

Eli A Stahl

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

22,079
citations

53794

45
h-index

76900

74
g-index

94
all docs

94
docs citations

94
times ranked

27010
citing authors

#	ARTICLE	IF	CITATIONS
1	Partitioning heritability by functional annotation using genome-wide association summary statistics. <i>Nature Genetics</i> , 2015, 47, 1228-1235.	21.4	2,045
2	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013, 45, 1150-1159.	21.4	1,395
3	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. <i>Nature Genetics</i> , 2018, 50, 381-389.	21.4	1,332
4	A polygenic burden of rare disruptive mutations in schizophrenia. <i>Nature</i> , 2014, 506, 185-190.	27.8	1,305
5	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	21.4	1,191
6	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	6.2	1,098
7	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	12.6	1,085
8	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	14.8	952
9	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. <i>Cell</i> , 2019, 179, 1469-1482.e11.	28.9	935
10	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
11	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	21.4	838
12	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	12.8	748
13	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	27.8	679
14	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
15	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	28.9	623
16	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. <i>American Journal of Human Genetics</i> , 2014, 95, 535-552.	6.2	569
17	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. <i>Cell</i> , 2019, 179, 589-603.	28.9	428
18	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1433-1441.	14.8	427

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19	Hyperuricemia, Acute and Chronic Kidney Disease, Hypertension, and Cardiovascular Disease: Report of a Scientific Workshop Organized by the National Kidney Foundation. <i>American Journal of Kidney Diseases</i> , 2018, 71, 851-865.	1.9	362
20	Rare coding variants in ten genes confer substantial risk for schizophrenia. <i>Nature</i> , 2022, 604, 509-516.	27.8	326
21	Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. <i>PLoS Genetics</i> , 2011, 7, e1002004.	3.5	307
22	A Role for Noncoding Variation in Schizophrenia. <i>Cell Reports</i> , 2014, 9, 1417-1429.	6.4	225
23	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	2.8	214
24	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	6.2	193
25	An update on the genetics of hyperuricaemia and gout. <i>Nature Reviews Rheumatology</i> , 2018, 14, 341-353.	8.0	186
26	GWAS of Suicide Attempt in Psychiatric Disorders and Association With Major Depression Polygenic Risk Scores. <i>American Journal of Psychiatry</i> , 2019, 176, 651-660.	7.2	186
27	Synergistic effects of common schizophrenia risk variants. <i>Nature Genetics</i> , 2019, 51, 1475-1485.	21.4	184
28	Penetrance and Pleiotropy of Polygenic Risk Scores for Schizophrenia in 106,160 Patients Across Four Health Care Systems. <i>American Journal of Psychiatry</i> , 2019, 176, 846-855.	7.2	168
29	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019, 51, 659-674.	21.4	154
30	Transcriptional signatures of schizophrenia in hiPSC-derived NPCs and neurons are concordant with post-mortem adult brains. <i>Nature Communications</i> , 2017, 8, 2225.	12.8	143
31	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
32	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. <i>Nature Communications</i> , 2018, 9, 989.	12.8	136
33	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. <i>American Journal of Human Genetics</i> , 2018, 102, 1169-1184.	6.2	128
34	TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. <i>PLoS ONE</i> , 2015, 10, e0122271.	2.5	120
35	Quantifying Missing Heritability at Known GWAS Loci. <i>PLoS Genetics</i> , 2013, 9, e1003993.	3.5	115
36	Exome Sequencing of Familial Bipolar Disorder. <i>JAMA Psychiatry</i> , 2016, 73, 590.	11.0	97

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37	Genome-wide association study implicates CHRNA2 in cannabis use disorder. <i>Nature Neuroscience</i> , 2019, 22, 1066-1074.	14.8	94
38	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	11.0	88
39	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. <i>Genome Medicine</i> , 2017, 9, 114.	8.2	86
40	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways. <i>American Journal of Human Genetics</i> , 2019, 105, 334-350.	6.2	86
41	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. <i>Molecular Psychiatry</i> , 2020, 25, 2455-2467.	7.9	82
42	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016, 7, 12460.	12.8	73
43	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. <i>PLoS Genetics</i> , 2015, 11, e1005622.	3.5	70
44	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. <i>Nature Genetics</i> , 2022, 54, 541-547.	21.4	65
45	Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia. <i>Nature Neuroscience</i> , 2019, 22, 1402-1412.	14.8	63
46	A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases. <i>Nature Genetics</i> , 2016, 48, 803-810.	21.4	62
47	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. <i>Biological Psychiatry</i> , 2022, 91, 102-117.	1.3	61
48	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021, 26, 2070-2081.	7.9	48
49	Population-specific Resequencing Associates the ATP-binding Cassette Subfamily C Member 4 Gene With Gout in New Zealand Māori and Pacific Men. <i>Arthritis and Rheumatology</i> , 2017, 69, 1461-1469.	5.6	46
50	Contribution of Rare Copy Number Variants to Bipolar Disorder Risk Is Limited to Schizoaffective Cases. <i>Biological Psychiatry</i> , 2019, 86, 110-119.	1.3	45
51	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. <i>Cell Reports</i> , 2020, 31, 107716.	6.4	44
52	Dissecting clinical heterogeneity of bipolar disorder using multiple polygenic risk scores. <i>Translational Psychiatry</i> , 2020, 10, 314.	4.8	42
53	Collagenous Colitis Is Associated With HLA Signature and Shares Genetic Risks With Other Immune-Mediated Diseases. <i>Gastroenterology</i> , 2020, 159, 549-561.e8.	1.3	31
54	The Toll-Like Receptor 4 (TLR4) Variant rs2149356 and Risk of Gout in European and Polynesian Sample Sets. <i>PLoS ONE</i> , 2016, 11, e0147939.	2.5	31

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55	Mitochondrial genetic variation and gout in Māori and Pacific people living in Aotearoa New Zealand. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 571-578.	0.9	30
56	Fine-mapping of lipid regions in global populations discovers ethnic-specific signals and refines previously identified lipid loci. <i>Human Molecular Genetics</i> , 2016, 25, 5500-5512.	2.9	29
57	Genome-wide non-HLA donor-recipient genetic differences influence renal allograft survival via early allograft fibrosis. <i>Kidney International</i> , 2020, 98, 758-768.	5.2	25
58	Genetic validation of bipolar disorder identified by automated phenotyping using electronic health records. <i>Translational Psychiatry</i> , 2018, 8, 86.	4.8	24
59	Characterisation of age and polarity at onset in bipolar disorder. <i>British Journal of Psychiatry</i> , 2021, 219, 659-669.	2.8	20
60	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018, 14, e1005934.	3.2	17
61	Genetic risk for schizophrenia and autism, social impairment and developmental pathways to psychosis. <i>Translational Psychiatry</i> , 2018, 8, 204.	4.8	16
62	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	7.9	15
63	Rare protein-coding variants implicate genes involved in risk of suicide death. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 508-520.	1.7	14
64	Population-scale analysis of common and rare genetic variation associated with hearing loss in adults. <i>Communications Biology</i> , 2022, 5, .	4.4	12
65	Characterization of Single Gene Copy Number Variants in Schizophrenia. <i>Biological Psychiatry</i> , 2020, 87, 736-744.	1.3	10
66	mTADA is a framework for identifying risk genes from de novo mutations in multiple traits. <i>Nature Communications</i> , 2020, 11, 2929.	12.8	10
67	Heritability estimates of individual psychological distress symptoms from genetic variation. <i>Journal of Affective Disorders</i> , 2019, 252, 413-420.	4.1	9
68	Brief Report: The Role of Rare Protein-Coding Variants in Anti-Tumor Necrosis Factor Treatment Response in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2017, 69, 735-741.	5.6	8
69	Impact of schizophrenia GWAS loci converge onto distinct pathways in cortical interneurons vs glutamatergic neurons during development. <i>Molecular Psychiatry</i> , 2022, 27, 4218-4233.	7.9	6
70	Predicted gene expression in ancestrally diverse populations leads to discovery of susceptibility loci for lifestyle and cardiometabolic traits. <i>American Journal of Human Genetics</i> , 2022, 109, 669-679.	6.2	5
71	A loop-counting method for covariate-corrected low-rank biclustering of gene-expression and genome-wide association study data. <i>PLoS Computational Biology</i> , 2018, 14, e1006105.	3.2	3
72	The genetic architecture of bipolar disorder: Entering the road of discoveries. , 2020, , 215-225.		0