Andrew S Allen

List of Publications by Year
in descending order

67 papers	5,043 citations	304602 22 h-index	123376 61 g-index
74 all docs	74 docs citations	74 times ranked	11221 citing authors

#	Article	IF	Citations
1	De novo mutations in epileptic encephalopathies. Nature, 2013, 501, 217-221.	13.7	1,351
2	Genic Intolerance to Functional Variation and the Interpretation of Personal Genomes. PLoS Genetics, 2013, 9, e1003709.	1.5	844
3	Exome sequencing in amyotrophic lateral sclerosis identifies risk genes and pathways. Science, 2015, 347, 1436-1441.	6.0	823
4	Sequencing studies in human genetics: design and interpretation. Nature Reviews Genetics, 2013, 14, 460-470.	7.7	236
5	An Exome Sequencing Study to Assess the Role of Rare Genetic Variation in Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 82-93.	2.5	185
6	A Simple and Improved Correction for Population Stratification in Case-Control Studies. American Journal of Human Genetics, 2007, 80, 921-930.	2.6	150
7	Rare-variant collapsing analyses for complex traits: guidelines and applications. Nature Reviews Genetics, 2019, 20, 747-759.	7.7	147
8	The Intolerance of Regulatory Sequence to Genetic Variation Predicts Gene Dosage Sensitivity. PLoS Genetics, 2015, 11, e1005492.	1.5	123
9	The intolerance to functional genetic variation of protein domains predicts the localization of pathogenic mutations within genes. Genome Biology, 2016, 17, 9.	3.8	118
10	Loss of tubulin deglutamylase <scp>CCP</scp> 1 causes infantileâ€onset neurodegeneration. EMBO Journal, 2018, 37, .	3.5	86
11	Transversions have larger regulatory effects than transitions. BMC Genomics, 2017, 18, 394.	1.2	83
12	Informative Missingness in Genetic Association Studies: Case-Parent Designs. American Journal of Human Genetics, 2003, 72, 671-680.	2.6	67
13	Causal Genetic Variants in Stillbirth. New England Journal of Medicine, 2020, 383, 1107-1116.	13.9	67
14	Polymorphisms in HLA Class II Genes Are Associated With Susceptibility toStaphylococcus aureusInfection in a White Population. Journal of Infectious Diseases, 2016, 213, 816-823.	1.9	44
15	De novo and inherited private variants in MAP1B in periventricular nodular heterotopia. PLoS Genetics, 2018, 14, e1007281.	1.5	40
16	Exome-Based Rare-Variant Analyses in CKD. Journal of the American Society of Nephrology: JASN, 2019, 30, 1109-1122.	3.0	40
17	Sub-genic intolerance, ClinVar, and the epilepsies: A whole-exome sequencing study of 29,165 individuals. American Journal of Human Genetics, 2021, 108, 965-982.	2.6	35
18	Human genome-wide measurement of drug-responsive regulatory activity. Nature Communications, 2018, 9, 5317.	5.8	34

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19	Orion: Detecting regions of the human non-coding genome that are intolerant to variation using population genetics. PLoS ONE, 2017, 12, e0181604.	1.1	31
20	A novel haplotypeâ€sharing approach for genomeâ€wide caseâ€control association studies implicates the calpastatin gene in Parkinson's disease. Genetic Epidemiology, 2009, 33, 657-667.	0.6	29
21	Incorporating Functional Information in Tests of Excess De Novo Mutational Load. American Journal of Human Genetics, 2015, 97, 272-283.	2.6	29
22	Improved Pathogenic Variant Localization via a Hierarchical Model of Sub-regional Intolerance. American Journal of Human Genetics, 2019, 104, 299-309.	2.6	29
23	The Genetics of Neuropsychiatric Diseases: Looking In and Beyond the Exome. Annual Review of Neuroscience, 2015, 38, 47-68.	5.0	27
24	A case-control collapsing analysis identifies epilepsy genes implicated in trio sequencing studies focused on de novo mutations. PLoS Genetics, 2017, 13, e1007104.	1.5	25
25	Hypnotics with novel modes of action. British Journal of Clinical Pharmacology, 2020, 86, 244-249.	1.1	25
26	meaRtools: An R package for the analysis of neuronal networks recorded on microelectrode arrays. PLoS Computational Biology, 2018, 14, e1006506.	1.5	22
27	Locally-efficient robust estimation of haplotype-disease association in family-based studies. Biometrika, 2005, 92, 559-571.	1.3	21
28	Inference on haplotype/disease association using parent-affected-child data: the projection conditional on parental haplotypes method. Genetic Epidemiology, 2007, 31, 211-223.	0.6	21
29	Control for Confounding in Case-Control Studies Using the Stratification Score, a Retrospective Balancing Score. American Journal of Epidemiology, 2011, 173, 752-760.	1.6	21
30	Stratificationâ€Score Matching Improves Correction for Confounding by Population Stratification in Caseâ€Control Association Studies. Genetic Epidemiology, 2012, 36, 195-205.	0.6	21
31	A new approach for rare variation collapsing on functional protein domains implicates specific genic regions in ALS. Genome Research, 2019, 29, 809-818.	2.4	21
32	Statistical Models for Haplotype Sharing in Case-Parent Trio Data. Human Heredity, 2007, 64, 35-44.	0.4	19
33	Genome-wide association study (GWAS) of human host factors influencing viral severity of herpes simplex virus type 2 (HSV-2). Genes and Immunity, 2019, 20, 112-120.	2.2	17
34	Quantifying the Impact of Non-coding Variants on Transcription Factor-DNA Binding. Lecture Notes in Computer Science, 2017, 10229, 336-352.	1.0	16
35	Coding and noncoding variants in EBF3 are involved in HADDS and simplex autism. Human Genomics, 2021, 15, 44.	1.4	16
36	Utilizing Population Controls in Rare-Variant Case-Parent Association Tests. American Journal of Human Genetics, 2014, 94, 845-853.	2.6	15

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37	Effect of population stratification on the identification of significant single-nucleotide polymorphisms in genome-wide association studies. BMC Proceedings, 2009, 3, S13.	1.8	12
38	Exploiting expression patterns across multiple tissues to map expression quantitative trait loci. BMC Bioinformatics, 2016, 17, 257.	1.2	12
39	Evaluating Chromatin Accessibility Differences Across Multiple Primate Species Using a Joint Modeling Approach. Genome Biology and Evolution, 2019, 11, 3035-3053.	1.1	12
40	Diverse genetic causes of polymicrogyria with epilepsy. Epilepsia, 2021, 62, 973-983.	2.6	12
41	Correcting signal biases and detecting regulatory elements in STARR-seq data. Genome Research, 2021, 31, 877-889.	2.4	11
42	Genome-wide association analysis of rheumatoid arthritis data via haplotype sharing. BMC Proceedings, 2009, 3, S30.	1.8	9
43	Joint Models for Toxicology Studies with Doseâ€Dependent Number of Implantations. Risk Analysis, 2002, 22, 1165-1173.	1.5	8
44	Robust estimation and testing of haplotype effects in caseâ€control studies. Genetic Epidemiology, 2008, 32, 29-40.	0.6	8
45	Robust analysis of secondary phenotypes in caseâ€control genetic association studies. Statistics in Medicine, 2016, 35, 4226-4237.	0.8	8
46	Scoreâ€based adjustment for confounding by population stratification in genetic association studies. Genetic Epidemiology, 2010, 34, 383-385.	0.6	7
47	Response to Lee etÂal.. American Journal of Human Genetics, 2008, 82, 526-528.	2.6	6
48	A Regressionâ€based Association Test for Caseâ€control Studies that Uses Inferred Ancestral Haplotype Similarity. Annals of Human Genetics, 2009, 73, 520-526.	0.3	6
49	SNPs in CAST are associated with Parkinson disease: A confirmation study. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 973-979.	1.1	6
50	Robust testing of haplotype/disease association. BMC Genetics, 2005, 6, S69.	2.7	5
51	Testing the Effect of Rare Compoundâ€Heterozygous and Recessive Mutations in Caseâ€“Parent Sequencing Studies. Genetic Epidemiology, 2015, 39, 166-172.	0.6	5
52	Mapping eQTL by leveraging multiple tissues and DNA methylation. BMC Bioinformatics, 2017, 18, 455.	1.2	5
53	Incorporating external information to improve sparse signal detection in rareâ€variant geneâ€setâ€based analyses. Genetic Epidemiology, 2020, 44, 330-338.	0.6	5
54	Association mapping via a class of haplotype-sharing statistics. BMC Proceedings, 2007, 1, S123.	1.8	4

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55	<tt>bcSeq</tt>: an R package for fast sequence mapping in high-throughput shRNA and CRISPR screens. Bioinformatics, 2018, 34, 3581-3583.	1.8	4
56	Fast and Robust Association Tests for Untyped SNPs in Case-Control Studies. Human Heredity, 2010, 70, 167-176.	0.4	3
57	Leveraging population information in familyâ€based rare variant association analyses of quantitative traits. Genetic Epidemiology, 2017, 41, 98-107.	0.6	3
58	Lifting EMMeT to OWL Getting the Most from SKOS. Lecture Notes in Computer Science, 2016, , 69-80.	1.0	3
59	Summary of contributions to GAW15 Group 13: candidate gene association studies. Genetic Epidemiology, 2007, 31, S110-S117.	0.6	2
60	High-throughput interpretation of gene structure changes in human and nonhuman resequencing data, using ACE. Bioinformatics, 2017, 33, 1437-1446.	1.8	2
61	Ancestry adjustment improves genome-wide estimates of regional intolerance. Genetics, 2022, , .	1.2	2
62	Testing for risk and protective trends in genetic analyses of HIV acquisition. Biostatistics, 2015, 16, 268-280.	0.9	0
63	Facilitating the Calculation of the Efficient Score Using Symbolic Computing. American Statistician, 2018, 72, 199-205.	0.9	0
64	Bayesian estimation of genetic regulatory effects in high-throughput reporter assays. Bioinformatics, 2020, 36, 331-338.	1.8	0
65	Casual Genetic Variants in Stillbirth. Obstetrical and Gynecological Survey, 2021, 76, 79-81.	0.2	0
66	Focused goodness of fit tests for gene set analyses. Briefings in Bioinformatics, 2021, , .	3.2	0
67	Invited Keynote Talk: Haplotype Sharing for Genome-Wide Case-Control Association Studies. , 2008, , 183-183.		0