 case-control samples. <i>Epigenomics</i> , 2012, 4, 605-621.	2.1	86
14	Testing two models describing how methylome-wide studies in blood are informative for psychiatric conditions. <i>Epigenomics</i> , 2013, 5, 367-377.	2.1	81
15	Genome-wide association study of antipsychotic-induced QTc interval prolongation. <i>Pharmacogenomics Journal</i> , 2012, 12, 165-172.	2.0	78
16	Methylome-wide association findings for major depressive disorder overlap in blood and brain and replicate in independent brain samples. <i>Molecular Psychiatry</i> , 2020, 25, 1344-1354.	7.9	61
17	Pharmacogenomic study of side-effects for antidepressant treatment options in STAR*D. <i>Psychological Medicine</i> , 2012, 42, 1151-1162.	4.5	60
18	A methylation study of long-term depression risk. <i>Molecular Psychiatry</i> , 2020, 25, 1334-1343.	7.9	56

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19	An integrative study of five biological clocks in somatic and mental health. <i>ELife</i> , 2021, 10, .	6.0	52
20	Systematic Integration of Brain eQTL and GWAS Identifies <i>ZNF323</i> as a Novel Schizophrenia Risk Gene and Suggests Recent Positive Selection Based on Compensatory Advantage on Pulmonary Function. <i>Schizophrenia Bulletin</i> , 2015, 41, 1294-1308.	4.3	48
21	SNP-based analysis of neuroactive ligand-receptor interaction pathways implicates PGE2 as a novel mediator of antipsychotic treatment response: Data from the CATIE study. <i>Schizophrenia Research</i> , 2012, 135, 200-201.	2.0	47
22	Genome-wide association study of patient-rated and clinician-rated global impression of severity during antipsychotic treatment. <i>Pharmacogenetics and Genomics</i> , 2013, 23, 69-77.	1.5	43
23	A MBD-seq protocol for large-scale methylome-wide studies with (very) low amounts of DNA. <i>Epigenetics</i> , 2017, 12, 743-750.	2.7	42
24	RaMWAS: fast methylome-wide association study pipeline for enrichment platforms. <i>Bioinformatics</i> , 2018, 34, 2283-2285.	4.1	42
25	Genome-wide pharmacogenomic study of citalopram-induced side effects in STAR*D. <i>Translational Psychiatry</i> , 2012, 2, e129-e129.	4.8	41
26	A Whole Methylome CpG-SNP Association Study of Psychosis in Blood and Brain Tissue. <i>Schizophrenia Bulletin</i> , 2016, 42, 1018-1026.	4.3	41
27	Cell Type-Specific Methylome-wide Association Studies Implicate Neurotrophin and Innate Immune Signaling in Major Depressive Disorder. <i>Biological Psychiatry</i> , 2020, 87, 431-442.	1.3	35
28	Serotonin receptor 2C (HTR2C) and schizophrenia: Examination of possible medication and genetic influences on expression levels. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2005, 134B, 84-89.	1.7	32
29	Enrichment methods provide a feasible approach to comprehensive and adequately powered investigations of the brain methylome. <i>Nucleic Acids Research</i> , 2017, 45, e97-e97.	14.5	32
30	High quality methylome-wide investigations through next-generation sequencing of DNA from a single archived dry blood spot. <i>Epigenetics</i> , 2013, 8, 542-547.	2.7	31
31	A genome-wide linkage scan identifies multiple chromosomal regions influencing serum lipid levels in the population on the Samoan islands. <i>Journal of Lipid Research</i> , 2008, 49, 2169-2178.	4.2	29
32	Susceptibility Loci for Adiposity Phenotypes on 8p, 9p, and 16q in American Samoa and Samoa. <i>Obesity</i> , 2009, 17, 518-524.	3.0	28
33	DNA methylation and histone acetylation changes to cytochrome P450 2E1 regulation in normal aging and impact on rates of drug metabolism in the liver. <i>GeroScience</i> , 2020, 42, 819-832.	4.6	26
34	Evaluation of Methyl-Binding Domain Based Enrichment Approaches Revisited. <i>PLoS ONE</i> , 2015, 10, e0132205.	2.5	26
35	Methylome-wide comparison of human genomic DNA extracted from whole blood and from EBV-transformed lymphocyte cell lines. <i>European Journal of Human Genetics</i> , 2012, 20, 953-955.	2.8	25
36	Refinement of schizophrenia GWAS loci using methylome-wide association data. <i>Human Genetics</i> , 2015, 134, 77-87.	3.8	25

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37	Correcting for cell-type effects in DNA methylation studies: reference-based method outperforms latent variable approaches in empirical studies. <i>Genome Biology</i> , 2017, 18, 24.	8.8	25
38	Estimation of CpG coverage in whole methylome next-generation sequencing studies. <i>BMC Bioinformatics</i> , 2013, 14, 50.	2.6	24
39	Reconstruction of ancestral haplotypes in a 12-generation schizophrenia pedigree. <i>Psychiatric Genetics</i> , 2004, 14, 1-8.	1.1	22
40	Methyl-CpG-Binding Domain Sequencing: MBD-seq. <i>Methods in Molecular Biology</i> , 2018, 1708, 171-189.	0.9	21
41	Test-statistic inflation in methylome-wide association studies. <i>Epigenetics</i> , 2020, 15, 1163-1166.	2.7	20
42	A Genomewide Association Study of Citalopram Response in Major Depressive Disorder—A Psychometric Approach. <i>Biological Psychiatry</i> , 2010, 68, e25-e27.	1.3	18
43	MBD-seq - realities of a misunderstood method for high-quality methylome-wide association studies. <i>Epigenetics</i> , 2020, 15, 431-438.	2.7	17
44	MethylPCA: a toolkit to control for confounders in methylome-wide association studies. <i>BMC Bioinformatics</i> , 2013, 14, 74.	2.6	16
45	Convergence of evidence from a methylome-wide CpG-SNP association study and GWAS of major depressive disorder. <i>Translational Psychiatry</i> , 2018, 8, 162.	4.8	16
46	Early adversities accelerate epigenetic aging into adulthood: a 10-year, within-subject analysis. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2022, 63, 1308-1315.	5.2	16
47	Combined Whole Methylome and Genomewide Association Study Implicates <i>CNTN4</i> in Alcohol Use. <i>Alcoholism: Clinical and Experimental Research</i> , 2015, 39, 1396-1405.	2.4	15
48	Common Variants in the <i>MKL1</i> Gene Confer Risk of Schizophrenia. <i>Schizophrenia Bulletin</i> , 2015, 41, 715-727.	4.3	15
49	Independent Methylome-Wide Association Studies of Schizophrenia Detect Consistent Case-Control Differences. <i>Schizophrenia Bulletin</i> , 2020, 46, 319-327.	4.3	15
50	The genomics of major psychiatric disorders in a large pedigree from Northern Sweden. <i>Translational Psychiatry</i> , 2019, 9, 60.	4.8	15
51	Candidate gene methylation studies are at high risk of erroneous conclusions. <i>Epigenomics</i> , 2015, 7, 13-15.	2.1	14
52	Suggestive linkage detected for blood pressure related traits on 2q and 22q in the population on the Samoan islands. <i>BMC Medical Genetics</i> , 2009, 10, 107.	2.1	13
53	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 711-718.	2.4	13
54	A Whole Methylome Study of Ethanol Exposure in Brain and Blood: An Exploration of the Utility of Peripheral Blood as Proxy Tissue for Brain in Alcohol Methylation Studies. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 2360-2368.	2.4	12

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55	Methylomic Investigation of Problematic Adolescent Cannabis Use and Its Negative Mental Health Consequences. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2021, 60, 1524-1532.	0.5	12
56	Dual methylation and hydroxymethylation study of alcohol use disorder. <i>Addiction Biology</i> , 2022, 27, e13114.	2.6	12
57	Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. <i>Nicotine and Tobacco Research</i> , 2016, 18, 626-631.	2.6	10
58	Transcriptome-wide association study for postpartum depression implicates altered B-cell activation and insulin resistance. <i>Molecular Psychiatry</i> , 2022, 27, 2858-2867.	7.9	9
59	DNA methylation signatures of childhood trauma predict psychiatric disorders and other adverse outcomes 17 years after exposure. <i>Molecular Psychiatry</i> , 2022, 27, 3367-3373.	7.9	9
60	Support for schizophrenia susceptibility locus on chromosome 2q detected in a Swedish isolate using a dense map of microsatellites and SNPs. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008, 147B, 1238-1244.	1.7	8
61	DNA methylation of the KLK8 gene in depression symptomatology. <i>Clinical Epigenetics</i> , 2021, 13, 200.	4.1	7
62	Genotype-Based Ancestral Background Consistently Predicts Efficacy and Side Effects across Treatments in CATIE and STAR*D. <i>PLoS ONE</i> , 2013, 8, e55239.	2.5	6
63	Merging microsatellite data: enhanced methodology and software to combine genotype data for linkage and association analysis. <i>BMC Bioinformatics</i> , 2008, 9, 317.	2.6	5
64	Reply to: Epstein-Barr Virus Transformed DNA as a Source of False Positive Findings in Methylation Studies of Psychiatric Conditions. <i>Biological Psychiatry</i> , 2011, 70, e27-e28.	1.3	5
65	Applying Novel Genome-Wide Linkage Strategies to Search for Loci Influencing Type 2 Diabetes and Adult Height in American Samoa. <i>Human Biology</i> , 2008, 80, 99-123.	0.2	4
66	Successes and Challenges in Precision Medicine in Psychiatry. <i>JAMA Psychiatry</i> , 2018, 75, 1269.	11.0	4
67	A methylation study implicates the rewiring of brain neural circuits during puberty in the emergence of sex differences in depression symptoms. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2021, , .	5.2	4
68	A targeted solution for estimating the cell-type composition of bulk samples. <i>BMC Bioinformatics</i> , 2021, 22, 462.	2.6	4
69	Could monitoring methylation markers aid the management of schizophrenia?. <i>Biomarkers in Medicine</i> , 2014, 8, 607-611.	1.4	0
70	Family-Based Replication Study of Schizophrenia Genes. <i>JAMA Psychiatry</i> , 2014, 71, 1195.	11.0	0