Tim Aitman

List of Publications by Year
in descending order

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47 papers	4,435 citations	236925 25 h-index	214800 47 g-index
50 all docs	50 docs citations	50 times ranked	7378 citing authors

#	Article	IF	Citations
1	Identification of Cd36 (Fat) as an insulin-resistance gene causing defective fatty acid and glucose metabolism in hypertensive rats. Nature Genetics, 1999, 21, 76-83.	21.4	692
2	Copy number polymorphism in Fcgr3 predisposes to glomerulonephritis in rats and humans. Nature, 2006, 439, 851-855.	27.8	610
3	Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102.	27.8	338
4	Progress and prospects in rat genetics: a community view. Nature Genetics, 2008, 40, 516-522.	21.4	265
5	Malaria susceptibility and CD36 mutation. Nature, 2000, 405, 1015-1016.	27.8	230
6	Transgenic rescue of defective Cd36 ameliorates insulin resistance in spontaneously hypertensive rats. Nature Genetics, 2001, 27, 156-158.	21.4	186
7	Heritability and Tissue Specificity of Expression Quantitative Trait Loci. PLoS Genetics, 2006, 2, e172.	3.5	183
8	Changes in the Coding and Non-coding Transcriptome and DNA Methylome that Define the Schwann Cell Repair Phenotype after Nerve Injury. Cell Reports, 2017, 20, 2719-2734.	6.4	164
9	Genome Sequencing Reveals Loci under Artificial Selection that Underlie Disease Phenotypes in the Laboratory Rat. Cell, 2013, 154, 691-703.	28.9	154
10	C9ORF72 repeat expansion causes vulnerability of motor neurons to Ca2+-permeable AMPA receptor-mediated excitotoxicity. Nature Communications, 2018, 9, 347.	12.8	151
11	Integrated genomic approaches implicate osteoglycin (Ogn) in the regulation of left ventricular mass. Nature Genetics, 2008, 40, 546-552.	21.4	150
12	Quantitative trait loci for cellular defects in glucose and fatty acid metabolism in hypertensive rats. Nature Genetics, 1997, 16, 197-201.	21.4	138
13	The zinc transporter ZIP12 regulates the pulmonary vascular response to chronic hypoxia. Nature, 2015, 524, 356-360.	27.8	113
14	Periodontal Ehlers-Danlos Syndrome Is Caused by Mutations in C1R and C1S , which Encode Subcomponents C1r and C1s of Complement. American Journal of Human Genetics, 2016, 99, 1005-1014.	6.2	100
15	Genetics of Cd36 and the clustering of multiple cardiovascular risk factors in spontaneous hypertension. Journal of Clinical Investigation, 1999, 103, 1651-1657.	8.2	99
16	Identification of renal Cd36 as a determinant of blood pressure and risk for hypertension. Nature Genetics, 2008, 40, 952-954.	21.4	97
17	Genomic landscape of rat strain and substrain variation. BMC Genomics, 2015, 16, 357.	2.8	84
18	A Dominantly Inherited 5â€² UTR Variant Causing Methylation-Associated Silencing of BRCA1 as a Cause of Breast and Ovarian Cancer. American Journal of Human Genetics, 2018, 103, 213-220.	6.2	78

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19	Kcnn4 Is a Regulator of Macrophage Multinucleation in Bone Homeostasis and Inflammatory Disease. Cell Reports, 2014, 8, 1210-1224.	6.4	53
20	Inherited Thoracic Aortic Disease. Circulation, 2020, 141, 1570-1587.	1.6	53
21	A RATional choice for translational research?. DMM Disease Models and Mechanisms, 2016, 9, 1069-1072.	2.4	49
22	Targeted genetic testing for familial hypercholesterolaemia using next generation sequencing: a population-based study. BMC Medical Genetics, 2014, 15, 70.	2.1	47
23	Genetic epidemiology of motor neuron disease-associated variants in the Scottish population. Neurobiology of Aging, 2017, 51, 178.e11-178.e20.	3.1	37
24	Systems-level approaches reveal conservation of trans-regulated genes in the rat and genetic determinants of blood pressure in humans. Cardiovascular Research, 2013, 97, 653-665.	3.8	31
25	Performance evaluation of Sanger sequencing for the diagnosis of primary hyperoxaluria and comparison with targeted next generation sequencing. Molecular Genetics & Genomic Medicine, 2015, 3, 69-78.	1.2	31
26	Macrophage Epoxygenase Determines a Profibrotic Transcriptome Signature. Journal of Immunology, 2015, 194, 4705-4716.	0.8	28
27	Integrated genomic approaches to identification of candidate genes underlying metabolic and cardiovascular phenotypes in the spontaneously hypertensive rat. Physiological Genomics, 2011, 43, 1207-1218.	2.3	26
28	Complement Factor B Is a Determinant of Both Metabolic and Cardiovascular Features of Metabolic Syndrome. Hypertension, 2017, 70, 624-633.	2.7	26
29	Spatial transcriptomics identifies spatially dysregulated expression of GRM3 and USP47 in amyotrophic lateral sclerosis. Neuropathology and Applied Neurobiology, 2020, 46, 441-457.	3.2	25
30	Genetic Analysis of the Cardiac Methylome at Single Nucleotide Resolution in a Model of Human Cardiovascular Disease. PLoS Genetics, 2014, 10, e1004813.	3.5	19
31	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. Scientific Reports, 2019, 9, 10964.	3.3	17
32	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. PLoS Genetics, 2019, 15, e1008480.	3.5	17
33	Natural Polymorphisms in Tap2 Influence Negative Selection and CD4âˆ¶CD8 Lineage Commitment in the Rat. PLoS Genetics, 2014, 10, e1004151.	3.5	16
34	Epoxygenase inactivation exacerbates diet and aging-associated metabolic dysfunction resulting from impaired adipogenesis. Molecular Metabolism, 2018, 11, 18-32.	6.5	14
35	Functionally Conserved Noncoding Regulators of Cardiomyocyte Proliferation and Regeneration in Mouse and Human. Circulation Genomic and Precision Medicine, 2018, 11, e001805.	3.6	14
36	Genetic, physiological and comparative genomic studies of hypertension and insulin resistance in the spontaneously hypertensive rat. DMM Disease Models and Mechanisms, 2017, 10, 297-306.	2.4	13

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37	Genetic Mapping and Positional Cloning. Methods in Molecular Biology, 2010, 597, 13-32.	0.9	12
38	Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	12
39	Longitudinal measurement of HPV copy number in cell-free DNA is associated with patient outcomes in HPV-positive oropharyngeal cancer. European Journal of Surgical Oncology, 2022, 48, 1224-1234.	1.0	12
40	Identification of Ceruloplasmin as a Gene that Affects Susceptibility to Glomerulonephritis Through Macrophage Function. Genetics, 2017, 206, 1139-1151.	2.9	11
41	Absolute measurement of the tissue origins of cell-free DNA in the healthy state and following paracetamol overdose. BMC Medical Genomics, 2020, 13, 60.	1.5	10
42	De novo mutations in autosomal recessive congenital malformations. Genetics in Medicine, 2016, 18, 1325-1326.	2.4	8
43	New Wistar Kyoto and Spontaneously Hypertensive rat transgenic models with ubiquitous expression of green fluorescent protein. DMM Disease Models and Mechanisms, 2016, 9, 463-71.	2.4	8
44	A high-resolution radiation hybrid map of the proximal region of rat Chromosome 4. Mammalian Genome, 1999, 10, 471-476.	2.2	5
45	Multiplexed DNA Methylation Analysis of Target Regions Using Microfluidics (Fluidigm). Methods in Molecular Biology, 2018, 1708, 349-363.	0.9	5
46	Glomerulonephritis and autoimmune vasculitis are independent of <scp>P2RX7</scp> but may depend on alternative inflammasome pathways. Journal of Pathology, 2022, 257, 300-313.	4.5	3
47	Gene Expression Profiling of Sorted Peripheral Blood Cells Using Microarray and Next Generation Sequencing Reveals Distinct Molecular Signatures in the Polymorphonuclear and Mononuclear Cells of Patients with Polycythemia Vera and Primary Myelofibrosis. Blood, 2015, 126, 5201-5201.	1.4	0