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	Clinical assessment incorporating a personal genome. Lancet, The, 2010, 375, 1525-1535.	6.3	637
2	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
3	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
4	Identification of an IFN-γ/mast cell axis in a mouse model of chronic asthma. Journal of Clinical Investigation, 2011, 121, 3133-3143.	3.9	113
5	Integrated multi-cohort transcriptional meta-analysis of neurodegenerative diseases. Acta Neuropathologica Communications, 2014, 2, 93.	2.4	94
6	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
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	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
9	Whole genome sequencing in support of wellness and health maintenance. Genome Medicine, 2013, 5, 58.	3.6	46
10	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
11	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
12	Likelihood ratios for genome medicine. Genome Medicine, 2010, 2, 30.	3.6	27
13	Comparison of multiplex meta analysis techniques for understanding the acute rejection of solid organ transplants. BMC Bioinformatics, 2010, 11, S6.	1.2	20
14	Dynamism in gene expression across multiple studies. Physiological Genomics, 2010, 40, 128-140.	1.0	12
15	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
16	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
17	Multiplex meta-analysis of medulloblastoma expression studies with external controls. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 99-109.	0.7	1
18	MULTIPLEX META-ANALYSIS OF MEDULLOBLASTOMA EXPRESSION STUDIES WITH EXTERNAL CONTROLS. , 2013, , .		0