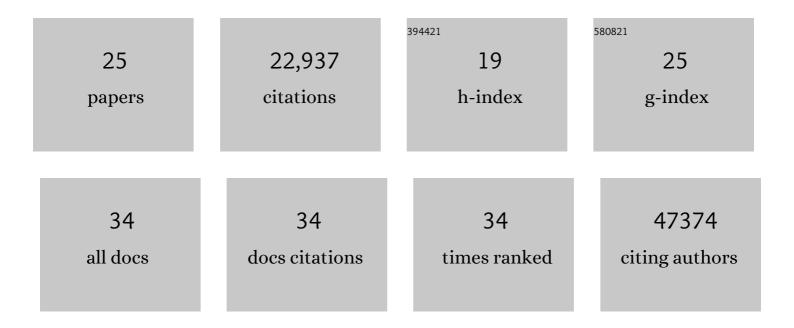
Alan Hodgkinson

List of Publications by Year in descending order

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ALAN HODCKINSON

#	Article	IF	CITATIONS
1	Genetic variation at mouse and human ribosomal DNA influences associated epigenetic states. Genome Biology, 2022, 23, 54.	8.8	11
2	Mitochondrial-nuclear cross-talk in the human brain is modulated by cell type and perturbed in neurodegenerative disease. Communications Biology, 2021, 4, 1262.	4.4	8
3	Intellectual disability-associated factor Zbtb11 cooperates with NRF-2/GABP to control mitochondrial function. Nature Communications, 2020, 11, 5469.	12.8	12
4	Analysis of mitochondrial m1A/G RNA modification reveals links to nuclear genetic variants and associated disease processes. Communications Biology, 2020, 3, 147.	4.4	22
5	Nuclear genetic regulation of the human mitochondrial transcriptome. ELife, 2019, 8, .	6.0	56
6	Gene-by-environment interactions in urban populations modulate risk phenotypes. Nature Communications, 2018, 9, 827.	12.8	84
7	Relaxed Selection During a Recent Human Expansion. Genetics, 2018, 208, 763-777.	2.9	49
8	Integrated genomic analysis of mitochondrial RNA processing in human cancers. Genome Medicine, 2017, 9, 36.	8.2	25
9	A haplotype-based normalization technique for the analysis and detection of allele specific expression. BMC Bioinformatics, 2016, 17, 364.	2.6	7
10	Gain-of-function missense variant in SLC12A2, encoding the bumetanide-sensitive NKCC1 cotransporter, identified in human schizophrenia. Journal of Psychiatric Research, 2016, 77, 22-26.	3.1	40
11	Replication study of MATR3 in familial and sporadic amyotrophic lateral sclerosis. Neurobiology of Aging, 2016, 37, 209.e17-209.e21.	3.1	53
12	Recombination affects accumulation of damaging and disease-associated mutations in human populations. Nature Genetics, 2015, 47, 400-404.	21.4	84
13	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
14	High-Resolution Genomic Analysis of Human Mitochondrial RNA Sequence Variation. Science, 2014, 344, 413-415.	12.6	90
15	Genetically encoded impairment of neuronal <scp>KCC</scp> 2 cotransporter function in human idiopathic generalized epilepsy. EMBO Reports, 2014, 15, 766-774.	4.5	163
16	Selective constraint, background selection, and mutation accumulation variability within and between human populations. BMC Genomics, 2013, 14, 495.	2.8	16
17	Exome sequencing identifies mutations in the gene <i>TTC7A</i> in French-Canadian cases with hereditary multiple intestinal atresia. Journal of Medical Genetics, 2013, 50, 324-329.	3.2	119
18	Whole-Exome Sequencing Reveals a Rapid Change in the Frequency of Rare Functional Variants in a Founding Population of Humans. PLoS Genetics, 2013, 9, e1003815.	3.5	70

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#	Article	IF	CITATIONS
19	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
20	The large-scale distribution of somatic mutations in cancer genomes. Human Mutation, 2012, 33, 136-143.	2.5	77
21	Variation in the mutation rate across mammalian genomes. Nature Reviews Genetics, 2011, 12, 756-766.	16.3	438
22	The Genomic Distribution and Local Context of Coincident SNPs in Human and Chimpanzee. Genome Biology and Evolution, 2010, 2, 547-557.	2.5	25
23	Human Triallelic Sites: Evidence for a New Mutational Mechanism?. Genetics, 2010, 184, 233-241.	2.9	76
24	Cryptic Variation in the Human Mutation Rate. PLoS Biology, 2009, 7, e1000027.	5.6	101
25	Prior infection of Manduca sexta with non-pathogenic Escherichia coli elicits immunity to pathogenic Photorhabdus luminescens: Roles of immune-related proteins shown by RNA interference. Insect Biochemistry and Molecular Biology, 2006, 36, 517-525.	2.7	108