Alan P Boyle

List of Publications by Citations

51 papers	22,432 citations	31 h-index	66 g-index
66 ext. papers	28,026 ext. citations	19.4 avg, IF	8.21 L-index

#	Paper	IF	Citations
51	An integrated encyclopedia of DNA elements in the human genome. *Nature*, **2012**, 489, 57-74	50.4	11449
50	Annotation of functional variation in personal genomes using RegulomeDB. *Genome Research*, **2012**, 22, 1790-7	9.7	1723
49	Architecture of the human regulatory network derived from ENCODE data. *Nature*, **2012**, 489, 91-100	50.4	1104
48	A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biology*, **2011**, 9, e1001046	9.7	1060
47	A comparative encyclopedia of DNA elements in the mouse genome. *Nature*, **2014**, 515, 355-64	50.4	1026
46	High-resolution mapping and characterization of open chromatin across the genome. *Cell*, **2008**, 132, 311-22	56.2	988
45	Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell*, **2012**, 148, 1293-307	56.2	921
44	Linking disease associations with regulatory information in the human genome. *Genome Research*, **2012**, 22, 1748-59	9.7	538
43	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. *Genome Research*, **2011**, 21, 1757-67	9.7	391
42	Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710	50.4	360
41	The ENCODE Blacklist: Identification of Problematic Regions of the Genome. *Scientific Reports*, **2019**, 9, 9354	4.9	319
40	F-Seq: a feature density estimator for high-throughput sequence tags. *Bioinformatics*, **2008**, 24, 2537-8	7.2	282
39	Extensive variation in chromatin states across humans. *Science*, **2013**, 342, 750-2	33.3	276
38	Heritable individual-specific and allele-specific chromatin signatures in humans. *Science*, **2010**, 328, 235-9	33.3	260
37	High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells. *Genome Research*, **2011**, 21, 456-64	9.7	250
36	Principles of regulatory information conservation between mouse and human. *Nature*, **2014**, 515, 371-375	50.4	190
35	Global epigenomic analysis of primary human pancreatic islets provides insights into type 2 diabetes susceptibility loci. *Cell Metabolism*, **2010**, 12, 443-55	24.6	168

34	Comparative analysis of regulatory information and circuits across distant species. *Nature*, **2014**, 512, 453-6	50.4	135
33	Sushi.R: flexible, quantitative and integrative genomic visualizations for publication-quality multi-panel figures. *Bioinformatics*, **2014**, 30, 2808-10	7.2	122
32	Dynamic trans-acting factor colocalization in human cells. *Cell*, **2013**, 155, 713-24	56.2	109
31	Mango: a bias-correcting ChIA-PET analysis pipeline. *Bioinformatics*, **2015**, 31, 3092-8	7.2	91
30	Regulatory analysis of the C. elegans genome with spatiotemporal resolution. *Nature*, **2014**, 512, 400-5	50.4	81
29	Both noncoding and protein-coding RNAs contribute to gene expression evolution in the primate brain. *Genome Biology and Evolution*, **2010**, 2, 67-79	3.9	76
28	Evidence-ranked motif identification. *Genome Biology*, **2010**, 11, R19	18.3	73
27	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
26	Mining the Unknown: Assigning Function to Noncoding Single Nucleotide Polymorphisms. *Trends in Genetics*, **2017**, 33, 34-45	8.5	60
25	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. *American Journal of Human Genetics*, **2018**, 102, 103-115	11	53
24	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. *Nature Communications*, **2017**, 8, 15481	17.4	52
23	Transposable elements contribute to cell and species-specific chromatin looping and gene regulation in mammalian genomes. *Nature Communications*, **2020**, 11, 1796	17.4	39
22	Deciphering ENCODE. *Trends in Genetics*, **2016**, 32, 238-249	8.5	37
21	Predicting functional variants in enhancer and promoter elements using RegulomeDB. *Human Mutation*, **2019**, 40, 1292-1298	4.7	32
20	Predicting the effects of SNPs on transcription factor binding affinity. *Bioinformatics*, **2020**, 36, 364-372	7.2	20
19	Integration of multiple epigenomic marks improves prediction of variant impact in saturation mutagenesis reporter assay. *Human Mutation*, **2019**, 40, 1280-1291	4.7	19
18	DNaseI hypersensitivity at gene-poor, FSH dystrophy-linked 4q35.2. *Nucleic Acids Research*, **2009**, 37, 7381-93	20.1	12
17	Cas9 targeted enrichment of mobile elements using nanopore sequencing. *Nature Communications*, **2021**, 12, 3586	17.4	10

16	Cell Specificity of Human Regulatory Annotations and Their Genetic Effects on Gene Expression. *Genetics*, **2019**, 211, 549-562	4	9
15	Conserved and species-specific transcription factor co-binding patterns drive divergent gene regulation in human and mouse. *Nucleic Acids Research*, **2018**, 46, 1878-1894	20.1	8
14	Broad noncoding transcription suggests genome surveillance by RNA polymerase V. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 30799-30804	11.5	6
13	Poly-Enrich: count-based methods for gene set enrichment testing with genomic regions. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa006	3.7	5
12	High-resolution mapping studies of chromatin and gene regulatory elements. *Epigenomics*, **2009**, 1, 319-329	4.4	4
11	TRACE: transcription factor footprinting using chromatin accessibility data and DNA sequence. *Genome Research*, **2020**, 30, 1040-1046	9.7	3
10	Visualization of aligned genomic open reading frame data*. *Biochemistry and Molecular Biology Education*, **2003**, 31, 64-68	1.3	2
9	A proximity-based graph clustering method for the identification and application of transcription factor clusters. *BMC Bioinformatics*, **2017**, 18, 530	3.6	1
8	SquiggleNet: real-time, direct classification of nanopore signals. *Genome Biology*, **2021**, 22, 298	18.3	1
7	SEMplMe: A tool for integrating DNA methylation effects in transcription factor binding affinity predictions		1
6	MapGL: Inferring evolutionary gain and loss of short genomic sequence features by phylogenetic maximum parsimony		1
5	Real-Time, Direct Classification of Nanopore Signals with SquiggleNet		1
4	MapGL: inferring evolutionary gain and loss of short genomic sequence features by phylogenetic maximum parsimony. *BMC Bioinformatics*, **2020**, 21, 416	3.6	0
3	F-Seq2: improving the feature density based peak caller with dynamic statistics. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab012	3.7	0
2	Comprehensive enhancer-target gene assignments improve gene set level interpretation of genome-wide regulatory data.. *Genome Biology*, **2022**, 23, 105	18.3	0
1	The Inducible Operator-Repressor System Is Functional in Zebrafish Cells. *Frontiers in Genetics*, **2021**, 12, 683394	4.5	