Adaikalavan Ramasamy

List of Publications by Year
in descending order

54 papers	11,235 citations	94433 37 h-index	149698 56 g-index
58 all docs	58 docs citations	58 times ranked	22322 citing authors

#	Article	IF	Citations
1	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Nature Genetics, 2014, 46, 989-993.	21.4	1,685
2	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	27.8	772
3	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	2.1	696
4	Genetic variability in the regulation of gene expression in ten regions of the human brain. Nature Neuroscience, 2014, 17, 1418-1428.	14.8	620
5	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	21.4	594
6	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
7	Key Issues in Conducting a Meta-Analysis of Gene Expression Microarray Datasets. PLoS Medicine, 2008, 5, e184.	8.4	471
8	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
9	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
10	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. Lancet Respiratory Medicine,the, 2015, 3, 769-781.	10.7	346
11	Identification of IL6R and chromosome 11q13.5 as risk loci for asthma. Lancet, The, 2011, 378, 1006-1014.	13.7	345
12	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	21.4	311
13	Frontotemporal dementia and its subtypes: a genome-wide association study. Lancet Neurology, The, 2014, 13, 686-699.	10.2	302
14	Gene expression changes with age in skin, adipose tissue, blood and brain. Genome Biology, 2013, 14, R75.	9.6	263
15	Discovery of estrogen receptor alpha target genes and response elements in breast tumor cells. Genome Biology, 2004, 5, R66.	9.6	257
16	Widespread sex differences in gene expression and splicing in the adult human brain. Nature Communications, 2013, 4, 2771.	12.8	255
17	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
18	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	21.4	223

#	Article	IF	Citations
19	Quality control parameters on a large dataset of regionally dissected human control brains for whole genome expression studies. Journal of Neurochemistry, 2011, 119, 275-282.	3.9	214
20	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
21	A genome-wide meta-analysis of genetic variants associated with allergic rhinitis and grass sensitization and their interaction with birth order. Journal of Allergy and Clinical Immunology, 2011, 128, 996-1005.	2.9	212
22	MAPT expression and splicing is differentially regulated by brain region: relation to genotype and implication for tauopathies. Human Molecular Genetics, 2012, 21, 4094-4103.	2.9	191
23	Epilepsy, hippocampal sclerosis and febrile seizures linked by common genetic variation around SCN1A. Brain, 2013, 136, 3140-3150.	7.6	168
24	Molecular changes from dysplastic nodule to hepatocellular carcinoma through gene expression profiling. Hepatology, 2005, 42, 809-818.	7.3	167
25	Insights into TREM2 biology by network analysis of human brain gene expression data. Neurobiology of Aging, 2013, 34, 2699-2714.	3.1	145
26	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
27	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	3.5	130
28	Genome-Wide Association Studies of Asthma in Population-Based Cohorts Confirm Known and Suggested Loci and Identify an Additional Association near HLA. PLoS ONE, 2012, 7, e44008.	2.5	111
29	Identification of Candidate Parkinson Disease Genes by Integrating Genome-Wide Association Study, Expression, and Epigenetic Data Sets. JAMA Neurology, 2021, 78, 464.	9.0	95
30	Genome-wide association study of lung function decline in adults with and without asthma. Journal of Allergy and Clinical Immunology, 2012, 129, 1218-1228.	2.9	94
31	Highly interconnected genes in disease-specific networks are enriched for disease-associated polymorphisms. Genome Biology, 2012, 13, R46.	9.6	60
32	Obesity-susceptibility loci have a limited influence on birth weight: a meta-analysis of up to 28,219 individuals. American Journal of Clinical Nutrition, 2011, 93, 851-860.	4.7	58
33	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
34	Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. Journal of Allergy and Clinical Immunology, 2014, 133, 885-888.	2.9	47
35	Transcriptomic and genetic analyses reveal potential causal drivers for intractable partial epilepsy. Brain, 2019, 142, 1616-1630.	7.6	47
36	Fine-Mapping, Gene Expression and Splicing Analysis of the Disease Associated LRRK2 Locus. PLoS ONE, 2013, 8, e70724.	2.5	45

#	Article	IF	Citations
37	Genetic evidence for a pathogenic role for the vitamin D3 metabolizing enzyme CYP24A1 in multiple sclerosis. Multiple Sclerosis and Related Disorders, 2014, 3, 211-219.	2.0	44
38	Genetic Variants of TSLP and Asthma in an Admixed Urban Population. PLoS ONE, 2011, 6, e25099.	2.5	39
39	Resolving the polymorphism-in-probe problem is critical for correct interpretation of expression QTL studies. Nucleic Acids Research, 2013, 41, e88-e88.	14.5	39
40	A C6orf10/LOC101929163 locus is associated with age of onset in C9orf72 carriers. Brain, 2018, 141, 2895-2907.	7.6	39
41	Assessment of common variability and expression quantitative trait loci for genome-wide associations for progressive supranuclear palsy. Neurobiology of Aging, 2014, 35, 1514.e1-1514.e12.	3.1	33
42	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
43	Interaction between gas cooking andGSTM1null genotype in bronchial responsiveness: results from the European Community Respiratory Health Survey. Thorax, 2014, 69, 558-564.	5.6	22
44	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. Nature Communications, 2020, 11, 1041.	12.8	22
45	Dysregulation of Complement System and CD4+ T Cell Activation Pathways Implicated in Allergic Response. PLoS ONE, 2013, 8, e74821.	2.5	14
46	Farm environment during infancy and lung function at the age of 31: a prospective birth cohort study in Finland. BMJ Open, 2015, 5, e007350.	1.9	12
47	Respiratory health and endotoxin: associations and modification by CD14/-260 genotype. European Respiratory Journal, 2012, 39, 573-581.	6.7	10
48	Gene Expression Imputation Across Multiple Tissue Types Provides Insight Into the Genetic Architecture of Frontotemporal Dementia and Its Clinical Subtypes. Biological Psychiatry, 2021, 89, 825-835.	1.3	10
49	Treating Spider Phobia Using Neuro Emotional Techniqueâ„¢: Findings from a Pilot Study. Journal of Alternative and Complementary Medicine, 2009, 15, 1363-1374.	2.1	9
50	Development of an objective gene expression panel as an alternative to self-reported symptom scores in human influenza challenge trials. Journal of Translational Medicine, 2017, 15, 134.	4.4	6
51	Improving General Flexibility with a Mind-Body Approach. Journal of Strength and Conditioning Research, 2012, 26, 2103-2112.	2.1	5
52	Quality control parameters on a large dataset of regionally dissected human control brains for whole genome expression studies. Journal of Neurochemistry, 2012, 120, 473-473.	3.9	4
53	Mendelian randomization implies no direct causal association between leukocyte telomere length and amyotrophic lateral sclerosis. Scientific Reports, 2020, 10, 12184.	3.3	4
54	The Benefits of Giving a Massage on the Mental State of Massage Therapists: A Randomized, Controlled Trial. Journal of Alternative and Complementary Medicine, 2012, 18, 1142-1146.	2.1	2