Nan Laird

List of Publications by Year
in descending order

64	42,632	76326	114465
papers	citations	40 h-index	63 g-index

64	64	64	46476
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Meta-analysis in clinical trials. Contemporary Clinical Trials, 1986, 7, 177-188.	1.9	33,020
2	Meta-analysis in clinical trials revisited. Contemporary Clinical Trials, 2015, 45, 139-145.	1.8	1,745
3	Impact of Overweight on the Risk of Developing Common Chronic Diseases During a 10-Year Period. Archives of Internal Medicine, 2001, 161, 1581.	3.8	1,286
4	A Unified Approach to Adjusting Association Tests for Population Admixture with Arbitrary Pedigree Structure and Arbitrary Missing Marker Information. Human Heredity, 2000, 50, 211-223.	0.8	580
5	Nonparametric Maximum Likelihood Estimation of a Mixing Distribution. Journal of the American Statistical Association, 1978, 73, 805-811.	3.1	574
6	Cutaneous Squamous-Cell Carcinoma in Patients Treated with PUVA. New England Journal of Medicine, 1984, 310, 1156-1161.	27.0	461
7	Relation of body composition, fat mass, and serum lipids to osteoporotic fractures and bone mineral density in Chinese men and women. American Journal of Clinical Nutrition, 2006, 83, 146-154.	4.7	441
8	Covariance Analysis of Censored Survival Data Using Log-Linear Analysis Techniques. Journal of the American Statistical Association, 1981, 76, 231-240.	3.1	428
9	The carcinogenic risk of treatments for severe psoriasis. Cancer, 1994, 73, 2759-2764.	4.1	408
10	Maximum Likelihood Computations with Repeated Measures: Application of the EM Algorithm. Journal of the American Statistical Association, 1987, 82, 97-105.	3.1	334
11	The transforming growth factor-Â1 (TGFB1) gene is associated with chronic obstructive pulmonary disease (COPD). Human Molecular Genetics, 2004, 13, 1649-1656.	2.9	203
12	Attempted Replication of Reported Chronic Obstructive Pulmonary Disease Candidate Gene Associations. American Journal of Respiratory Cell and Molecular Biology, 2005, 33, 71-78.	2.9	185
13	A Common Haplotype of the Nicotine Acetylcholine Receptor Î±4 Subunit Gene Is Associated with Vulnerability to Nicotine Addiction in Men. American Journal of Human Genetics, 2004, 75, 112-121.	6.2	180
14	Blood eosinophil count thresholds and exacerbations in patients with chronic obstructive pulmonary disease. Journal of Allergy and Clinical Immunology, 2018, 141, 2037-2047.e10.	2.9	138
15	Nonparametric Maximum Likelihood Estimation of a Mixing Distribution. Journal of the American Statistical Association, 1978, 73, 805.	3.1	137
16	The Association of a SNP Upstream of INSIG2 with Body Mass Index is Reproduced in Several but Not All Cohorts. PLoS Genetics, 2007, 3, e61.	3.5	134
17	A Random-Effects Model for Multiple Characteristics with Possibly Missing Data. Journal of the American Statistical Association, 1997, 92, 775-779.	3.1	131
18	On the Replication of Genetic Associations: Timing Can Be Everything!. American Journal of Human Genetics, 2008, 82, 849-858.	6.2	130

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19	Exome sequencing in schizophrenia-affected parentâ€“offspring trios reveals risk conferred by protein-coding de novo mutations. Nature Neuroscience, 2020, 23, 185-193.	14.8	125
20	Distinct Quantitative Computed Tomography Emphysema Patterns Are Associated with Physiology and Function in Smokers. American Journal of Respiratory and Critical Care Medicine, 2013, 188, 1083-1090.	5.6	118
21	Covariance Analysis of Censored Survival Data Using Log-Linear Analysis Techniques. Journal of the American Statistical Association, 1981, 76, 231.	3.1	110
22	Evaluating the Effect of Coaching on SAT Scores: A Meta-Analysis. Harvard Educational Review, 1983, 53, 1-15.	0.9	103
23	Variation in genes involved in the RANKL/RANK/OPG bone remodeling pathway are associated with bone mineral density at different skeletal sites in men. Human Genetics, 2006, 118, 568-577.	3.8	103
24	A Reanalysis of the Stanford Heart Transplant Data. Journal of the American Statistical Association, 1983, 78, 264-274.	3.1	91
25	Weight Cycling and the Risk of Developing Type 2 Diabetes among Adult Women in the United States. Obesity, 2004, 12, 267-274.	4.0	87
26	The Association of Genome-Wide Significant Spirometric Loci with Chronic Obstructive Pulmonary Disease Susceptibility. American Journal of Respiratory Cell and Molecular Biology, 2011, 45, 1147-1153.	2.9	87
27	IL10 gene polymorphisms are associated with asthma phenotypes in children. Genetic Epidemiology, 2004, 26, 155-165.	1.3	86
28	Rare Variant Analysis for Family-Based Design. PLoS ONE, 2013, 8, e48495.	2.5	85
29	Genome-Wide Association Identifies Regulatory Loci Associated with Distinct Local Histogram Emphysema Patterns. American Journal of Respiratory and Critical Care Medicine, 2014, 190, 399-409.	5.6	77
30	A candidate gene association study on preterm delivery: application of high-throughput genotyping technology and advanced statistical methods. Human Molecular Genetics, 2004, 13, 683-691.	2.9	73
31	Cluster analysis in severe emphysema subjects using phenotype and genotype data: an exploratory investigation. Respiratory Research, 2010, 11, 30.	3.6	72
32	Maximum Likelihood Computations with Repeated Measures: Application of the EM Algorithm. Journal of the American Statistical Association, 1987, 82, 97.	3.1	67
33	Meta-Analysis of the INSIG2 Association with Obesity Including 74,345 Individuals: Does Heterogeneity of Estimates Relate to Study Design?. PLoS Genetics, 2009, 5, e1000694.	3.5	62
34	Predicting recovery from idiopathic sudden hearing loss. American Journal of Otolaryngology - Head and Neck Medicine and Surgery, 1983, 4, 161-164.	1.3	59
35	Further Comparative Analyses of Pretest-Posttest Research Designs. American Statistician, 1983, 37, 329-330.	1.6	59
36	Polymorphism in Maternal LRP8 Gene Is Associated with Fetal Growth. American Journal of Human Genetics, 2006, 78, 770-777.	6.2	59

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37	Genetic association analysis of behavioral inhibition using candidate loci from mouse models. American Journal of Medical Genetics Part A, 2001, 105, 226-235.	2.4	58
38	Socioeconomic disadvantage and neural development from infancy through early childhood. International Journal of Epidemiology, 2015, 44, 1889-1899.	1.9	55
39	Genetic Association and Risk Scores in a Chronic Obstructive Pulmonary Disease Meta-analysis of 16,707 Subjects. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 35-46.	2.9	55
40	Machine Learning Characterization of COPD Subtypes. Chest, 2020, 157, 1147-1157.	0.8	44
41	An efficient family-based association test using multiple markers. Genetic Epidemiology, 2006, 30, 620-626.	1.3	41
42	Lobar Emphysema Distribution Is Associated With 5-Year Radiological Disease Progression. Chest, 2018, 153, 65-76.	0.8	36
43	Electronystagmographic findings in idiopathic sudden hearing loss. American Journal of Otolaryngology - Head and Neck Medicine and Surgery, 1982, 3, 279-285.	1.3	35
44	The Relationship Of Idiopathic Sudden Hearing Loss To Diabetes Mellitus. Laryngoscope, 1982, 92, 155-160.	2.0	34
45	Identification of Novel Alzheimerâ€™s Disease Loci Using Sex-Specific Family-Based Association Analysis of Whole-Genome Sequence Data. Scientific Reports, 2020, 10, 5029.	3.3	31
46	Sex-Based Genetic Association Study Identifies CELSR1 as a Possible Chronic Obstructive Pulmonary Disease Risk Locus among Women. American Journal of Respiratory Cell and Molecular Biology, 2017, 56, 332-341.	2.9	28
47	A Random-Effects Model for Multiple Characteristics With Possibly Missing Data. Journal of the American Statistical Association, 1997, 92, 775.	3.1	25
48	Nonparametric Mixed-Effects Models for Repeated Binary Data Arising in Serial Dilution Assays: An Application to Estimating Viral Burden in AIDS. Journal of the American Statistical Association, 1996, 91, 52-61.	3.1	24
49	Growth Changes. Evaluation Review, 1983, 7, 80-95.	1.0	15
50	Comments on â€˜Empirical vs natural weighting in random effects metaâ€analysisâ€™. Statistics in Medicine, 2010, 29, 1266-1267.	1.6	15
51	Integrative Genomics Analysis Identifies ACVR1B as a Candidate Causal Gene of Emphysema Distribution. American Journal of Respiratory Cell and Molecular Biology, 2019, 60, 388-398.	2.9	15
52	Exact family-based association tests for biallelic data. Genetic Epidemiology, 2005, 29, 185-194.	1.3	14
53	Identifying causal rare variants of disease through family-based analysis of Genetics Analysis Workshop 17 data set. BMC Proceedings, 2011, 5, S21.	1.6	13
54	Joint models for efficient estimation in proportional hazards regression models. Statistics in Medicine, 2003, 22, 2137-2148.	1.6	10

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55	New Powerful Approaches for Familyâ€based Association Tests with Longitudinal Measurements. Annals of Human Genetics, 2009, 73, 74-83.	0.8	9
56	Region-based analysis of rare genomic variants in whole-genome sequencing datasets reveal two novel Alzheimerâ€™s disease-associated genes: DTNB and DLG2. Molecular Psychiatry, 2022, 27, 1963-1969.	7.9	9
57	A comparison of popular TDTâ€generalizations for familyâ€based association analysis. Genetic Epidemiology, 2019, 43, 300-317.	1.3	7
58	EFBAT: exact family-based association tests. BMC Genetics, 2007, 8, 86.	2.7	6
59	Power Evaluations for Family-Based Tests of Association With Incomplete Parental Genotypes. Genetics, 2003, 164, 399-406.	2.9	5
60	Family-based tests for associating haplotypes with general phenotype data. Genetic Epidemiology, 2018, 42, 123-126.	1.3	4
61	Family-Based Association Tests with Longitudinal Measurements: Handling Missing Data. Human Heredity, 2009, 68, 98-105.	0.8	3
62	Nonparametric Mixed-Effects Models for Repeated Binary Data Arising in Serial Dilution Assays: An Application to Estimating Viral Burden in AIDS. Journal of the American Statistical Association, 1996, 91, 52.	3.1	2
63	Comment: Bayes, Oracle Bayes, and Empirical Bayes. Statistical Science, 2019, 34, .	2.8	1
64	Categorical Auxiliary Data in the Discrete Time Proportional Hazards Model. Handbook of Statistics, 2003, 23, 363-382.	0.6	0