Alan Hodgkinson

List of Publications by Year
in descending order

25	22,937	394421 19	580821 25
papers	citations	h-index	g-index

34	34	34	47374
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
3	Variation in the mutation rate across mammalian genomes. Nature Reviews Genetics, 2011, 12, 756-766.	16.3	438
4	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
5	Exome sequencing identifies mutations in the geneTTC7Ain French-Canadian cases with hereditary multiple intestinal atresia. Journal of Medical Genetics, 2013, 50, 324-329.	3.2	119
6	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
7	Cryptic Variation in the Human Mutation Rate. PLoS Biology, 2009, 7, e1000027.	5.6	101
8	High-Resolution Genomic Analysis of Human Mitochondrial RNA Sequence Variation. Science, 2014, 344, 413-415.	12.6	90
9	Recombination affects accumulation of damaging and disease-associated mutations in human populations. Nature Genetics, 2015, 47, 400-404.	21.4	84
10	Gene-by-environment interactions in urban populations modulate risk phenotypes. Nature Communications, 2018, 9, 827.	12.8	84
11	The large-scale distribution of somatic mutations in cancer genomes. Human Mutation, 2012, 33, 136-143.	2.5	77
12	Human Triallelic Sites: Evidence for a New Mutational Mechanism?. Genetics, 2010, 184, 233-241.	2.9	76
13	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
14	Nuclear genetic regulation of the human mitochondrial transcriptome. ELife, 2019, 8, .	6.0	56
15	Replication study of MATR3 in familial and sporadic amyotrophic lateral sclerosis. Neurobiology of Aging, 2016, 37, 209.e17-209.e21.	3.1	53
16	Relaxed Selection During a Recent Human Expansion. Genetics, 2018, 208, 763-777.	2.9	49
17	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
18	The Genomic Distribution and Local Context of Coincident SNPs in Human and Chimpanzee. Genome Biology and Evolution, 2010, 2, 547-557.	2.5	25

#	Article	IF	Citations
19	Integrated genomic analysis of mitochondrial RNA processing in human cancers. Genome Medicine, 2017, 9, 36.	8.2	25
20	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
21	Selective constraint, background selection, and mutation accumulation variability within and between human populations. BMC Genomics, 2013, 14, 495.	2.8	16
22	Intellectual disability-associated factor Zbtb11 cooperates with NRF-2/GABP to control mitochondrial function. Nature Communications, 2020, 11, 5469.	12.8	12
23	Genetic variation at mouse and human ribosomal DNA influences associated epigenetic states. Genome Biology, 2022, 23, 54.	8.8	11
24	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
25	A haplotype-based normalization technique for the analysis and detection of allele specific expression. BMC Bioinformatics, 2016, 17, 364.	2.6	7