Alexander A Morgan

List of Publications by Year
in descending order

18 papers	1,647 citations	686830 13 h-index	887659 17 g-index
19 all docs	19 docs citations	19 times ranked	3366 citing authors

#	Article	IF	Citations
1	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. Human Mutation, 2017, 38, 1182-1192.	1.1	39
2	Disease Variant Landscape of a Large Multiethnic Population of Moyamoya Patients by Exome Sequencing. G3: Genes, Genomes, Genetics, 2016, 6, 41-49.	0.8	42
3	Mouse models rarely mimic the transcriptome of human neurodegenerative diseases: A systematic bioinformatics-based critique of preclinical models. European Journal of Pharmacology, 2015, 759, 101-117.	1.7	60
4	Integrated multi-cohort transcriptional meta-analysis of neurodegenerative diseases. Acta Neuropathologica Communications, 2014, 2, 93.	2.4	94
5	Multiplex meta-analysis of medulloblastoma expression studies with external controls. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 99-109.	0.7	1
6	A common rejection module (CRM) for acute rejection across multiple organs identifies novel therapeutics for organ transplantation. Journal of Experimental Medicine, 2013, 210, 2205-2221.	4.2	201
7	Analysis of the Genetic Basis of Disease in the Context of Worldwide Human Relationships and Migration. PLoS Genetics, 2013, 9, e1003447.	1.5	67
8	Whole genome sequencing in support of wellness and health maintenance. Genome Medicine, 2013, 5, 58.	3.6	46
9	MULTIPLEX META-ANALYSIS OF MEDULLOBLASTOMA EXPRESSION STUDIES WITH EXTERNAL CONTROLS. , 2013, , .		0
10	Proline: The Distribution, Frequency, Positioning, and Common Functional Roles of Proline and Polyproline Sequences in the Human Proteome. PLoS ONE, 2013, 8, e53785.	1.1	203
11	Clinical utility of sequence-based genotype compared with that derivable from genotyping arrays. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, e21-e27.	2.2	4
12	Multiplex meta-analysis of RNA expression to identify genes with variants associated with immune dysfunction. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 284-288.	2.2	3
13	Identification of an IFN-Î³/mast cell axis in a mouse model of chronic asthma. Journal of Clinical Investigation, 2011, 121, 3133-3143.	3.9	113
14	Comparison of multiplex meta analysis techniques for understanding the acute rejection of solid organ transplants. BMC Bioinformatics, 2010, 11, S6.	1.2	20
15	Differentially Expressed RNA from Public Microarray Data Identifies Serum Protein Biomarkers for Cross-Organ Transplant Rejection and Other Conditions. PLoS Computational Biology, 2010, 6, e1000940.	1.5	72
16	Clinical assessment incorporating a personal genome. Lancet, The, 2010, 375, 1525-1535.	6.3	637
17	Likelihood ratios for genome medicine. Genome Medicine, 2010, 2, 30.	3.6	27
18	Dynamism in gene expression across multiple studies. Physiological Genomics, 2010, 40, 128-140.	1.0	12